

(19) World Intellectual Property Organization  
International Bureau(43) International Publication Date  
20 September 2001 (20.09.2001)

PCT

(10) International Publication Number  
WO 01/68848 A2

- (51) International Patent Classification<sup>7</sup>: C12N 15/12, 15/62, C07K 14/47, 14/705, 16/18, G01N 33/53, C12Q 1/68 60/000,000 15 September 2000 (15.09.2000) US PCT/US00/30952 8 November 2000 (08.11.2000) US PCT/US00/32678 1 December 2000 (01.12.2000) US PCT/US00/34956 20 December 2000 (20.12.2000) US
- (21) International Application Number: PCT/US01/06520
- (22) International Filing Date: 28 February 2001 (28.02.2001)
- (25) Filing Language: English
- (26) Publication Language: English
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- (30) Priority Data:
- |                |                             |    |
|----------------|-----------------------------|----|
| PCT/US00/05601 | 1 March 2000 (01.03.2000)   | US |
| PCT/US00/05841 | 2 March 2000 (02.03.2000)   | US |
| 60/187,202     | 3 March 2000 (03.03.2000)   | US |
| 60/186,968     | 6 March 2000 (06.03.2000)   | US |
| 60/189,328     | 14 March 2000 (14.03.2000)  | US |
| 60/189,320     | 14 March 2000 (14.03.2000)  | US |
| PCT/US00/06884 | 15 March 2000 (15.03.2000)  | US |
| 60/191,048     | 21 March 2000 (21.03.2000)  | US |
| 60/190,828     | 21 March 2000 (21.03.2000)  | US |
| 60/191,314     | 21 March 2000 (21.03.2000)  | US |
| 60/191,007     | 21 March 2000 (21.03.2000)  | US |
| 60/192,655     | 28 March 2000 (28.03.2000)  | US |
| 60/193,032     | 29 March 2000 (29.03.2000)  | US |
| 60/193,053     | 29 March 2000 (29.03.2000)  | US |
| PCT/US00/08439 | 30 March 2000 (30.03.2000)  | US |
| 60/194,647     | 4 April 2000 (04.04.2000)   | US |
| 60/194,449     | 4 April 2000 (04.04.2000)   | US |
| 60/196,820     | 11 April 2000 (11.04.2000)  | US |
| 60/195,975     | 11 April 2000 (11.04.2000)  | US |
| 60/196,000     | 11 April 2000 (11.04.2000)  | US |
| 60/196,187     | 11 April 2000 (11.04.2000)  | US |
| 60/196,690     | 11 April 2000 (11.04.2000)  | US |
| 60/198,121     | 18 April 2000 (18.04.2000)  | US |
| 60/198,585     | 18 April 2000 (18.04.2000)  | US |
| 60/199,654     | 25 April 2000 (25.04.2000)  | US |
| 60/199,397     | 25 April 2000 (25.04.2000)  | US |
| 60/199,550     | 25 April 2000 (25.04.2000)  | US |
| 60/201,516     | 3 May 2000 (03.05.2000)     | US |
| PCT/US00/13705 | 17 May 2000 (17.05.2000)    | US |
| PCT/US00/14042 | 22 May 2000 (22.05.2000)    | US |
| PCT/US00/14941 | 30 May 2000 (30.05.2000)    | US |
| PCT/US00/15264 | 2 June 2000 (02.06.2000)    | US |
| 60/209,832     | 5 June 2000 (05.06.2000)    | US |
| PCT/US00/20710 | 28 July 2000 (28.07.2000)   | US |
| 09/644,848     | 22 August 2000 (22.08.2000) | US |
| PCT/US00/23328 | 24 August 2000 (24.08.2000) | US |
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- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

WO 01/68848 A2

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**Published:**

— without international search report and to be republished  
upon receipt of that report

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

## SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

### FIELD OF THE INVENTION

5 The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

### BACKGROUND OF THE INVENTION

10 Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of  
15 action in the extracellular environment.

Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts  
20 are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.* 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

Membrane-bound proteins and receptors can play important roles in, among other things, the formation,  
25 differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins.  
30 Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and

nerve growth factor receptor.

Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

5 Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

#### SUMMARY OF THE INVENTION

10 In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94%



nucleic acid sequence identity, alternatively at least about 95 % nucleic acid sequence identity, alternatively at least about 96 % nucleic acid sequence identity, alternatively at least about 97 % nucleic acid sequence identity, alternatively at least about 98 % nucleic acid sequence identity and alternatively at least about 99 % nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80 % nucleic acid sequence identity, alternatively at least about 81 % nucleic acid sequence identity, alternatively at least about 82 % nucleic acid sequence identity, alternatively at least about 83 % nucleic acid sequence identity, alternatively at least about 84 % nucleic acid sequence identity, alternatively at least about 85 % nucleic acid sequence identity, alternatively at least about 86 % nucleic acid sequence identity, alternatively at least about 87 % nucleic acid sequence identity, alternatively at least about 88 % nucleic acid sequence identity, alternatively at least about 89 % nucleic acid sequence identity, alternatively at least about 90 % nucleic acid sequence identity, alternatively at least about 91 % nucleic acid sequence identity, alternatively at least about 92 % nucleic acid sequence identity, alternatively at least about 93 % nucleic acid sequence identity, alternatively at least about 94 % nucleic acid sequence identity, alternatively at least about 95 % nucleic acid sequence identity, alternatively at least about 96 % nucleic acid sequence identity, alternatively at least about 97 % nucleic acid sequence identity, alternatively at least about 98 % nucleic acid sequence identity and alternatively at least about 99 % nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either *transmembrane domain-deleted* or *transmembrane domain-inactivated*, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length,

alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83%

amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described

polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

In yet other embodiments, the invention provides oligonucleotide probes which may be useful for isolating genomic and cDNA nucleotide sequences, measuring or detecting expression of an associated gene or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences. Preferred probe lengths are described above.

In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO276 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA16435-1208".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figure 1.

Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO284 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA23318-1211".

Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

Figure 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO193 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA23322-1393".

Figure 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in Figure 5.

Figure 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO190 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA23334-1392".

Figure 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in Figure 7.

Figure 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO180 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA26843-1389".

Figure 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in Figure 9.

Figure 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO194 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA26844-1394".

Figure 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 11.

5 Figure 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO218 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA30867-1335".

Figure 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in Figure 13.

Figure 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO260 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA33470-1175".

10 Figure 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in Figure 15.

Figure 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO233 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA34436-1238".

15 Figure 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 17.

Figure 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO234 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA35557-1137".

Figure 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in Figure 19.

20 Figure 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO236 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA35599-1168".

Figure 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in Figure 21.

25 Figure 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO244 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA35668-1171".

Figure 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO262 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA36992-1168".

30 Figure 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO271 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA39423-1182".

35 Figure 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO268 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA39427-1179".

Figure 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in Figure 29.

Figure 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO270 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA39510-1181".

5 Figure 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in Figure 31.

Figure 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO355 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA39518-1247".

Figure 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figure 33.

10 Figure 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO298 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA39975-1210".

Figure 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in Figure 35.

15 Figure 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO299 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA39976-1215".

Figure 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO296 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA39979-1213".

20 Figure 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in Figure 39.

Figure 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO329 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA40594-1233".

25 Figure 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in Figure 41.

Figure 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO330 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA40603-1232".

Figure 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in Figure 43.

30 Figure 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO294 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA40604-1187".

Figure 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in Figure 45.

35 Figure 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO300 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA40625-1189".

Figure 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in Figure 47.

Figure 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO307 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA41225-1217".

Figure 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in Figure 49.

5 Figure 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO334 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA41379-1236".

Figure 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 51.

Figure 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO352 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA41386-1316".

10 Figure 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO710 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA44161-1434".

15 Figure 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in Figure 55.

Figure 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO873 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA44179-1362".

Figure 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in Figure 57.

20 Figure 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO354 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA44192-1246".

Figure 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in Figure 59.

25 Figure 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO1151 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA44694-1500".

Figure 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in Figure 61.

Figure 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO382 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA45234-1277".

30 Figure 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 63.

Figure 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO1864 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA45409-2511".

35 Figure 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in Figure 65.

Figure 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO386 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA45415-1318".

Figure 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in Figure 67.

Figure 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO541 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA45417-1432".

5 Figure 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in Figure 69.

Figure 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO852 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA45493-1349".

Figure 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in Figure 71.

10 Figure 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO700 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA46776-1284".

Figure 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 73.

15 Figures 75A-75B show a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO708 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA48296-1292".

Figure 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in Figures 75A-75B.

Figure 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO707 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA48306-1291".

20 Figure 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO864 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA48328-1355".

25 Figure 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in Figure 79.

Figure 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO706 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA48329-1290".

Figure 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in Figure 81.

30 Figure 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO732 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA48334-1435".

Figure 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 83.

35 Figure 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO537 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA49141-1431".

Figure 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in Figure 85.



Figure 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO545 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA49624-1279".

Figure 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in Figure 87.

5 Figure 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO718 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA49647-1398".

Figure 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 89.

Figure 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO872 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA49819-1439".

10 Figure 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in Figure 91.

Figure 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO704 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA50911-1288".

15 Figure 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in Figure 93.

Figure 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO705 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA50914-1289".

Figure 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figure 95.

20 Figure 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO871 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA50919-1361".

Figure 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in Figure 97.

25 Figure 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO702 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA50980-1286".

Figure 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in Figure 99.

Figure 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO944 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA52185-1370".

30 Figure 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 101.

Figure 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO739 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA52756".

35 Figure 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 103.

Figure 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO941 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA53906-1368".

Figure 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in Figure 105.

Figure 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO1082 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA53912-1457".

5 Figure 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in Figure 107.

Figure 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO1133 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA53913-1490".

Figure 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in Figure 109.

10 Figure 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO983 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA53977-1371".

Figure 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in Figure 111.

15 Figure 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO784 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA53978-1443".

Figure 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in Figure 113.

Figure 115 shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO783 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA53996-1442".

20 Figure 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115 shown in Figure 115.

Figure 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO940 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA54002-1367".

25 Figure 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in Figure 117.

Figure 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO768 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA55737-1345".

Figure 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in Figure 119.

30 Figure 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO1079 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA56050-1455".

Figure 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in Figure 121.

35 Figure 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO1078 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA56052-1454".

Figure 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in Figure 123.

Figure 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO1018 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA56107-1415".

Figure 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in Figure 125.

5 Figure 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO793 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA56110-1437".

Figure 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in Figure 127.

Figure 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO1773 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA56406-1704".

10 Figure 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in Figure 129.

Figure 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO1014 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA56409-1377".

15 Figure 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in Figure 131.

Figure 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO1013 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA56410-1414".

Figure 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in Figure 133.

20 Figure 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO937 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA56436-1448".

Figure 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in Figure 135.

25 Figure 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO1477 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA56529-1647".

Figure 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in Figure 137.

Figure 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO842 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA56855-1447".

30 Figure 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in Figure 139.

Figure 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO839 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA56859-1445".

35 Figure 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in Figure 141.

Figure 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO1180 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA56860-1510".

Figure 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in Figure 143.

Figure 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO1134 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA56865-1491".

5 Figure 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in Figure 145.

Figure 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO1115 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA56868-1478".

Figure 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in Figure 147.

10 Figure 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO1277 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA56869-1545".

Figure 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in Figure 149.

15 Figure 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO1135 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA56870-1492".

Figure 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in Figure 151.

Figure 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO827 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA57039-1402".

20 Figure 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in Figure 153.

Figure 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO1057 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA57253-1382".

25 Figure 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in Figure 155.

Figure 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO1113 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA57254-1477".

Figure 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in Figure 157.

30 Figure 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO1006 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA57699-1412".

Figure 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in Figure 159.

35 Figure 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO1074 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA57704-1452".

Figure 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in Figure 161.

Figure 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO1073 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA57710-1451".

Figure 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in Figure 163.

5 Figure 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO1136 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA57827-1493".

Figure 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in Figure 165.

Figure 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO1004 cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA57844-1410".

10 Figure 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in Figure 167.

Figure 169 shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO1344 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "DNA58723-1588".

15 Figure 170 shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in Figure 169.

Figure 171 shows a nucleotide sequence (SEQ ID NO:171) of a native sequence PRO1110 cDNA, wherein SEQ ID NO:171 is a clone designated herein as "DNA58727-1474".

Figure 172 shows the amino acid sequence (SEQ ID NO:172) derived from the coding sequence of SEQ ID NO:171 shown in Figure 171.

20 Figure 173 shows a nucleotide sequence (SEQ ID NO:173) of a native sequence PRO1378 cDNA, wherein SEQ ID NO:173 is a clone designated herein as "DNA58730-1607".

Figure 174 shows the amino acid sequence (SEQ ID NO:174) derived from the coding sequence of SEQ ID NO:173 shown in Figure 173.

25 Figure 175 shows a nucleotide sequence (SEQ ID NO:175) of a native sequence PRO1481 cDNA, wherein SEQ ID NO:175 is a clone designated herein as "DNA58732-1650".

Figure 176 shows the amino acid sequence (SEQ ID NO:176) derived from the coding sequence of SEQ ID NO:175 shown in Figure 175.

Figure 177 shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO1109 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "DNA58737-1473".

30 Figure 178 shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in Figure 177.

Figure 179 shows a nucleotide sequence (SEQ ID NO:179) of a native sequence PRO1383 cDNA, wherein SEQ ID NO:179 is a clone designated herein as "DNA58743-1609".

35 Figure 180 shows the amino acid sequence (SEQ ID NO:180) derived from the coding sequence of SEQ ID NO:179 shown in Figure 179.

Figure 181 shows a nucleotide sequence (SEQ ID NO:181) of a native sequence PRO1072 cDNA, wherein SEQ ID NO:181 is a clone designated herein as "DNA58747-1384".

Figure 182 shows the amino acid sequence (SEQ ID NO:182) derived from the coding sequence of SEQ ID NO:181 shown in Figure 181.

Figure 183 shows a nucleotide sequence (SEQ ID NO:183) of a native sequence PRO1189 cDNA, wherein SEQ ID NO:183 is a clone designated herein as "DNA58828-1519".

5     Figure 184 shows the amino acid sequence (SEQ ID NO:184) derived from the coding sequence of SEQ ID NO:183 shown in Figure 183.

Figure 185 shows a nucleotide sequence (SEQ ID NO:185) of a native sequence PRO1003 cDNA, wherein SEQ ID NO:185 is a clone designated herein as "DNA58846-1409".

Figure 186 shows the amino acid sequence (SEQ ID NO:186) derived from the coding sequence of SEQ ID NO:185 shown in Figure 185.

10     Figure 187 shows a nucleotide sequence (SEQ ID NO:187) of a native sequence PRO1108 cDNA, wherein SEQ ID NO:187 is a clone designated herein as "DNA58848-1472".

Figure 188 shows the amino acid sequence (SEQ ID NO:188) derived from the coding sequence of SEQ ID NO:187 shown in Figure 187.

15     Figure 189 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO1137 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "DNA58849-1494".

Figure 190 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in Figure 189.

Figure 191 shows a nucleotide sequence (SEQ ID NO:191) of a native sequence PRO1138 cDNA, wherein SEQ ID NO:191 is a clone designated herein as "DNA58850-1495".

20     Figure 192 shows the amino acid sequence (SEQ ID NO:192) derived from the coding sequence of SEQ ID NO:191 shown in Figure 191.

Figure 193 shows a nucleotide sequence (SEQ ID NO:193) of a native sequence PRO1415 cDNA, wherein SEQ ID NO:193 is a clone designated herein as "DNA58852-1637".

25     Figure 194 shows the amino acid sequence (SEQ ID NO:194) derived from the coding sequence of SEQ ID NO:193 shown in Figure 193.

Figure 195 shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO1054 cDNA, wherein SEQ ID NO:195 is a clone designated herein as "DNA58853-1423".

Figure 196 shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in Figure 195.

30     Figure 197 shows a nucleotide sequence (SEQ ID NO:197) of a native sequence PRO994 cDNA, wherein SEQ ID NO:197 is a clone designated herein as "DNA58855-1422".

Figure 198 shows the amino acid sequence (SEQ ID NO:198) derived from the coding sequence of SEQ ID NO:197 shown in Figure 197.

35     Figure 199 shows a nucleotide sequence (SEQ ID NO:199) of a native sequence PRO1069 cDNA, wherein SEQ ID NO:199 is a clone designated herein as "DNA59211-1450".

Figure 200 shows the amino acid sequence (SEQ ID NO:200) derived from the coding sequence of SEQ ID NO:199 shown in Figure 199.

Figure 201 shows a nucleotide sequence (SEQ ID NO:201) of a native sequence PRO1411 cDNA, wherein SEQ ID NO:201 is a clone designated herein as "DNA59212-1627".

Figure 202 shows the amino acid sequence (SEQ ID NO:202) derived from the coding sequence of SEQ ID NO:201 shown in Figure 201.

5 Figure 203 shows a nucleotide sequence (SEQ ID NO:203) of a native sequence PRO1129 cDNA, wherein SEQ ID NO:203 is a clone designated herein as "DNA59213-1487".

Figure 204 shows the amino acid sequence (SEQ ID NO:204) derived from the coding sequence of SEQ ID NO:203 shown in Figure 203.

Figure 205 shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO1359 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "DNA59219-1613".

10 Figure 206 shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in Figure 205.

Figure 207 shows a nucleotide sequence (SEQ ID NO:207) of a native sequence PRO1139 cDNA, wherein SEQ ID NO:207 is a clone designated herein as "DNA59497-1496".

15 Figure 208 shows the amino acid sequence (SEQ ID NO:208) derived from the coding sequence of SEQ ID NO:207 shown in Figure 207.

Figure 209 shows a nucleotide sequence (SEQ ID NO:209) of a native sequence PRO1065 cDNA, wherein SEQ ID NO:209 is a clone designated herein as "DNA59602-1436".

Figure 210 shows the amino acid sequence (SEQ ID NO:210) derived from the coding sequence of SEQ ID NO:209 shown in Figure 209.

20 Figure 211 shows a nucleotide sequence (SEQ ID NO:211) of a native sequence PRO1028 cDNA, wherein SEQ ID NO:211 is a clone designated herein as "DNA59603-1419".

Figure 212 shows the amino acid sequence (SEQ ID NO:212) derived from the coding sequence of SEQ ID NO:211 shown in Figure 211.

25 Figure 213 shows a nucleotide sequence (SEQ ID NO:213) of a native sequence PRO1027 cDNA, wherein SEQ ID NO:213 is a clone designated herein as "DNA59605-1418".

Figure 214 shows the amino acid sequence (SEQ ID NO:214) derived from the coding sequence of SEQ ID NO:213 shown in Figure 213.

Figure 215 shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO1140 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "DNA59607-1497".

30 Figure 216 shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in Figure 215.

Figure 217 shows a nucleotide sequence (SEQ ID NO:217) of a native sequence PRO1291 cDNA, wherein SEQ ID NO:217 is a clone designated herein as "DNA59610-1556".

35 Figure 218 shows the amino acid sequence (SEQ ID NO:218) derived from the coding sequence of SEQ ID NO:217 shown in Figure 217.

Figure 219 shows a nucleotide sequence (SEQ ID NO:219) of a native sequence PRO1105 cDNA, wherein SEQ ID NO:219 is a clone designated herein as "DNA59612-1466".

Figure 220 shows the amino acid sequence (SEQ ID NO:220) derived from the coding sequence of SEQ ID NO:219 shown in Figure 219.

Figure 221 shows a nucleotide sequence (SEQ ID NO:221) of a native sequence PRO1026 cDNA, wherein SEQ ID NO:221 is a clone designated herein as "DNA59613-1417".

5 Figure 222 shows the amino acid sequence (SEQ ID NO:222) derived from the coding sequence of SEQ ID NO:221 shown in Figure 221.

Figure 223 shows a nucleotide sequence (SEQ ID NO:223) of a native sequence PRO1104 cDNA, wherein SEQ ID NO:223 is a clone designated herein as "DNA59616-1465".

Figure 224 shows the amino acid sequence (SEQ ID NO:224) derived from the coding sequence of SEQ ID NO:223 shown in Figure 223.

10 Figure 225 shows a nucleotide sequence (SEQ ID NO:225) of a native sequence PRO1100 cDNA, wherein SEQ ID NO:225 is a clone designated herein as "DNA59619-1464".

Figure 226 shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225 shown in Figure 225.

15 Figure 227 shows a nucleotide sequence (SEQ ID NO:227) of a native sequence PRO1141 cDNA, wherein SEQ ID NO:227 is a clone designated herein as "DNA59625-1498".

Figure 228 shows the amino acid sequence (SEQ ID NO:228) derived from the coding sequence of SEQ ID NO:227 shown in Figure 227.

Figure 229 shows a nucleotide sequence (SEQ ID NO:229) of a native sequence PRO1772 cDNA, wherein SEQ ID NO:229 is a clone designated herein as "DNA59817-1703".

20 Figure 230 shows the amino acid sequence (SEQ ID NO:230) derived from the coding sequence of SEQ ID NO:229 shown in Figure 229.

Figure 231 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO1064 cDNA, wherein SEQ ID NO:231 is a clone designated herein as "DNA59827-1426".

25 Figure 232 shows the amino acid sequence (SEQ ID NO:232) derived from the coding sequence of SEQ ID NO:231 shown in Figure 231.

Figure 233 shows a nucleotide sequence (SEQ ID NO:233) of a native sequence PRO1379 cDNA, wherein SEQ ID NO:233 is a clone designated herein as "DNA59828-1608".

Figure 234 shows the amino acid sequence (SEQ ID NO:234) derived from the coding sequence of SEQ ID NO:233 shown in Figure 233.

30 Figure 235 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO3573 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "DNA59837-2545".

Figure 236 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in Figure 235.

35 Figure 237 shows a nucleotide sequence (SEQ ID NO:237) of a native sequence PRO3566 cDNA, wherein SEQ ID NO:237 is a clone designated herein as "DNA59844-2542".

Figure 238 shows the amino acid sequence (SEQ ID NO:238) derived from the coding sequence of SEQ ID NO:237 shown in Figure 237.



Figure 239 shows a nucleotide sequence (SEQ ID NO:239) of a native sequence PRO1156 cDNA, wherein SEQ ID NO:239 is a clone designated herein as "DNA59853-1505".

Figure 240 shows the amino acid sequence (SEQ ID NO:240) derived from the coding sequence of SEQ ID NO:239 shown in Figure 239.

5 Figure 241 shows a nucleotide sequence (SEQ ID NO:241) of a native sequence PRO1098 cDNA, wherein SEQ ID NO:241 is a clone designated herein as "DNA59854-1459".

Figure 242 shows the amino acid sequence (SEQ ID NO:242) derived from the coding sequence of SEQ ID NO:241 shown in Figure 241.

Figure 243 shows a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO1128 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "DNA59855-1485".

10 Figure 244 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in Figure 243.

Figure 245 shows a nucleotide sequence (SEQ ID NO:245) of a native sequence PRO1248 cDNA, wherein SEQ ID NO:245 is a clone designated herein as "DNA60278-1530".

15 Figure 246 shows the amino acid sequence (SEQ ID NO:246) derived from the coding sequence of SEQ ID NO:245 shown in Figure 245.

Figure 247 shows a nucleotide sequence (SEQ ID NO:247) of a native sequence PRO1127 cDNA, wherein SEQ ID NO:247 is a clone designated herein as "DNA60283-1484".

Figure 248 shows the amino acid sequence (SEQ ID NO:248) derived from the coding sequence of SEQ ID NO:247 shown in Figure 247.

20 Figure 249 shows a nucleotide sequence (SEQ ID NO:249) of a native sequence PRO1316 cDNA, wherein SEQ ID NO:249 is a clone designated herein as "DNA60608-1577".

Figure 250 shows the amino acid sequence (SEQ ID NO:250) derived from the coding sequence of SEQ ID NO:249 shown in Figure 249.

25 Figure 251 shows a nucleotide sequence (SEQ ID NO:251) of a native sequence PRO1197 cDNA, wherein SEQ ID NO:251 is a clone designated herein as "DNA60611-1524".

Figure 252 shows the amino acid sequence (SEQ ID NO:252) derived from the coding sequence of SEQ ID NO:251 shown in Figure 251.

Figure 253 shows a nucleotide sequence (SEQ ID NO:253) of a native sequence PRO1125 cDNA, wherein SEQ ID NO:253 is a clone designated herein as "DNA60619-1482".

30 Figure 254 shows the amino acid sequence (SEQ ID NO:254) derived from the coding sequence of SEQ ID NO:253 shown in Figure 253.

Figure 255 shows a nucleotide sequence (SEQ ID NO:255) of a native sequence PRO1158 cDNA, wherein SEQ ID NO:255 is a clone designated herein as "DNA60625-1507".

35 Figure 256 shows the amino acid sequence (SEQ ID NO:256) derived from the coding sequence of SEQ ID NO:255 shown in Figure 255.

Figure 257 shows a nucleotide sequence (SEQ ID NO:257) of a native sequence PRO1124 cDNA, wherein SEQ ID NO:257 is a clone designated herein as "DNA60629-1481".

Figure 258 shows the amino acid sequence (SEQ ID NO:258) derived from the coding sequence of SEQ ID NO:257 shown in Figure 257.

Figure 259 shows a nucleotide sequence (SEQ ID NO:259) of a native sequence PRO1380 cDNA, wherein SEQ ID NO:259 is a clone designated herein as "DNA60740-1615".

5 Figure 260 shows the amino acid sequence (SEQ ID NO:260) derived from the coding sequence of SEQ ID NO:259 shown in Figure 259.

Figure 261 shows a nucleotide sequence (SEQ ID NO:261) of a native sequence PRO1377 cDNA, wherein SEQ ID NO:261 is a clone designated herein as "DNA61608-1606".

Figure 262 shows the amino acid sequence (SEQ ID NO:262) derived from the coding sequence of SEQ ID NO:261 shown in Figure 261.

10 Figure 263 shows a nucleotide sequence (SEQ ID NO:263) of a native sequence PRO1287 cDNA, wherein SEQ ID NO:263 is a clone designated herein as "DNA61755-1554".

Figure 264 shows the amino acid sequence (SEQ ID NO:264) derived from the coding sequence of SEQ ID NO:263 shown in Figure 263.

15 Figure 265 shows a nucleotide sequence (SEQ ID NO:265) of a native sequence PRO1249 cDNA, wherein SEQ ID NO:265 is a clone designated herein as "DNA62809-1531".

Figure 266 shows the amino acid sequence (SEQ ID NO:266) derived from the coding sequence of SEQ ID NO:265 shown in Figure 265.

Figure 267 shows a nucleotide sequence (SEQ ID NO:267) of a native sequence PRO1335 cDNA, wherein SEQ ID NO:267 is a clone designated herein as "DNA62812-1594".

20 Figure 268 shows the amino acid sequence (SEQ ID NO:268) derived from the coding sequence of SEQ ID NO:267 shown in Figure 267.

Figure 269 shows a nucleotide sequence (SEQ ID NO:269) of a native sequence PRO3572 cDNA, wherein SEQ ID NO:269 is a clone designated herein as "DNA62813-2544".

25 Figure 270 shows the amino acid sequence (SEQ ID NO:270) derived from the coding sequence of SEQ ID NO:269 shown in Figure 269.

Figure 271 shows a nucleotide sequence (SEQ ID NO:271) of a native sequence PRO1599 cDNA, wherein SEQ ID NO:271 is a clone designated herein as "DNA62845-1684".

Figure 272 shows the amino acid sequence (SEQ ID NO:272) derived from the coding sequence of SEQ ID NO:271 shown in Figure 271.

30 Figure 273 shows a nucleotide sequence (SEQ ID NO:273) of a native sequence PRO1374 cDNA, wherein SEQ ID NO:273 is a clone designated herein as "DNA64849-1604".

Figure 274 shows the amino acid sequence (SEQ ID NO:274) derived from the coding sequence of SEQ ID NO:273 shown in Figure 273.

35 Figure 275 shows a nucleotide sequence (SEQ ID NO:275) of a native sequence PRO1345 cDNA, wherein SEQ ID NO:275 is a clone designated herein as "DNA64852-1589".

Figure 276 shows the amino acid sequence (SEQ ID NO:276) derived from the coding sequence of SEQ ID NO:275 shown in Figure 275.

Figure 277 shows a nucleotide sequence (SEQ ID NO:277) of a native sequence PRO1311 cDNA, wherein SEQ ID NO:277 is a clone designated herein as "DNA64863-1573".

Figure 278 shows the amino acid sequence (SEQ ID NO:278) derived from the coding sequence of SEQ ID NO:277 shown in Figure 277.

5 Figure 279 shows a nucleotide sequence (SEQ ID NO:279) of a native sequence PRO1357 cDNA, wherein SEQ ID NO:279 is a clone designated herein as "DNA64881-1602".

Figure 280 shows the amino acid sequence (SEQ ID NO:280) derived from the coding sequence of SEQ ID NO:279 shown in Figure 279.

Figure 281 shows a nucleotide sequence (SEQ ID NO:281) of a native sequence PRO1557 cDNA, wherein SEQ ID NO:281 is a clone designated herein as "DNA64902-1667".

10 Figure 282 shows the amino acid sequence (SEQ ID NO:282) derived from the coding sequence of SEQ ID NO:281 shown in Figure 281.

Figure 283 shows a nucleotide sequence (SEQ ID NO:283) of a native sequence PRO1305 cDNA, wherein SEQ ID NO:283 is a clone designated herein as "DNA64952-1568".

15 Figure 284 shows the amino acid sequence (SEQ ID NO:284) derived from the coding sequence of SEQ ID NO:283 shown in Figure 283.

Figure 285 shows a nucleotide sequence (SEQ ID NO:285) of a native sequence PRO1302 cDNA, wherein SEQ ID NO:285 is a clone designated herein as "DNA65403-1565".

Figure 286 shows the amino acid sequence (SEQ ID NO:286) derived from the coding sequence of SEQ ID NO:285 shown in Figure 285.

20 Figure 287 shows a nucleotide sequence (SEQ ID NO:287) of a native sequence PRO1266 cDNA, wherein SEQ ID NO:287 is a clone designated herein as "DNA65413-1534".

Figure 288 shows the amino acid sequence (SEQ ID NO:288) derived from the coding sequence of SEQ ID NO:287 shown in Figure 287.

25 Figures 289A-289B show a nucleotide sequence (SEQ ID NO:289) of a native sequence PRO1336 cDNA, wherein SEQ ID NO:289 is a clone designated herein as "DNA65423-1595".

Figure 290 shows the amino acid sequence (SEQ ID NO:290) derived from the coding sequence of SEQ ID NO:289 shown in Figures 289A-289B.

Figure 291 shows a nucleotide sequence (SEQ ID NO:291) of a native sequence PRO1278 cDNA, wherein SEQ ID NO:291 is a clone designated herein as "DNA66304-1546".

30 Figure 292 shows the amino acid sequence (SEQ ID NO:292) derived from the coding sequence of SEQ ID NO:291 shown in Figure 291.

Figure 293 shows a nucleotide sequence (SEQ ID NO:293) of a native sequence PRO1270 cDNA, wherein SEQ ID NO:293 is a clone designated herein as "DNA66308-1537".

35 Figure 294 shows the amino acid sequence (SEQ ID NO:294) derived from the coding sequence of SEQ ID NO:293 shown in Figure 293.

Figure 295 shows a nucleotide sequence (SEQ ID NO:295) of a native sequence PRO1298 cDNA, wherein SEQ ID NO:295 is a clone designated herein as "DNA66511-1563".

Figure 296 shows the amino acid sequence (SEQ ID NO:296) derived from the coding sequence of SEQ ID NO:295 shown in Figure 295.

Figure 297 shows a nucleotide sequence (SEQ ID NO:297) of a native sequence PRO1301 cDNA, wherein SEQ ID NO:297 is a clone designated herein as "DNA66512-1564".

5 Figure 298 shows the amino acid sequence (SEQ ID NO:298) derived from the coding sequence of SEQ ID NO:297 shown in Figure 297.

Figure 299 shows a nucleotide sequence (SEQ ID NO:299) of a native sequence PRO1268 cDNA, wherein SEQ ID NO:299 is a clone designated herein as "DNA66519-1535".

Figure 300 shows the amino acid sequence (SEQ ID NO:300) derived from the coding sequence of SEQ ID NO:299 shown in Figure 299.

10 Figure 301 shows a nucleotide sequence (SEQ ID NO:301) of a native sequence PRO1327 cDNA, wherein SEQ ID NO:301 is a clone designated herein as "DNA66521-1583".

Figure 302 shows the amino acid sequence (SEQ ID NO:302) derived from the coding sequence of SEQ ID NO:301 shown in Figure 301.

15 Figure 303 shows a nucleotide sequence (SEQ ID NO:303) of a native sequence PRO1328 cDNA, wherein SEQ ID NO:303 is a clone designated herein as "DNA66658-1584".

Figure 304 shows the amino acid sequence (SEQ ID NO:304) derived from the coding sequence of SEQ ID NO:303 shown in Figure 303.

Figure 305 shows a nucleotide sequence (SEQ ID NO:305) of a native sequence PRO1329 cDNA, wherein SEQ ID NO:305 is a clone designated herein as "DNA66660-1585".

20 Figure 306 shows the amino acid sequence (SEQ ID NO:306) derived from the coding sequence of SEQ ID NO:305 shown in Figure 305.

Figure 307 shows a nucleotide sequence (SEQ ID NO:307) of a native sequence PRO1339 cDNA, wherein SEQ ID NO:307 is a clone designated herein as "DNA66669-1597".

25 Figure 308 shows the amino acid sequence (SEQ ID NO:308) derived from the coding sequence of SEQ ID NO:307 shown in Figure 307.

Figure 309 shows a nucleotide sequence (SEQ ID NO:309) of a native sequence PRO1342 cDNA, wherein SEQ ID NO:309 is a clone designated herein as "DNA66674-1599".

Figure 310 shows the amino acid sequence (SEQ ID NO:310) derived from the coding sequence of SEQ ID NO:309 shown in Figure 309.

30 Figures 311A-311B show a nucleotide sequence (SEQ ID NO:311) of a native sequence PRO1487 cDNA, wherein SEQ ID NO:311 is a clone designated herein as "DNA68836-1656".

Figure 312 shows the amino acid sequence (SEQ ID NO:312) derived from the coding sequence of SEQ ID NO:311 shown in Figures 311A-311B.

35 Figure 313 shows a nucleotide sequence (SEQ ID NO:313) of a native sequence PRO3579 cDNA, wherein SEQ ID NO:313 is a clone designated herein as "DNA68862-2546".

Figure 314 shows the amino acid sequence (SEQ ID NO:314) derived from the coding sequence of SEQ ID NO:313 shown in Figure 313.

Figure 315 shows a nucleotide sequence (SEQ ID NO:315) of a native sequence PRO1472 cDNA, wherein SEQ ID NO:315 is a clone designated herein as "DNA68866-1644".

Figure 316 shows the amino acid sequence (SEQ ID NO:316) derived from the coding sequence of SEQ ID NO:315 shown in Figure 315.

5 Figure 317 shows a nucleotide sequence (SEQ ID NO:317) of a native sequence PRO1385 cDNA, wherein SEQ ID NO:317 is a clone designated herein as "DNA68869-1610".

Figure 318 shows the amino acid sequence (SEQ ID NO:318) derived from the coding sequence of SEQ ID NO:317 shown in Figure 317.

Figure 319 shows a nucleotide sequence (SEQ ID NO:319) of a native sequence PRO1461 cDNA, wherein SEQ ID NO:319 is a clone designated herein as "DNA68871-1638".

10 Figure 320 shows the amino acid sequence (SEQ ID NO:320) derived from the coding sequence of SEQ ID NO:319 shown in Figure 319.

Figure 321 shows a nucleotide sequence (SEQ ID NO:321) of a native sequence PRO1429 cDNA, wherein SEQ ID NO:321 is a clone designated herein as "DNA68879-1631".

15 Figure 322 shows the amino acid sequence (SEQ ID NO:322) derived from the coding sequence of SEQ ID NO:321 shown in Figure 321.

Figure 323 shows a nucleotide sequence (SEQ ID NO:323) of a native sequence PRO1568 cDNA, wherein SEQ ID NO:323 is a clone designated herein as "DNA68880-1676".

Figure 324 shows the amino acid sequence (SEQ ID NO:324) derived from the coding sequence of SEQ ID NO:323 shown in Figure 323.

20 Figure 325 shows a nucleotide sequence (SEQ ID NO:325) of a native sequence PRO1569 cDNA, wherein SEQ ID NO:325 is a clone designated herein as "DNA68882-1677".

Figure 326 shows the amino acid sequence (SEQ ID NO:326) derived from the coding sequence of SEQ ID NO:325 shown in Figure 325.

25 Figure 327 shows a nucleotide sequence (SEQ ID NO:327) of a native sequence PRO1753 cDNA, wherein SEQ ID NO:327 is a clone designated herein as "DNA68883-1691".

Figure 328 shows the amino acid sequence (SEQ ID NO:328) derived from the coding sequence of SEQ ID NO:327 shown in Figure 327.

Figure 329 shows a nucleotide sequence (SEQ ID NO:329) of a native sequence PRO1570 cDNA, wherein SEQ ID NO:329 is a clone designated herein as "DNA68885-1678".

30 Figure 330 shows the amino acid sequence (SEQ ID NO:330) derived from the coding sequence of SEQ ID NO:329 shown in Figure 329.

Figure 331 shows a nucleotide sequence (SEQ ID NO:331) of a native sequence PRO1559 cDNA, wherein SEQ ID NO:331 is a clone designated herein as "DNA68886".

35 Figure 332 shows the amino acid sequence (SEQ ID NO:332) derived from the coding sequence of SEQ ID NO:331 shown in Figure 331.

Figure 333 shows a nucleotide sequence (SEQ ID NO:333) of a native sequence PRO1486 cDNA, wherein SEQ ID NO:333 is a clone designated herein as "DNA71180-1655".

Figure 334 shows the amino acid sequence (SEQ ID NO:334) derived from the coding sequence of SEQ ID NO:333 shown in Figure 333.

Figure 335 shows a nucleotide sequence (SEQ ID NO:335) of a native sequence PRO1433 cDNA, wherein SEQ ID NO:335 is a clone designated herein as "DNA71184-1634".

5 Figure 336 shows the amino acid sequence (SEQ ID NO:336) derived from the coding sequence of SEQ ID NO:335 shown in Figure 335.

Figure 337 shows a nucleotide sequence (SEQ ID NO:337) of a native sequence PRO1490 cDNA, wherein SEQ ID NO:337 is a clone designated herein as "DNA71213-1659".

Figure 338 shows the amino acid sequence (SEQ ID NO:338) derived from the coding sequence of SEQ ID NO:337 shown in Figure 337.

10 Figure 339 shows a nucleotide sequence (SEQ ID NO:339) of a native sequence PRO1482 cDNA, wherein SEQ ID NO:339 is a clone designated herein as "DNA71234-1651".

Figure 340 shows the amino acid sequence (SEQ ID NO:340) derived from the coding sequence of SEQ ID NO:339 shown in Figure 339.

15 Figure 341 shows a nucleotide sequence (SEQ ID NO:341) of a native sequence PRO1409 cDNA, wherein SEQ ID NO:341 is a clone designated herein as "DNA71269-1621".

Figure 342 shows the amino acid sequence (SEQ ID NO:342) derived from the coding sequence of SEQ ID NO:341 shown in Figure 341.

Figure 343 shows a nucleotide sequence (SEQ ID NO:343) of a native sequence PRO1446 cDNA, wherein SEQ ID NO:343 is a clone designated herein as "DNA71277-1636".

20 Figure 344 shows the amino acid sequence (SEQ ID NO:344) derived from the coding sequence of SEQ ID NO:343 shown in Figure 343.

Figure 345 shows a nucleotide sequence (SEQ ID NO:345) of a native sequence PRO1604 cDNA, wherein SEQ ID NO:345 is a clone designated herein as "DNA71286-1687".

25 Figure 346 shows the amino acid sequence (SEQ ID NO:346) derived from the coding sequence of SEQ ID NO:345 shown in Figure 345.

Figure 347 shows a nucleotide sequence (SEQ ID NO:347) of a native sequence PRO1491 cDNA, wherein SEQ ID NO:347 is a clone designated herein as "DNA71883-1660".

Figure 348 shows the amino acid sequence (SEQ ID NO:348) derived from the coding sequence of SEQ ID NO:347 shown in Figure 347.

30 Figure 349 shows a nucleotide sequence (SEQ ID NO:349) of a native sequence PRO1431 cDNA, wherein SEQ ID NO:349 is a clone designated herein as "DNA73401-1633".

Figure 350 shows the amino acid sequence (SEQ ID NO:350) derived from the coding sequence of SEQ ID NO:349 shown in Figure 349.

35 Figures 351A-351B show a nucleotide sequence (SEQ ID NO:351) of a native sequence PRO1563 cDNA, wherein SEQ ID NO:351 is a clone designated herein as "DNA73492-1671".

Figure 352 shows the amino acid sequence (SEQ ID NO:352) derived from the coding sequence of SEQ ID NO:351 shown in Figures 351A-351B.

Figure 353 shows a nucleotide sequence (SEQ ID NO:353) of a native sequence PRO1571 cDNA, wherein SEQ ID NO:353 is a clone designated herein as "DNA73730-1679".

Figure 354 shows the amino acid sequence (SEQ ID NO:354) derived from the coding sequence of SEQ ID NO:353 shown in Figure 353.

5 Figure 355 shows a nucleotide sequence (SEQ ID NO:355) of a native sequence PRO1572 cDNA, wherein SEQ ID NO:355 is a clone designated herein as "DNA73734-1680".

Figure 356 shows the amino acid sequence (SEQ ID NO:356) derived from the coding sequence of SEQ ID NO:355 shown in Figure 355.

Figure 357 shows a nucleotide sequence (SEQ ID NO:357) of a native sequence PRO1573 cDNA, wherein SEQ ID NO:357 is a clone designated herein as "DNA73735-1681".

10 Figure 358 shows the amino acid sequence (SEQ ID NO:358) derived from the coding sequence of SEQ ID NO:357 shown in Figure 357.

Figure 359 shows a nucleotide sequence (SEQ ID NO:359) of a native sequence PRO1508 cDNA, wherein SEQ ID NO:359 is a clone designated herein as "DNA73742-1662".

15 Figure 360 shows the amino acid sequence (SEQ ID NO:360) derived from the coding sequence of SEQ ID NO:359 shown in Figure 359.

Figure 361 shows a nucleotide sequence (SEQ ID NO:361) of a native sequence PRO1485 cDNA, wherein SEQ ID NO:361 is a clone designated herein as "DNA73746-1654".

Figure 362 shows the amino acid sequence (SEQ ID NO:362) derived from the coding sequence of SEQ ID NO:361 shown in Figure 361.

20 Figure 363 shows a nucleotide sequence (SEQ ID NO:363) of a native sequence PRO1564 cDNA, wherein SEQ ID NO:363 is a clone designated herein as "DNA73760-1672".

Figure 364 shows the amino acid sequence (SEQ ID NO:364) derived from the coding sequence of SEQ ID NO:363 shown in Figure 363.

25 Figure 365 shows a nucleotide sequence (SEQ ID NO:365) of a native sequence PRO1550 cDNA, wherein SEQ ID NO:365 is a clone designated herein as "DNA76393-1664".

Figure 366 shows the amino acid sequence (SEQ ID NO:366) derived from the coding sequence of SEQ ID NO:365 shown in Figure 365.

Figure 367 shows a nucleotide sequence (SEQ ID NO:367) of a native sequence PRO1757 cDNA, wherein SEQ ID NO:367 is a clone designated herein as "DNA76398-1699".

30 Figure 368 shows the amino acid sequence (SEQ ID NO:368) derived from the coding sequence of SEQ ID NO:367 shown in Figure 367.

Figure 369 shows a nucleotide sequence (SEQ ID NO:369) of a native sequence PRO1758 cDNA, wherein SEQ ID NO:369 is a clone designated herein as "DNA76399-1700".

35 Figure 370 shows the amino acid sequence (SEQ ID NO:370) derived from the coding sequence of SEQ ID NO:369 shown in Figure 369.

Figure 371 shows a nucleotide sequence (SEQ ID NO:371) of a native sequence PRO1781 cDNA, wherein SEQ ID NO:371 is a clone designated herein as "DNA76522-2500".

Figure 372 shows the amino acid sequence (SEQ ID NO:372) derived from the coding sequence of SEQ ID NO:371 shown in Figure 371.

Figure 373 shows a nucleotide sequence (SEQ ID NO:373) of a native sequence PRO1606 cDNA, wherein SEQ ID NO:373 is a clone designated herein as "DNA76533-1689".

5     Figure 374 shows the amino acid sequence (SEQ ID NO:374) derived from the coding sequence of SEQ ID NO:373 shown in Figure 373.

Figure 375 shows a nucleotide sequence (SEQ ID NO:375) of a native sequence PRO1784 cDNA, wherein SEQ ID NO:375 is a clone designated herein as "DNA77303-2502".

Figure 376 shows the amino acid sequence (SEQ ID NO:376) derived from the coding sequence of SEQ ID NO:375 shown in Figure 375.

10     Figure 377 shows a nucleotide sequence (SEQ ID NO:377) of a native sequence PRO1774 cDNA, wherein SEQ ID NO:377 is a clone designated herein as "DNA77626-1705".

Figure 378 shows the amino acid sequence (SEQ ID NO:378) derived from the coding sequence of SEQ ID NO:377 shown in Figure 377.

15     Figure 379 shows a nucleotide sequence (SEQ ID NO:379) of a native sequence PRO1605 cDNA, wherein SEQ ID NO:379 is a clone designated herein as "DNA77648-1688".

Figure 380 shows the amino acid sequence (SEQ ID NO:380) derived from the coding sequence of SEQ ID NO:379 shown in Figure 379.

Figure 381 shows a nucleotide sequence (SEQ ID NO:381) of a native sequence PRO1928 cDNA, wherein SEQ ID NO:381 is a clone designated herein as "DNA81754-2532".

20     Figure 382 shows the amino acid sequence (SEQ ID NO:382) derived from the coding sequence of SEQ ID NO:381 shown in Figure 381.

Figure 383 shows a nucleotide sequence (SEQ ID NO:383) of a native sequence PRO1865 cDNA, wherein SEQ ID NO:383 is a clone designated herein as "DNA81757-2512".

25     Figure 384 shows the amino acid sequence (SEQ ID NO:384) derived from the coding sequence of SEQ ID NO:383 shown in Figure 383.

Figure 385 shows a nucleotide sequence (SEQ ID NO:385) of a native sequence PRO1925 cDNA, wherein SEQ ID NO:385 is a clone designated herein as "DNA82302-2529".

Figure 386 shows the amino acid sequence (SEQ ID NO:386) derived from the coding sequence of SEQ ID NO:385 shown in Figure 385.

30     Figure 387 shows a nucleotide sequence (SEQ ID NO:387) of a native sequence PRO1926 cDNA, wherein SEQ ID NO:387 is a clone designated herein as "DNA82340-2530".

Figure 388 shows the amino acid sequence (SEQ ID NO:388) derived from the coding sequence of SEQ ID NO:387 shown in Figure 387.

35     Figure 389 shows a nucleotide sequence (SEQ ID NO:389) of a native sequence PRO2630 cDNA, wherein SEQ ID NO:389 is a clone designated herein as "DNA83551".

Figure 390 shows the amino acid sequence (SEQ ID NO:390) derived from the coding sequence of SEQ ID NO:389 shown in Figure 389.



Figure 391 shows a nucleotide sequence (SEQ ID NO:391) of a native sequence PRO3443 cDNA, wherein SEQ ID NO:391 is a clone designated herein as "DNA87991-2540".

Figure 392 shows the amino acid sequence (SEQ ID NO:392) derived from the coding sequence of SEQ ID NO:391 shown in Figure 391.

5 Figure 393 shows a nucleotide sequence (SEQ ID NO:393) of a native sequence PRO3301 cDNA, wherein SEQ ID NO:393 is a clone designated herein as "DNA88002".

Figure 394 shows the amino acid sequence (SEQ ID NO:394) derived from the coding sequence of SEQ ID NO:393 shown in Figure 393.

Figure 395 shows a nucleotide sequence (SEQ ID NO:395) of a native sequence PRO3442 cDNA, wherein SEQ ID NO:395 is a clone designated herein as "DNA92238-2539".

10 Figure 396 shows the amino acid sequence (SEQ ID NO:396) derived from the coding sequence of SEQ ID NO:395 shown in Figure 395.

Figure 397 shows a nucleotide sequence (SEQ ID NO:397) of a native sequence PRO4978 cDNA, wherein SEQ ID NO:397 is a clone designated herein as "DNA95930".

15 Figure 398 shows the amino acid sequence (SEQ ID NO:398) derived from the coding sequence of SEQ ID NO:397 shown in Figure 397.

Figure 399 shows a nucleotide sequence (SEQ ID NO:399) of a native sequence PRO5801 cDNA, wherein SEQ ID NO:399 is a clone designated herein as "DNA115291-2681".

Figure 400 shows the amino acid sequence (SEQ ID NO:400) derived from the coding sequence of SEQ ID NO:399 shown in Figure 399.

20 Figure 401 shows a nucleotide sequence (SEQ ID NO:401) of a native sequence PRO19630 cDNA, wherein SEQ ID NO:401 is a clone designated herein as "DNA23336-2861".

Figure 402 shows the amino acid sequence (SEQ ID NO:402) derived from the coding sequence of SEQ ID NO:401 shown in Figure 401.

25 Figure 403 shows a nucleotide sequence (SEQ ID NO:403) of a native sequence PRO203 cDNA, wherein SEQ ID NO:403 is a clone designated herein as "DNA30862-1396".

Figure 404 shows the amino acid sequence (SEQ ID NO:404) derived from the coding sequence of SEQ ID NO:403 shown in Figure 403.

Figure 405 shows a nucleotide sequence (SEQ ID NO:405) of a native sequence PRO204 cDNA, wherein SEQ ID NO:405 is a clone designated herein as "DNA30871-1157".

30 Figure 406 shows the amino acid sequence (SEQ ID NO:406) derived from the coding sequence of SEQ ID NO:405 shown in Figure 405.

Figure 407 shows a nucleotide sequence (SEQ ID NO:407) of a native sequence PRO210 cDNA, wherein SEQ ID NO:407 is a clone designated herein as "DNA32279-1131".

35 Figure 408 shows the amino acid sequence (SEQ ID NO:408) derived from the coding sequence of SEQ ID NO:407 shown in Figure 407.

Figure 409 shows a nucleotide sequence (SEQ ID NO:409) of a native sequence PRO223 cDNA, wherein SEQ ID NO:409 is a clone designated herein as "DNA33206-1165".

Figure 410 shows the amino acid sequence (SEQ ID NO:410) derived from the coding sequence of SEQ ID NO:409 shown in Figure 409.

Figure 411 shows a nucleotide sequence (SEQ ID NO:411) of a native sequence PRO247 cDNA, wherein SEQ ID NO:411 is a clone designated herein as "DNA35673-1201".

5      Figure 412 shows the amino acid sequence (SEQ ID NO:412) derived from the coding sequence of SEQ ID NO:411 shown in Figure 411.

Figure 413 shows a nucleotide sequence (SEQ ID NO:413) of a native sequence PRO358 cDNA, wherein SEQ ID NO:413 is a clone designated herein as "DNA47361-1154-2".

Figure 414 shows the amino acid sequence (SEQ ID NO:414) derived from the coding sequence of SEQ ID NO:413 shown in Figure 413.

10      Figure 415 shows a nucleotide sequence (SEQ ID NO:415) of a native sequence PRO724 cDNA, wherein SEQ ID NO:415 is a clone designated herein as "DNA49631-1328".

Figure 416 shows the amino acid sequence (SEQ ID NO:416) derived from the coding sequence of SEQ ID NO:415 shown in Figure 415.

15      Figure 417 shows a nucleotide sequence (SEQ ID NO:417) of a native sequence PRO868 cDNA, wherein SEQ ID NO:417 is a clone designated herein as "DNA52594-1270".

Figure 418 shows the amino acid sequence (SEQ ID NO:418) derived from the coding sequence of SEQ ID NO:417 shown in Figure 417.

Figure 419 shows a nucleotide sequence (SEQ ID NO:419) of a native sequence PRO740 cDNA, wherein SEQ ID NO:419 is a clone designated herein as "DNA55800-1263".

20      Figure 420 shows the amino acid sequence (SEQ ID NO:420) derived from the coding sequence of SEQ ID NO:419 shown in Figure 419.

Figure 421 shows a nucleotide sequence (SEQ ID NO:421) of a native sequence PRO1478 cDNA, wherein SEQ ID NO:421 is a clone designated herein as "DNA56531-1648".

25      Figure 422 shows the amino acid sequence (SEQ ID NO:422) derived from the coding sequence of SEQ ID NO:421 shown in Figure 421.

Figure 423 shows a nucleotide sequence (SEQ ID NO:423) of a native sequence PRO162 cDNA, wherein SEQ ID NO:423 is a clone designated herein as "DNA56965-1356".

Figure 424 shows the amino acid sequence (SEQ ID NO:424) derived from the coding sequence of SEQ ID NO:423 shown in Figure 423.

30      Figure 425 shows a nucleotide sequence (SEQ ID NO:425) of a native sequence PRO828 cDNA, wherein SEQ ID NO:425 is a clone designated herein as "DNA57037-1444".

Figure 426 shows the amino acid sequence (SEQ ID NO:426) derived from the coding sequence of SEQ ID NO:425 shown in Figure 425.

35      Figure 427 shows a nucleotide sequence (SEQ ID NO:427) of a native sequence PRO819 cDNA, wherein SEQ ID NO:427 is a clone designated herein as "DNA57695-1340".

Figure 428 shows the amino acid sequence (SEQ ID NO:428) derived from the coding sequence of SEQ ID NO:427 shown in Figure 427.

Figure 429 shows a nucleotide sequence (SEQ ID NO:429) of a native sequence PRO813 cDNA, wherein SEQ ID NO:429 is a clone designated herein as "DNA57834-1339".

Figure 430 shows the amino acid sequence (SEQ ID NO:430) derived from the coding sequence of SEQ ID NO:429 shown in Figure 429.

5 Figure 431 shows a nucleotide sequence (SEQ ID NO:431) of a native sequence PRO1194 cDNA, wherein SEQ ID NO:431 is a clone designated herein as "DNA57841-1522".

Figure 432 shows the amino acid sequence (SEQ ID NO:432) derived from the coding sequence of SEQ ID NO:431 shown in Figure 431.

Figure 433 shows a nucleotide sequence (SEQ ID NO:433) of a native sequence PRO887 cDNA, wherein SEQ ID NO:433 is a clone designated herein as "DNA58130".

10 Figure 434 shows the amino acid sequence (SEQ ID NO:434) derived from the coding sequence of SEQ ID NO:433 shown in Figure 433.

Figure 435 shows a nucleotide sequence (SEQ ID NO:435) of a native sequence PRO1071 cDNA, wherein SEQ ID NO:435 is a clone designated herein as "DNA58847-1383".

15 Figure 436 shows the amino acid sequence (SEQ ID NO:436) derived from the coding sequence of SEQ ID NO:435 shown in Figure 435.

Figure 437 shows a nucleotide sequence (SEQ ID NO:437) of a native sequence PRO1029 cDNA, wherein SEQ ID NO:437 is a clone designated herein as "DNA59493-1420".

Figure 438 shows the amino acid sequence (SEQ ID NO:438) derived from the coding sequence of SEQ ID NO:437 shown in Figure 437.

20 Figure 439 shows a nucleotide sequence (SEQ ID NO:439) of a native sequence PRO1190 cDNA, wherein SEQ ID NO:439 is a clone designated herein as "DNA59586-1520".

Figure 440 shows the amino acid sequence (SEQ ID NO:440) derived from the coding sequence of SEQ ID NO:439 shown in Figure 439.

25 Figure 441 shows a nucleotide sequence (SEQ ID NO:441) of a native sequence PRO4334 cDNA, wherein SEQ ID NO:441 is a clone designated herein as "DNA59608-2577".

Figure 442 shows the amino acid sequence (SEQ ID NO:442) derived from the coding sequence of SEQ ID NO:441 shown in Figure 441.

Figure 443 shows a nucleotide sequence (SEQ ID NO:443) of a native sequence PRO1155 cDNA, wherein SEQ ID NO:443 is a clone designated herein as "DNA59849-1504".

30 Figure 444 shows the amino acid sequence (SEQ ID NO:444) derived from the coding sequence of SEQ ID NO:443 shown in Figure 443.

Figure 445 shows a nucleotide sequence (SEQ ID NO:445) of a native sequence PRO1157 cDNA, wherein SEQ ID NO:445 is a clone designated herein as "DNA60292-1506".

35 Figure 446 shows the amino acid sequence (SEQ ID NO:446) derived from the coding sequence of SEQ ID NO:445 shown in Figure 445.

Figure 447 shows a nucleotide sequence (SEQ ID NO:447) of a native sequence PRO1122 cDNA, wherein SEQ ID NO:447 is a clone designated herein as "DNA62377-1381-1".

Figure 448 shows the amino acid sequence (SEQ ID NO:448) derived from the coding sequence of SEQ ID NO:447 shown in Figure 447.

Figure 449 shows a nucleotide sequence (SEQ ID NO:449) of a native sequence PRO1183 cDNA, wherein SEQ ID NO:449 is a clone designated herein as "DNA62880-1513".

5     Figure 450 shows the amino acid sequence (SEQ ID NO:450) derived from the coding sequence of SEQ ID NO:449 shown in Figure 449.

Figure 451 shows a nucleotide sequence (SEQ ID NO:451) of a native sequence PRO1337 cDNA, wherein SEQ ID NO:451 is a clone designated herein as "DNA66672-1586".

Figure 452 shows the amino acid sequence (SEQ ID NO:452) derived from the coding sequence of SEQ ID NO:451 shown in Figure 451.

10     Figure 453 shows a nucleotide sequence (SEQ ID NO:453) of a native sequence PRO1480 cDNA, wherein SEQ ID NO:453 is a clone designated herein as "DNA67962-1649".

Figure 454 shows the amino acid sequence (SEQ ID NO:454) derived from the coding sequence of SEQ ID NO:453 shown in Figure 453.

15     Figure 455 shows a nucleotide sequence (SEQ ID NO:455) of a native sequence PRO19645 cDNA, wherein SEQ ID NO:455 is a clone designated herein as "DNA69555-2867".

Figure 456 shows the amino acid sequence (SEQ ID NO:456) derived from the coding sequence of SEQ ID NO:455 shown in Figure 455.

Figure 457 shows a nucleotide sequence (SEQ ID NO:457) of a native sequence PRO9782 cDNA, wherein SEQ ID NO:457 is a clone designated herein as "DNA71162-2764".

20     Figure 458 shows the amino acid sequence (SEQ ID NO:458) derived from the coding sequence of SEQ ID NO:457 shown in Figure 457.

Figure 459 shows a nucleotide sequence (SEQ ID NO:459) of a native sequence PRO1419 cDNA, wherein SEQ ID NO:459 is a clone designated herein as "DNA71290-1630".

25     Figure 460 shows the amino acid sequence (SEQ ID NO:460) derived from the coding sequence of SEQ ID NO:459 shown in Figure 459.

Figure 461 shows a nucleotide sequence (SEQ ID NO:461) of a native sequence PRO1575 cDNA, wherein SEQ ID NO:461 is a clone designated herein as "DNA76401-1683".

Figure 462 shows the amino acid sequence (SEQ ID NO:462) derived from the coding sequence of SEQ ID NO:461 shown in Figure 461.

30     Figure 463 shows a nucleotide sequence (SEQ ID NO:463) of a native sequence PRO1567 cDNA, wherein SEQ ID NO:463 is a clone designated herein as "DNA76541-1675".

Figure 464 shows the amino acid sequence (SEQ ID NO:464) derived from the coding sequence of SEQ ID NO:463 shown in Figure 463.

35     Figure 465 shows a nucleotide sequence (SEQ ID NO:465) of a native sequence PRO1891 cDNA, wherein SEQ ID NO:465 is a clone designated herein as "DNA76788-2526".

Figure 466 shows the amino acid sequence (SEQ ID NO:466) derived from the coding sequence of SEQ ID NO:465 shown in Figure 465.

Figure 467 shows a nucleotide sequence (SEQ ID NO:467) of a native sequence PRO1889 cDNA, wherein SEQ ID NO:467 is a clone designated herein as "DNA77623-2524".

Figure 468 shows the amino acid sequence (SEQ ID NO:468) derived from the coding sequence of SEQ ID NO:467 shown in Figure 467.

5 Figure 469 shows a nucleotide sequence (SEQ ID NO:469) of a native sequence PRO1785 cDNA, wherein SEQ ID NO:469 is a clone designated herein as "DNA80136-2503".

Figure 470 shows the amino acid sequence (SEQ ID NO:470) derived from the coding sequence of SEQ ID NO:469 shown in Figure 469.

Figure 471 shows a nucleotide sequence (SEQ ID NO:471) of a native sequence PRO6003 cDNA, wherein SEQ ID NO:471 is a clone designated herein as "DNA83568-2692".

10 Figure 472 shows the amino acid sequence (SEQ ID NO:472) derived from the coding sequence of SEQ ID NO:471 shown in Figure 471.

Figure 473 shows a nucleotide sequence (SEQ ID NO:473) of a native sequence PRO4333 cDNA, wherein SEQ ID NO:473 is a clone designated herein as "DNA84210-2576".

15 Figure 474 shows the amino acid sequence (SEQ ID NO:474) derived from the coding sequence of SEQ ID NO:473 shown in Figure 473.

Figure 475 shows a nucleotide sequence (SEQ ID NO:475) of a native sequence PRO4356 cDNA, wherein SEQ ID NO:475 is a clone designated herein as "DNA86576-2595".

Figure 476 shows the amino acid sequence (SEQ ID NO:476) derived from the coding sequence of SEQ ID NO:475 shown in Figure 475.

20 Figure 477 shows a nucleotide sequence (SEQ ID NO:477) of a native sequence PRO4352 cDNA, wherein SEQ ID NO:477 is a clone designated herein as "DNA87976-2593".

Figure 478 shows the amino acid sequence (SEQ ID NO:478) derived from the coding sequence of SEQ ID NO:477 shown in Figure 477.

25 Figure 479 shows a nucleotide sequence (SEQ ID NO:479) of a native sequence PRO4354 cDNA, wherein SEQ ID NO:479 is a clone designated herein as "DNA92256-2596".

Figure 480 shows the amino acid sequence (SEQ ID NO:480) derived from the coding sequence of SEQ ID NO:479 shown in Figure 479.

Figure 481 shows a nucleotide sequence (SEQ ID NO:481) of a native sequence PRO4369 cDNA, wherein SEQ ID NO:481 is a clone designated herein as "DNA92289-2598".

30 Figure 482 shows the amino acid sequence (SEQ ID NO:482) derived from the coding sequence of SEQ ID NO:481 shown in Figure 481.

Figure 483 shows a nucleotide sequence (SEQ ID NO:483) of a native sequence PRO6030 cDNA, wherein SEQ ID NO:483 is a clone designated herein as "DNA96850-2705".

35 Figure 484 shows the amino acid sequence (SEQ ID NO:484) derived from the coding sequence of SEQ ID NO:483 shown in Figure 483.

Figure 485 shows a nucleotide sequence (SEQ ID NO:485) of a native sequence PRO4433 cDNA, wherein SEQ ID NO:485 is a clone designated herein as "DNA96855-2629".

Figure 486 shows the amino acid sequence (SEQ ID NO:486) derived from the coding sequence of SEQ ID NO:485 shown in Figure 485.

Figure 487 shows a nucleotide sequence (SEQ ID NO:487) of a native sequence PRO4424 cDNA, wherein SEQ ID NO:487 is a clone designated herein as "DNA96857-2636".

5     Figure 488 shows the amino acid sequence (SEQ ID NO:488) derived from the coding sequence of SEQ ID NO:487 shown in Figure 487.

Figure 489 shows a nucleotide sequence (SEQ ID NO:489) of a native sequence PRO6017 cDNA, wherein SEQ ID NO:489 is a clone designated herein as "DNA96860-2700".

Figure 490 shows the amino acid sequence (SEQ ID NO:490) derived from the coding sequence of SEQ ID NO:489 shown in Figure 489.

10     Figure 491 shows a nucleotide sequence (SEQ ID NO:491) of a native sequence PRO19563 cDNA, wherein SEQ ID NO:491 is a clone designated herein as "DNA96861-2844".

Figure 492 shows the amino acid sequence (SEQ ID NO:492) derived from the coding sequence of SEQ ID NO:491 shown in Figure 491.

15     Figure 493 shows a nucleotide sequence (SEQ ID NO:493) of a native sequence PRO6015 cDNA, wherein SEQ ID NO:493 is a clone designated herein as "DNA96866-2698".

Figure 494 shows the amino acid sequence (SEQ ID NO:494) derived from the coding sequence of SEQ ID NO:493 shown in Figure 493.

Figure 495 shows a nucleotide sequence (SEQ ID NO:495) of a native sequence PRO5779 cDNA, wherein SEQ ID NO:495 is a clone designated herein as "DNA96870-2676".

20     Figure 496 shows the amino acid sequence (SEQ ID NO:496) derived from the coding sequence of SEQ ID NO:495 shown in Figure 495.

Figure 497 shows a nucleotide sequence (SEQ ID NO:497) of a native sequence PRO5776 cDNA, wherein SEQ ID NO:497 is a clone designated herein as "DNA96872-2674".

25     Figure 498 shows the amino acid sequence (SEQ ID NO:498) derived from the coding sequence of SEQ ID NO:497 shown in Figure 497.

Figure 499 shows a nucleotide sequence (SEQ ID NO:499) of a native sequence PRO4430 cDNA, wherein SEQ ID NO:499 is a clone designated herein as "DNA96878-2626".

Figure 500 shows the amino acid sequence (SEQ ID NO:500) derived from the coding sequence of SEQ ID NO:499 shown in Figure 499.

30     Figure 501 shows a nucleotide sequence (SEQ ID NO:501) of a native sequence PRO4421 cDNA, wherein SEQ ID NO:501 is a clone designated herein as "DNA96879-2619".

Figure 502 shows the amino acid sequence (SEQ ID NO:502) derived from the coding sequence of SEQ ID NO:501 shown in Figure 501.

35     Figure 503 shows a nucleotide sequence (SEQ ID NO:503) of a native sequence PRO4499 cDNA, wherein SEQ ID NO:503 is a clone designated herein as "DNA96889-2641".

Figure 504 shows the amino acid sequence (SEQ ID NO:504) derived from the coding sequence of SEQ ID NO:503 shown in Figure 503.

Figure 505 shows a nucleotide sequence (SEQ ID NO:505) of a native sequence PRO4423 cDNA, wherein SEQ ID NO:505 is a clone designated herein as "DNA96893-2621".

Figure 506 shows the amino acid sequence (SEQ ID NO:506) derived from the coding sequence of SEQ ID NO:505 shown in Figure 505.

5 Figure 507 shows a nucleotide sequence (SEQ ID NO:507) of a native sequence PRO5998 cDNA, wherein SEQ ID NO:507 is a clone designated herein as "DNA96897-2688".

Figure 508 shows the amino acid sequence (SEQ ID NO:508) derived from the coding sequence of SEQ ID NO:507 shown in Figure 507.

Figure 509 shows a nucleotide sequence (SEQ ID NO:509) of a native sequence PRO4501 cDNA, wherein SEQ ID NO:509 is a clone designated herein as "DNA98564-2643".

10 Figure 510 shows the amino acid sequence (SEQ ID NO:510) derived from the coding sequence of SEQ ID NO:509 shown in Figure 509.

Figure 511 shows a nucleotide sequence (SEQ ID NO:511) of a native sequence PRO6240 cDNA, wherein SEQ ID NO:511 is a clone designated herein as "DNA107443-2718".

15 Figure 512 shows the amino acid sequence (SEQ ID NO:512) derived from the coding sequence of SEQ ID NO:511 shown in Figure 511.

Figure 513 shows a nucleotide sequence (SEQ ID NO:513) of a native sequence PRO6245 cDNA, wherein SEQ ID NO:513 is a clone designated herein as "DNA107786-2723".

Figure 514 shows the amino acid sequence (SEQ ID NO:514) derived from the coding sequence of SEQ ID NO:513 shown in Figure 513.

20 Figure 515 shows a nucleotide sequence (SEQ ID NO:515) of a native sequence PRO6175 cDNA, wherein SEQ ID NO:515 is a clone designated herein as "DNA108682-2712".

Figure 516 shows the amino acid sequence (SEQ ID NO:516) derived from the coding sequence of SEQ ID NO:515 shown in Figure 515.

25 Figure 517 shows a nucleotide sequence (SEQ ID NO:517) of a native sequence PRO9742 cDNA, wherein SEQ ID NO:517 is a clone designated herein as "DNA108684-2761".

Figure 518 shows the amino acid sequence (SEQ ID NO:518) derived from the coding sequence of SEQ ID NO:517 shown in Figure 517.

Figure 519 shows a nucleotide sequence (SEQ ID NO:519) of a native sequence PRO7179 cDNA, wherein SEQ ID NO:519 is a clone designated herein as "DNA108701-2749".

30 Figure 520 shows the amino acid sequence (SEQ ID NO:520) derived from the coding sequence of SEQ ID NO:519 shown in Figure 519.

Figure 521 shows a nucleotide sequence (SEQ ID NO:521) of a native sequence PRO6239 cDNA, wherein SEQ ID NO:521 is a clone designated herein as "DNA108720-2717".

35 Figure 522 shows the amino acid sequence (SEQ ID NO:522) derived from the coding sequence of SEQ ID NO:521 shown in Figure 521.

Figure 523 shows a nucleotide sequence (SEQ ID NO:523) of a native sequence PRO6493 cDNA, wherein SEQ ID NO:523 is a clone designated herein as "DNA108726-2729".

Figure 524 shows the amino acid sequence (SEQ ID NO:524) derived from the coding sequence of SEQ ID NO:523 shown in Figure 523.

Figures 525A-525B show a nucleotide sequence (SEQ ID NO:525) of a native sequence PRO9741 cDNA, wherein SEQ ID NO:525 is a clone designated herein as "DNA108728-2760".

5 Figure 526 shows the amino acid sequence (SEQ ID NO:526) derived from the coding sequence of SEQ ID NO:525 shown in Figures 525A-525B.

Figure 527 shows a nucleotide sequence (SEQ ID NO:527) of a native sequence PRO9822 cDNA, wherein SEQ ID NO:527 is a clone designated herein as "DNA108738-2767".

Figure 528 shows the amino acid sequence (SEQ ID NO:528) derived from the coding sequence of SEQ ID NO:527 shown in Figure 527.

10 Figure 529 shows a nucleotide sequence (SEQ ID NO:529) of a native sequence PRO6244 cDNA, wherein SEQ ID NO:529 is a clone designated herein as "DNA108743-2722".

Figure 530 shows the amino acid sequence (SEQ ID NO:530) derived from the coding sequence of SEQ ID NO:529 shown in Figure 529.

15 Figure 531 shows a nucleotide sequence (SEQ ID NO:531) of a native sequence PRO9740 cDNA, wherein SEQ ID NO:531 is a clone designated herein as "DNA108758-2759".

Figure 532 shows the amino acid sequence (SEQ ID NO:532) derived from the coding sequence of SEQ ID NO:531 shown in Figure 531.

Figure 533 shows a nucleotide sequence (SEQ ID NO:533) of a native sequence PRO9739 cDNA, wherein SEQ ID NO:533 is a clone designated herein as "DNA108765-2758".

20 Figure 534 shows the amino acid sequence (SEQ ID NO:534) derived from the coding sequence of SEQ ID NO:533 shown in Figure 533.

Figure 535 shows a nucleotide sequence (SEQ ID NO:535) of a native sequence PRO7177 cDNA, wherein SEQ ID NO:535 is a clone designated herein as "DNA108783-2747".

25 Figure 536 shows the amino acid sequence (SEQ ID NO:536) derived from the coding sequence of SEQ ID NO:535 shown in Figure 535.

Figure 537 shows a nucleotide sequence (SEQ ID NO:537) of a native sequence PRO7178 cDNA, wherein SEQ ID NO:537 is a clone designated herein as "DNA108789-2748".

Figure 538 shows the amino acid sequence (SEQ ID NO:538) derived from the coding sequence of SEQ ID NO:537 shown in Figure 537.

30 Figure 539 shows a nucleotide sequence (SEQ ID NO:539) of a native sequence PRO6246 cDNA, wherein SEQ ID NO:539 is a clone designated herein as "DNA108806-2724".

Figure 540 shows the amino acid sequence (SEQ ID NO:540) derived from the coding sequence of SEQ ID NO:539 shown in Figure 539.

35 Figure 541 shows a nucleotide sequence (SEQ ID NO:541) of a native sequence PRO6241 cDNA, wherein SEQ ID NO:541 is a clone designated herein as "DNA108936-2719".

Figure 542 shows the amino acid sequence (SEQ ID NO:542) derived from the coding sequence of SEQ ID NO:541 shown in Figure 541.



Figure 543 shows a nucleotide sequence (SEQ ID NO:543) of a native sequence PRO9835 cDNA, wherein SEQ ID NO:543 is a clone designated herein as "DNA119510-2771".

Figure 544 shows the amino acid sequence (SEQ ID NO:544) derived from the coding sequence of SEQ ID NO:543 shown in Figure 543.

5 Figure 545 shows a nucleotide sequence (SEQ ID NO:545) of a native sequence PRO9857 cDNA, wherein SEQ ID NO:545 is a clone designated herein as "DNA119517-2778".

Figure 546 shows the amino acid sequence (SEQ ID NO:546) derived from the coding sequence of SEQ ID NO:545 shown in Figure 545.

Figure 547 shows a nucleotide sequence (SEQ ID NO:547) of a native sequence PRO7436 cDNA, wherein SEQ ID NO:547 is a clone designated herein as "DNA119535-2756".

10 Figure 548 shows the amino acid sequence (SEQ ID NO:548) derived from the coding sequence of SEQ ID NO:547 shown in Figure 547.

Figure 549 shows a nucleotide sequence (SEQ ID NO:549) of a native sequence PRO9856 cDNA, wherein SEQ ID NO:549 is a clone designated herein as "DNA119537-2777".

15 Figure 550 shows the amino acid sequence (SEQ ID NO:550) derived from the coding sequence of SEQ ID NO:549 shown in Figure 549.

Figure 551 shows a nucleotide sequence (SEQ ID NO:551) of a native sequence PRO19605 cDNA, wherein SEQ ID NO:551 is a clone designated herein as "DNA119714-2851".

Figure 552 shows the amino acid sequence (SEQ ID NO:552) derived from the coding sequence of SEQ ID NO:551 shown in Figure 551.

20 Figure 553 shows a nucleotide sequence (SEQ ID NO:553) of a native sequence PRO9859 cDNA, wherein SEQ ID NO:553 is a clone designated herein as "DNA125170-2780".

Figure 554 shows the amino acid sequence (SEQ ID NO:554) derived from the coding sequence of SEQ ID NO:553 shown in Figure 553.

25 Figure 555 shows a nucleotide sequence (SEQ ID NO:555) of a native sequence PRO12970 cDNA, wherein SEQ ID NO:555 is a clone designated herein as "DNA129594-2841".

Figure 556 shows the amino acid sequence (SEQ ID NO:556) derived from the coding sequence of SEQ ID NO:555 shown in Figure 555.

Figure 557 shows a nucleotide sequence (SEQ ID NO:557) of a native sequence PRO19626 cDNA, wherein SEQ ID NO:557 is a clone designated herein as "DNA129793-2857".

30 Figure 558 shows the amino acid sequence (SEQ ID NO:558) derived from the coding sequence of SEQ ID NO:557 shown in Figure 557.

Figure 559 shows a nucleotide sequence (SEQ ID NO:559) of a native sequence PRO9833 cDNA, wherein SEQ ID NO:559 is a clone designated herein as "DNA130809-2769".

35 Figure 560 shows the amino acid sequence (SEQ ID NO:560) derived from the coding sequence of SEQ ID NO:559 shown in Figure 559.

Figure 561 shows a nucleotide sequence (SEQ ID NO:561) of a native sequence PRO19670 cDNA, wherein SEQ ID NO:561 is a clone designated herein as "DNA131639-2874".

Figure 562 shows the amino acid sequence (SEQ ID NO:562) derived from the coding sequence of SEQ ID NO:561 shown in Figure 561.

Figure 563 shows a nucleotide sequence (SEQ ID NO:563) of a native sequence PRO19624 cDNA, wherein SEQ ID NO:563 is a clone designated herein as "DNA131649-2855".

5 Figure 564 shows the amino acid sequence (SEQ ID NO:564) derived from the coding sequence of SEQ ID NO:563 shown in Figure 563.

Figure 565 shows a nucleotide sequence (SEQ ID NO:565) of a native sequence PRO19680 cDNA, wherein SEQ ID NO:565 is a clone designated herein as "DNA131652-2876".

Figure 566 shows the amino acid sequence (SEQ ID NO:566) derived from the coding sequence of SEQ ID NO:565 shown in Figure 565.

10 Figure 567 shows a nucleotide sequence (SEQ ID NO:567) of a native sequence PRO19675 cDNA, wherein SEQ ID NO:567 is a clone designated herein as "DNA131658-2875".

Figure 568 shows the amino acid sequence (SEQ ID NO:568) derived from the coding sequence of SEQ ID NO:567 shown in Figure 567.

15 Figure 569 shows a nucleotide sequence (SEQ ID NO:569) of a native sequence PRO9834 cDNA, wherein SEQ ID NO:569 is a clone designated herein as "DNA132162-2770".

Figure 570 shows the amino acid sequence (SEQ ID NO:570) derived from the coding sequence of SEQ ID NO:569 shown in Figure 569.

Figure 571 shows a nucleotide sequence (SEQ ID NO:571) of a native sequence PRO9744 cDNA, wherein SEQ ID NO:571 is a clone designated herein as "DNA136110-2763".

20 Figure 572 shows the amino acid sequence (SEQ ID NO:572) derived from the coding sequence of SEQ ID NO:571 shown in Figure 571.

Figure 573 shows a nucleotide sequence (SEQ ID NO:573) of a native sequence PRO19644 cDNA, wherein SEQ ID NO:573 is a clone designated herein as "DNA139592-2866".

25 Figure 574 shows the amino acid sequence (SEQ ID NO:574) derived from the coding sequence of SEQ ID NO:573 shown in Figure 573.

Figure 575 shows a nucleotide sequence (SEQ ID NO:575) of a native sequence PRO19625 cDNA, wherein SEQ ID NO:575 is a clone designated herein as "DNA139608-2856".

Figure 576 shows the amino acid sequence (SEQ ID NO:576) derived from the coding sequence of SEQ ID NO:575 shown in Figure 575.

30 Figure 577 shows a nucleotide sequence (SEQ ID NO:577) of a native sequence PRO19597 cDNA, wherein SEQ ID NO:577 is a clone designated herein as "DNA143292-2848".

Figure 578 shows the amino acid sequence (SEQ ID NO:578) derived from the coding sequence of SEQ ID NO:577 shown in Figure 577.

35 Figure 579 shows a nucleotide sequence (SEQ ID NO:579) of a native sequence PRO16090 cDNA, wherein SEQ ID NO:579 is a clone designated herein as "DNA144844-2843".

Figure 580 shows the amino acid sequence (SEQ ID NO:580) derived from the coding sequence of SEQ ID NO:579 shown in Figure 579.

Figure 581 shows a nucleotide sequence (SEQ ID NO:581) of a native sequence PRO19576 cDNA, wherein SEQ ID NO:581 is a clone designated herein as "DNA144857-2845".

Figure 582 shows the amino acid sequence (SEQ ID NO:582) derived from the coding sequence of SEQ ID NO:581 shown in Figure 581.

5 Figure 583 shows a nucleotide sequence (SEQ ID NO:583) of a native sequence PRO19646 cDNA, wherein SEQ ID NO:583 is a clone designated herein as "DNA145841-2868".

Figure 584 shows the amino acid sequence (SEQ ID NO:584) derived from the coding sequence of SEQ ID NO:583 shown in Figure 583.

Figure 585 shows a nucleotide sequence (SEQ ID NO:585) of a native sequence PRO19814 cDNA, wherein SEQ ID NO:585 is a clone designated herein as "DNA148004-2882".

10 Figure 586 shows the amino acid sequence (SEQ ID NO:586) derived from the coding sequence of SEQ ID NO:585 shown in Figure 585.

Figure 587 shows a nucleotide sequence (SEQ ID NO:587) of a native sequence PRO19669 cDNA, wherein SEQ ID NO:587 is a clone designated herein as "DNA149893-2873".

15 Figure 588 shows the amino acid sequence (SEQ ID NO:588) derived from the coding sequence of SEQ ID NO:587 shown in Figure 587.

Figure 589 shows a nucleotide sequence (SEQ ID NO:589) of a native sequence PRO19818 cDNA, wherein SEQ ID NO:589 is a clone designated herein as "DNA149930-2884".

Figure 590 shows the amino acid sequence (SEQ ID NO:590) derived from the coding sequence of SEQ ID NO:589 shown in Figure 589.

20 Figure 591 shows a nucleotide sequence (SEQ ID NO:591) of a native sequence PRO20088 cDNA, wherein SEQ ID NO:591 is a clone designated herein as "DNA150157-2898".

Figure 592 shows the amino acid sequence (SEQ ID NO:592) derived from the coding sequence of SEQ ID NO:591 shown in Figure 591.

25 Figure 593 shows a nucleotide sequence (SEQ ID NO:593) of a native sequence PRO16089 cDNA, wherein SEQ ID NO:593 is a clone designated herein as "DNA150163-2842".

Figure 594 shows the amino acid sequence (SEQ ID NO:594) derived from the coding sequence of SEQ ID NO:593 shown in Figure 593.

Figure 595 shows a nucleotide sequence (SEQ ID NO:595) of a native sequence PRO20025 cDNA, wherein SEQ ID NO:595 is a clone designated herein as "DNA153579-2894".

30 Figure 596 shows the amino acid sequence (SEQ ID NO:596) derived from the coding sequence of SEQ ID NO:595 shown in Figure 595.

Figure 597 shows a nucleotide sequence (SEQ ID NO:597) of a native sequence PRO20040 cDNA, wherein SEQ ID NO:597 is a clone designated herein as "DNA164625-2890".

35 Figure 598 shows the amino acid sequence (SEQ ID NO:598) derived from the coding sequence of SEQ ID NO:597 shown in Figure 597.

Figure 599 shows a nucleotide sequence (SEQ ID NO:599) of a native sequence PRO791 cDNA, wherein SEQ ID NO:599 is a clone designated herein as "DNA57838-1337".

Figure 600 shows the amino acid sequence (SEQ ID NO:600) derived from the coding sequence of SEQ ID NO:599 shown in Figure 599.

Figure 601 shows a nucleotide sequence (SEQ ID NO:601) of a native sequence PRO1131 cDNA, wherein SEQ ID NO:601 is a clone designated herein as "DNA59777-1480".

5 Figure 602 shows the amino acid sequence (SEQ ID NO:602) derived from the coding sequence of SEQ ID NO:601 shown in Figure 601.

Figure 603 shows a nucleotide sequence (SEQ ID NO:603) of a native sequence PRO1343 cDNA, wherein SEQ ID NO:603 is a clone designated herein as "DNA66675-1587".

Figure 604 shows the amino acid sequence (SEQ ID NO:604) derived from the coding sequence of SEQ ID NO:603 shown in Figure 603.

10 Figure 605 shows a nucleotide sequence (SEQ ID NO:605) of a native sequence PRO1760 cDNA, wherein SEQ ID NO:605 is a clone designated herein as "DNA76532-1702".

Figure 606 shows the amino acid sequence (SEQ ID NO:606) derived from the coding sequence of SEQ ID NO:605 shown in Figure 605.

15 Figure 607 shows a nucleotide sequence (SEQ ID NO:607) of a native sequence PRO6029 cDNA, wherein SEQ ID NO:607 is a clone designated herein as "DNA105849-2704".

Figure 608 shows the amino acid sequence (SEQ ID NO:608) derived from the coding sequence of SEQ ID NO:607 shown in Figure 607.

Figure 609 shows a nucleotide sequence (SEQ ID NO:609) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:609 is a clone designated herein as "DNA83500-2506".

20 Figure 610 shows the amino acid sequence (SEQ ID NO:610) derived from the coding sequence of SEQ ID NO:609 shown in Figure 609.

## DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

### I. Definitions

25 The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein  
30 may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing,  
35 treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as

the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (*e.g.*, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (*e.g.*, Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO

polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through

Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X", "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the

National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

"PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.



Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent

different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions,

to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polyepitopic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially

homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1 % sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding

specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

5 "Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an  
10 antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically  
15 include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

20 "Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an  
25 acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

30 Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable  
35 carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine,

asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

5 "Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')<sub>2</sub>, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to  
10 crystallize readily. Pepsin treatment yields an F(ab')<sub>2</sub> fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-  
15 binding site on the surface of the V<sub>H</sub>-V<sub>L</sub> dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the  
20 carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')<sub>2</sub> antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one  
25 of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA,  
30 and IgA2.

"Single-chain Fv" or "sFv" antibody fragments comprise the V<sub>H</sub> and V<sub>L</sub> domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V<sub>H</sub> and V<sub>L</sub> domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113,  
35 Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) in the same

polypeptide chain ( $V_H$ - $V_L$ ). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

5 An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence  
10 by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

15 An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical  
20 alteration of a substrate compound or composition which is detectable.

By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay  
25 plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of  
30 biological membranes.

A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide disclosed herein or an agonist or antagonist thereof is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner, in relation to the stated purpose.  
35

Table 1

```

/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
5  * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define _M      -8      /* value of a match with a stop */

10 int  _day[26][26] = {
/*   A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */   { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */   { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */   { -2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
15 /* D */   { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */   { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */   { -4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */   { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */   { -1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
20 /* I */   { -1, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */   { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */   { -1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */   { -2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */   { -1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
25 /* N */   { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */   { _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, 0, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */   { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */   { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */   { -2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
30 /* S */   { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */   { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */   { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */   { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */   { -6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
35 /* X */   { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */   { -3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */   { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};

```



**Table 1 (cont')**

```

/*
*/
#include <stdio.h>
#include <ctype.h>

5
#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
10
#define MX          4      /* save if there's at least MX-1 bases since last jmp */

#define DMAT        3      /* value of matching bases */
#define DMIS        0      /* penalty for mismatched bases */
#define DINS0       8      /* penalty for a gap */
15
#define DINS1       1      /* penalty per base */
#define PINS0       8      /* penalty for a gap */
#define PINS1       4      /* penalty per residue */

struct jmp {
20
    short          n[MAXJMP]; /* size of jmp (neg for dely) */
    unsigned short x[MAXJMP]; /* base no. of jmp in seq x */
}; /* limits seq to 2^16 -1 */

struct diag {
25
    int            score;      /* score at last jmp */
    long           offset;     /* offset of prev block */
    short          ijmp;       /* current jmp index */
    struct jmp     jp;         /* list of jmps */
};

30
struct path {
    int            spc;        /* number of leading spaces */
    short          n[JMPS];    /* size of jmp (gap) */
    int            x[JMPS];    /* loc of jmp (last elem before gap) */
35
};

char            *ofile;      /* output file name */
char            *namex[2];   /* seq names: getseqs() */
char            *prog;       /* prog name for err msgs */
40
char            *seqx[2];     /* seqs: getseqs() */
int             dmax;         /* best diag: nw() */
int             dmax0;        /* final diag */
int             dna;          /* set if dna: main() */
int             endgaps;      /* set if penalizing end gaps */
45
int             gapx, gapy;    /* total gaps in seqs */
int             len0, len1;    /* seq lens */
int             ngapx, ngapy;  /* total size of gaps */
int             smax;         /* max score: nw() */
int             *xbm;         /* bitmap for matching */
50
long            offset;       /* current offset in jmp file */
struct          diag          /* holds diagonals */
struct          path          /* holds path for seqs */
pp[2];

char            *calloc(), *malloc(), *index(), *strcpy();
55
char            *getseq(), *g_calloc();

```

60

Table 1 (cont')

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
* where file1 and file2 are two dna or two protein sequences.
5  * The sequences can be in upper- or lower-case and may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
10 * Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
15 #include "nw.h"
#include "day.h"

static _dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
20 };

static _pbval[26] = {
    1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
25 1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
    1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)                                main
30     int      ac;
     char      *av[];
{
    prog = av[0];
    if (ac != 3) {
35         fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
40     }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
45     xbm = (dna)? _dbval : _pbval;

    endgaps = 0;                                /* 1 to penalize endgaps */
    ofile = "align.out";                        /* output file */

50     nw();                                /* fill in the matrix, get the possible jmps */
    readjmps();                                /* get the actual jmps */
    print();                                /* print stats, alignment */

55     cleanup(0);                            /* unlink any tmp files */
}

```

**Table 1 (cont')**

```

/* do the alignment, return best score: main()
* dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
* pro: PAM 250 values
* When scores are equal, we prefer mismatches to any gap, prefer
5  * a new gap to extending an ongoing gap, and prefer a gap in seqx
  * to a gap in seq y.
  */
nw()
{
10  char      *px, *py;      /* seqs and ptrs */
   int      *ndely, *dely;  /* keep track of dely */
   int      ndelx, delx;    /* keep track of delx */
   int      *tmp;          /* for swapping row0, row1 */
15  int      mis;           /* score for each type */
   int      ins0, ins1;     /* insertion penalties */
   register id;            /* diagonal index */
   register ij;            /* jmp index */
   register *col0, *col1;  /* score for curr, last row */
   register xx, yy;        /* index into seqs */

20  dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

   ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
   dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
25  col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
   col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
   ins0 = (dna)? DINS0 : PINS0;
   ins1 = (dna)? DINS1 : PINS1;

30  smax = -10000;
   if (endgaps) {
       for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
           col0[yy] = dely[yy] = col0[yy-1] - ins1;
           ndely[yy] = yy;
35       }
       col0[0] = 0;      /* Waterman Bull Math Biol 84 */
   }
   else
       for (yy = 1; yy <= len1; yy++)
40       dely[yy] = -ins0;

   /* fill in match matrix
   */
45  for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
       /* initialize first entry in col
       */
       if (endgaps) {
           if (xx == 1)
50               col1[0] = delx = -(ins0+ins1);
           else
               col1[0] = delx = col0[0] - ins1;
           ndelx = xx;
       }
       else {
55           col1[0] = 0;
           delx = -ins0;
           ndelx = 0;
       }
   }
60

```

**Table 1 (cont')****...nw**

```

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
    mis = col0[yy-1];
    if (dna)
        mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
    else
        mis += _day[*px-'A'][*py-'A'];

    /* update penalty for del in x seq;
     * favor new del over ongoing del
     * ignore MAXGAP if weighting endgaps
     */
    if (endgaps || ndely[yy] < MAXGAP) {
        if (col0[yy] - ins0 >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else {
            dely[yy] -= ins1;
            ndely[yy]++;
        }
    } else {
        if (col0[yy] - (ins0+ins1) >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else
            ndely[yy]++;
    }

    /* update penalty for del in y seq;
     * favor new del over ongoing del
     */
    if (endgaps || ndelx < MAXGAP) {
        if (col1[yy-1] - ins0 >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else {
            delx -= ins1;
            ndelx++;
        }
    } else {
        if (col1[yy-1] - (ins0+ins1) >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else
            ndelx++;
    }

    /* pick the maximum score; we're favoring
     * mis over any del and delx over dely
     */

```

**Table 1 (cont')**

...nw

```

5      id = xx - yy + len1 - 1;
      if (mis >= delx && mis >= dely[yy])
          col1[yy] = mis;
      else if (delx >= dely[yy]) {
10          col1[yy] = delx;
          ij = dx[id].ijmp;
          if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
&& xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
15              dx[id].ijmp++;
              if (++ij >= MAXJMP) {
                  writeimps(id);
                  ij = dx[id].ijmp = 0;
                  dx[id].offset = offset;
                  offset += sizeof(struct jmp) + sizeof(offset);
              }
              dx[id].jp.n[ij] = ndelx;
              dx[id].jp.x[ij] = xx;
              dx[id].score = delx;
          }
      }
      else {
25          col1[yy] = dely[yy];
          ij = dx[id].ijmp;
          if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
&& xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
30              dx[id].ijmp++;
              if (++ij >= MAXJMP) {
                  writeimps(id);
                  ij = dx[id].ijmp = 0;
                  dx[id].offset = offset;
                  offset += sizeof(struct jmp) + sizeof(offset);
              }
              dx[id].jp.n[ij] = -ndely[yy];
              dx[id].jp.x[ij] = xx;
              dx[id].score = dely[yy];
          }
      }
      if (xx == len0 && yy < len1) {
40          /* last col
          */
          if (endgaps)
              col1[yy] -= ins0+ins1*(len1-yy);
          if (col1[yy] > smax) {
45              smax = col1[yy];
              dmax = id;
          }
      }
  }
  if (endgaps && xx < len0)
      col1[yy-1] -= ins0+ins1*(len0-xx);
  if (col1[yy-1] > smax) {
50      smax = col1[yy-1];
      dmax = id;
  }
  tmp = col0; col0 = col1; col1 = tmp;
55
}
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
60 (void) free((char *)col1);

```

Table 1 (cont')

```

/*
 *
 * print() -- only routine visible outside this module
 *
5  * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
10  * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

15  #include "nw.h"

#define SPC      3
#define P_LINE  256 /* maximum output line */
#define P_SPC    3  /* space between name or num and seq */

20  extern _day[26][26];
int olen; /* set output line length */
FILE *fx; /* output file */

25  print() print
{
    int lx, ly, firstgap, lastgap; /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
30      fprintf(stderr, "%s: can't write %s\n", prog, ofile);
      cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
35    olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
40      pp[0].spc = firstgap = len1 - dmax - 1;
      ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
45      pp[1].spc = firstgap = dmax - (len1 - 1);
      lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
50      lastgap = len0 - dmax0 - 1;
      lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
      lastgap = dmax0 - (len0 - 1);
      ly -= lastgap;
55    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

60

```

Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
static
5  getmat(lx, ly, firstgap, lastgap)                                getmat
    int      lx, ly;                                /* "core" (minus endgaps) */
    int      firstgap, lastgap;                      /* leading trailing overlap */
{
    int      nm, i0, i1, siz0, siz1;
10   char      outx[32];
    double    pct;
    register  n0, n1;
    register char *p0, *p1;

15   /* get total matches, score
    */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
20   n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while ( *p0 && *p1 ) {
25         if (siz0) {
            p1++;
            n1++;
            siz0--;
        }
        else if (siz1) {
30             p0++;
            n0++;
            siz1--;
        }
        else {
35             if (xbm[*p0-'A']&xbm[*p1-'A'])
                nm++;
            if (n0++ == pp[0].x[i0])
                siz0 = pp[0].n[i0++];
40             if (n1++ == pp[1].x[i1])
                siz1 = pp[1].n[i1++];
            p0++;
            p1++;
        }
45     }

    /* pct homology:
    * if penalizing endgaps, base is the shorter seq
    * else, knock off overhangs and take shorter core
    */
50   if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
55   pct = 100.*(double)nm/(double)lx;
    fprintf(fx, "\n");
    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);
60

```

**Table 1 (cont')**

```

    fprintf(fx, "< gaps in first sequence: %d", gapx);
    if (gapx) {
        (void) sprintf(outx, " (%d %s%s)",
            ngapx, (dna)? "base":"residue", (ngapx == 1)? "":"s");
        fprintf(fx, "%s", outx);

    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, " (%d %s%s)",
            ngapy, (dna)? "base":"residue", (ngapy == 1)? "":"s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
            "\n< score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINSO, DINS1);
    else
        fprintf(fx,
            "\n< score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINSO, PINS1);
    if (endgaps)
        fprintf(fx,
            "< endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
            lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
    else
        fprintf(fx, "< endgaps not penalized\n");
}

static      nm;          /* matches in core -- for checking */
static      lmax;        /* lengths of stripped file names */
static      ij[2];       /* jmp index for a path */
static      nc[2];       /* number at start of current line */
static      ni[2];       /* current elem number -- for gapping */
static      siz[2];
static char *ps[2];      /* ptr to current element */
static char *po[2];      /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int      nn;          /* char count */
    int      more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(nameex[i]);
        if (nn > lmax)
            lmax = nn;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
}

```

...getmat

pr\_align



Table 1 (cont')

```

for (nn = nm = 0, more = 1; more;) {
    for (i = more = 0; i < 2; i++) {
        /*
5         * do we have more of this sequence?
        */
        if (!*ps[i])
            continue;

10         more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
15         }
        else if (siz[i]) { /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
20         }
        else { /* we're putting a seq element
            */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
25             po[i]++;
            ps[i]++;

            /*
30             * are we at next gap for this seq?
            */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
35                 * we need to merge all gaps
                 * at this location
                */
                siz[i] = pp[i].n[ij[i]++];
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i]++];
40             }
            ni[i]++;
        }
    }
    if (++nn == olen || !more && nn) {
45         dumpblock();
        for (i = 0; i < 2; i++)
            po[i] = out[i];
        nn = 0;
    }
50 }

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
55 static
dumpblock()
{
    register i;

60     for (i = 0; i < 2; i++)
        *po[i]-- = '\0';

```

...pr\_align

dumpblock

Table 1 (cont')

...dumpblock

```

5      (void) putc('\n', fx);
      for (i = 0; i < 2; i++) {
          if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
              if (i == 0)
                  nums(i);
              if (i == 0 && *out[1])
                  stars();
10             putline(i);
              if (i == 0 && *out[1])
                  fprintf(fx, star);
              if (i == 1)
                  nums(i);
15             }
          }
      }

/*
20  * put out a number line: dumpblock()
  */
  static
  nums(ix)
25  {
      int      ix;      /* index in out[] holding seq line */

      char      nline[P_LINE];
      register  i, j;
      register char *pn, *px, *py;

30      for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
          *pn = ' ';
      for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
          if (*py == ' ' || *py == '-')
              *pn = ' ';
35          else {
              if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                  j = (i < 0)? -i : i;
                  for (px = pn; j /= 10, px--)
                      *px = j%10 + '0';
40                  if (i < 0)
                      *px = '-';

                  }
              else
                  *pn = ' ';
45              i++;
          }
      }
      *pn = '\0';
      nc[ix] = i;
50      for (pn = nline; *pn; pn++)
          (void) putc(*pn, fx);
      (void) putc('\n', fx);
  }

55  /*
  * put out a line (name, [num], seq, [num]): dumpblock()
  */
  static
  putline(ix)
60      int      ix;      {

```

nums

putline

Table 1 (cont')

...putline

```

5      int          i;
      register char *px;

      for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
          (void) putc(*px, fx);
      for (; i < lmax+P_SPC; i++)
          (void) putc(' ', fx);

10     /* these count from 1:
       * ni[] is current element (from 1)
       * nc[] is number at start of current line
       */

15     for (px = out[ix]; *px; px++)
          (void) putc(*px&0x7F, fx);
      (void) putc('\n', fx);
  }

20  /*
   * put a line of stars (seqs always in out[0], out[1]): dumpblock()
   */
  static
25  stars()
  {
      int          i;
      register char *p0, *p1, cx, *px;

30     if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
        !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
          return;
      px = star;
      for (i = lmax+P_SPC; i; i--)
35         *px++ = ' ';

      for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
          if (isalpha(*p0) && isalpha(*p1)) {

40             if (xbm[*p0-'A']&xbm[*p1-'A']) {
                 cx = '*';
                 nm++;
             }
             else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
45                 cx = '.';
             else
                 cx = ' ';
          }
          else
50             cx = ' ';
          *px++ = cx;
      }
      *px++ = '\n';
      *px = '\0';
55  }

```

stars

**Table 1 (cont')**

```

/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
5 stripname(pn)                                stripname
    char    *pn;    /* file name (may be path) */
{
    register char    *px, *py;
10     py = 0;
    for (px = pn; *px; px++)
        if (*px == '/')
            py = px + 1;
15     if (py)
        (void) strcpy(pn, py);
    return(strlen(pn));
}
20
25
30
35
40
45
50
55
60

```

**Table 1 (cont')**

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
5  * readjumps() -- get the good jumps; from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>
10
char    *jname = "/tmp/homgXXXXXX";    /* tmp file for jumps */
FILE    *fj;

int      cleanup();                    /* cleanup tmp file */
15 long    lseek();

/*
 * remove any tmp file if we blow
 */
20 cleanup(i)                            cleanup
{
    int    i;
    if (fj)
        (void) unlink(jname);
25    exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
30 char    *
getseq(file, len)                            getseq
35     char    *file;    /* file name */
     int      *len;    /* seq len */
{
     char    line[1024], *pseq;
     register char    *px, *py;
     int      natgc, tlen;
     FILE    *fp;

     if ((fp = fopen(file, "r")) == 0) {
45         fprintf(stderr, "%s: can't read %s\n", prog, file);
         exit(1);
     }
     tlen = natgc = 0;
     while (fgets(line, 1024, fp)) {
50         if (*line == ';' || *line == '<' || *line == '>')
             continue;
         for (px = line; *px != '\n'; px++)
             if (isupper(*px) || islower(*px))
                 tlen++;
     }
55     if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
         fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
         exit(1);
     }
     pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
60

```

**Table 1 (cont')**

```

...getseq
py = pseq + 4;
*len = tlen;
rewind(fp);
5
while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
10        if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU", *(py-1)))
15            natgc++;
    }
    *py++ = '\0';
    *py = '\0';
    (void) fclose(fp);
    dna = natgc > (tlen/3);
    return(pseq+4);
}

25 char *
g_calloc(msg, nx, sz)
char *msg; /* program, calling routine */
int nx, sz; /* number and size of elements */
{
30     char *px, *calloc();

    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
35             fprintf(stderr, "%s: g_calloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
    return(px);
}

40 /*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjmps()
45 {
    int fd = -1;
    int siz, i0, i1;
    register i, j, xx;

50     if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
55         }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; i++) {
        while (1) {
60             for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)

```

**Table 1 (cont')****...readjumps**

```

5         if (j < 0 && dx[dmax].offset && fj) {
            (void) lseek(fd, dx[dmax].offset, 0);
            (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
            (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
            dx[dmax].ijmp = MAXJMP-1;
        }
        else
10             break;
    }
    if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
    }
15    if (j >= 0) {
        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
        if (siz < 0) { /* gap in second seq */
20             pp[1].n[i1] = -siz;
             xx += siz;
             /* id = xx - yy + len1 - 1
              */
             pp[1].x[i1] = xx - dmax + len1 - 1;
             gapy++;
             ngapy -= siz;
            /* ignore MAXGAP when doing endgaps */
             siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
             i1++;
30         }
        else if (siz > 0) { /* gap in first seq */
            pp[0].n[i0] = siz;
            pp[0].x[i0] = xx;
            gapx++;
            ngapx += siz;
35            /* ignore MAXGAP when doing endgaps */
             siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
             i0++;
        }
    }
40    else
        break;
}

45    /* reverse the order of jumps
    */
    for (j = 0, i0--; j < i0; j++, i0--) {
        i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
        i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
50    }
    for (j = 0, i1--; j < i1; j++, i1--) {
        i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
        i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
55    }
    if (fd >= 0)
        (void) close(fd);
    if (fj) {
        (void) unlink(jname);
        fj = 0;
        offset = 0;
60    }
}

```

**Table 1 (cont')**

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
5  writejumps(ix)                                writejumps
    int    ix;
    {
        char    *mktemp();
10         if (!fj) {
            if (mktemp(jname) < 0) {
                fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                cleanup(1);
            }
15         if ((fj = fopen(jname, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, jname);
            exit(1);
        }
20         (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
    }
}

25

30

35

40

45

50

55

60

```



**Table 2**

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYYY	(Length = 12 amino acids)

5    % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

10    5 divided by 15 = 33.3%

**Table 3**

PRO	XXXXXXXXXX	(Length = 10 amino acids)
15    Comparison Protein	XXXXXXXXYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

20    (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

**Table 4**

25

PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

30

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

6 divided by 14 = 42.9%

35

Table 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

5     % nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

10    4 divided by 12 = 33.3%

## II.           Compositions and Methods of the Invention

### A.       Full-Length PRO Polypeptides

15     The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

20     As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

### B.   PRO Polypeptide Variants

30     In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

35     Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative

mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by  
5 comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by  
10 systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO  
15 polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired  
20 fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading  
25 of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

	<u>Original Residue</u>	<u>Exemplary Substitutions</u>	<u>Preferred Substitutions</u>
5	Ala (A)	val; leu; ile	val
	Arg (R)	lys; gln; asn	lys
	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
	Cys (C)	ser	ser
10	Gln (Q)	asn	asn
	Glu (E)	asp	asp
	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
	Ile (I)	leu; val; met; ala; phe;	
15		norleucine	leu
	Leu (L)	norleucine; ile; val;	
		met; ala; phe	ile
	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
20	Phe (F)	leu; val; ile; ala; tyr	leu
	Pro (P)	ala	ala
	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
25	Tyr (Y)	trp; phe; thr; ser	phe
	Val (V)	ile; leu; met; phe;	
		ala; norleucine	leu

30 Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- 35 (1) hydrophobic: norleucine, met, ala, val, leu, ile;  
 (2) neutral hydrophilic: cys, ser, thr;  
 (3) acidic: asp, glu;  
 (4) basic: asn, gln, his, lys, arg;  
 (5) residues that influence chain orientation: gly, pro; and  
 40 (6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

45 The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al.,

Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

### C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the  $\alpha$ -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding

the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an  $\alpha$ -tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27,

1995.

#### D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., **85**:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

##### 1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like <sup>32</sup>P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and

processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

## 2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example,  $\text{CaCl}_2$ ,  $\text{CaPO}_4$ , liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA*; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC



55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan<sup>r</sup>*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan<sup>r</sup>*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

5 In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilum* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolyocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylophilic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylophilic, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

### 3. Selection and Use of a Replicable Vector

35 The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an

appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

5           The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces*  $\alpha$ -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as  
10           signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

15           Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the  $2\mu$  plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for  
20           cloning vectors in mammalian cells.

            Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

25           An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979);  
30           Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

            Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well  
35           known. Promoters suitable for use with prokaryotic hosts include the  $\beta$ -lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (trp) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid

promoters such as the tac promoter [deBoer et al., *Proc. Natl. Acad. Sci. USA*, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

5 Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., *J. Biol. Chem.*, 255:2073 (1980)] or other glycolytic enzymes [Hess et al., *J. Adv. Enzyme Reg.*, 7:149 (1968); Holland, *Biochemistry*, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

10 Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytchrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

15 PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

20 Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin,  $\alpha$ -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

30 Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

35 Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., *Nature*, 293:620-625 (1981); Mantei et al., *Nature*, 281:40-46 (1979); EP 117,060; and EP 117,058.

#### 4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

#### 5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

#### E. Uses for PRO

Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding

naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as  $^{32}\text{P}$  or  $^{35}\text{S}$ , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example,  $\text{CaPO}_4$ -mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an

antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

5           Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

10           Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

15           Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

20           The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

          Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

25           When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified.

30           Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules

35           contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional

gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane.

5 (Zamecnik *et al.*, Proc. Natl. Acad. Sci. USA 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau *et al.*, Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu *et al.*, J. Biol. Chem. 262, 4429-4432 (1987); and Wagner *et al.*, Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson *et al.*, Science 256, 808-813 (1992).

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The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

25 The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

30 The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

35 The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient



having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, PLURONICS™ or PEG.

10       The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

15       The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

20       Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In *Toxicokinetics and New Drug Development*, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

25       When *in vivo* administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 µg/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

30       Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon- (rhIFN-), interleukin-2, and MN rgp120. Johnson et al., *Nat. Med.*, 2:795-799 (1996); Yasuda, *Biomed. Ther.*, 27:1221-1223 (1993); Hora et al., *Bio/Technology*, 8:755-758 (1990); Cleland, "Design and Production of Single Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in *Vaccine Design: The Subunit*

and Adjuvant Approach, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

5 The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA; lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability  
of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis,  
"Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.),  
Biodegradable Polymers as Drug Delivery Systems (Marcel Dekker: New York, 1990), pp. 1-41.

10 This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides encoded by  
the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other  
cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical  
libraries, making them particularly suitable for identifying small molecule drug candidates.

15 The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

20 In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of  
the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific  
for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed  
25 by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected.  
When the originally non-immobilized component carries a detectable label, the detection of label immobilized on  
the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry  
30 a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by  
a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting  
protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-  
immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-  
protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers  
35 (Fields and Song, Nature (London), 340:245-246 (1989); Chien et al., Proc. Natl. Acad. Sci. USA, 88:9578-9582

(1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-*lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for  $\beta$ -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single

clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the PRO polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA.

Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, Current Biology, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

5 Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

10 These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

#### F. Anti-PRO Antibodies

15 The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

##### 1. Polyclonal Antibodies

20 The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such  
25 immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

##### 30 2. Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically  
35 bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or

lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding

sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5       The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

10       *In vitro* methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

### 3.       Human and Humanized Antibodies

15       The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a  
20       complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially  
25       all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*,  
30       2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers  
35       [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeven et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No.

4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10, 779-783 (1992); Lonberg *et al.*, *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

#### 4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., *EMBO J.*, 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least



one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

5 According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large  
10 amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')<sub>2</sub> bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical  
15 linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')<sub>2</sub> fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar  
20 amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')<sub>2</sub> molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to  
25 directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers.  
30 Kostelny *et al.*, J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for  
35 making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V<sub>H</sub>) connected to a light-chain variable domain (V<sub>L</sub>) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V<sub>H</sub> and V<sub>L</sub> domains of one fragment are forced to pair with the complementary

V<sub>L</sub> and V<sub>H</sub> domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, J. Immunol. 147:60 (1991).

5 Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic  
10 agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

#### 5. Heteroconjugate Antibodies

15 Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example,  
20 immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

#### 6. Effector Function Engineering

25 It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, J. Exp Med., 176:  
30 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.* Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, Anti-Cancer Drug Design,  
35 3: 219-230 (1989).

#### 7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent

such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include  $^{212}\text{Bi}$ ,  $^{131}\text{I}$ ,  $^{131}\text{In}$ ,  $^{90}\text{Y}$ , and  $^{186}\text{Re}$ .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, **238**: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is conjugated to a cytotoxic agent (*e.g.*, a radionucleotide).

#### 8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, **82**: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, **77**: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.*, J. Biol. Chem., **257**: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., **81**(19): 1484 (1989).

#### 9. Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified

by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, *e.g.*, Marasco *et al.*, Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, *supra*.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and  $\gamma$  ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT<sup>TM</sup> (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulphydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

#### G. Uses for anti-PRO Antibodies

The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, *e.g.*, detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as  $^3\text{H}$ ,  $^{14}\text{C}$ ,  $^{32}\text{P}$ ,  $^{35}\text{S}$ , or  $^{125}\text{I}$ , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such as Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

#### EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

##### EXAMPLE 1: Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (*e.g.*, Dayhoff, GenBank), and proprietary databases (*e.g.* LIFESEQ<sup>TM</sup>, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or

BLAST-2 (Altschul *et al.*, Methods in Enzymology, 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, WA).

5 Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel *et al.*, Current  
10 Protocols in Molecular Biology, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized  
20 appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; *see*, Holmes *et al.*, Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

#### EXAMPLE 2: Isolation of cDNA clones by Amylase Screening

##### 25 1. Preparation of oligo dT primed cDNA library

mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, CA (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the SalI/NotI linkered cDNA  
30 was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

##### 2. Preparation of random primed cDNA library

A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary  
35 cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was

sized to 500-1000 bp, linked with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

### 3. Transformation and Detection

DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37°C for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37°C). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, *e.g.* CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha, ura3-52, leu2-3, leu2-112, his3-11, his3-15, MAL<sup>+</sup>, SUC<sup>+</sup>, GAL<sup>+</sup>. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in *sec71*, *sec72*, *sec62*, with truncated *sec71* being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (*e.g.*, SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

Transformation was performed based on the protocol outlined by Gietz *et al.*, Nucl. Acid. Res., 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30°C. The YEPD broth was prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 207 (1994). The overnight culture was then diluted to about 2 x 10<sup>6</sup> cells/ml (approx. OD<sub>600</sub>=0.1) into fresh YEPD broth (500 ml) and regrown to 1 x 10<sup>7</sup> cells/ml (approx. OD<sub>600</sub>=0.4-0.5).

The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM Li<sub>2</sub>OOCCH<sub>3</sub>), and resuspended into LiAc/TE (2.5 ml).

Transformation took place by mixing the prepared cells (100 µl) with freshly denatured single stranded

salmon testes DNA (Lofstrand Labs, Gaithersburg, MD) and transforming DNA (1  $\mu$ g, vol. < 10  $\mu$ l) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600  $\mu$ l, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li<sub>2</sub>OOCCH<sub>3</sub>, pH 7.5) was added. This mixture was gently mixed and incubated at 30°C while agitating for 30 minutes. The cells were then heat shocked at 42°C for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500  $\mu$ l, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted into TE (1 ml) and aliquots (200  $\mu$ l) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 208-210 (1994). Transformants were grown at 30°C for 2-3 days.

The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely *et al.*, Anal. Biochem., 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

#### 4. Isolation of DNA by PCR Amplification

When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30  $\mu$ l) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5  $\mu$ l) was used as a template for the PCR reaction in a 25  $\mu$ l volume containing: 0.5  $\mu$ l KlenTaq (Clontech, Palo Alto, CA); 4.0  $\mu$ l 10 mM dNTP's (Perkin Elmer-Cetus); 2.5  $\mu$ l Kentaq buffer (Clontech); 0.25  $\mu$ l forward oligo 1; 0.25  $\mu$ l reverse oligo 2; 12.5  $\mu$ l distilled water. The sequence of the forward oligonucleotide 1 was:

5'-TGTAACGACGGCCAGTTAAATAGACCTGCAATTATTAATCT-3' (SEQ ID NO:611)

The sequence of reverse oligonucleotide 2 was:

5'-CAGGAAACAGCTATGACCACCTGCACACCTGCAAAATCCATT-3' (SEQ ID NO:612)

PCR was then performed as follows:

- |    |              |                  |
|----|--------------|------------------|
| a. | Denature     | 92°C, 5 minutes  |
| b. | 3 cycles of: |                  |
|    | Denature     | 92°C, 30 seconds |
|    | Anneal       | 59°C, 30 seconds |



		Extend	72°C, 60 seconds
5	c.	3 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	57°C, 30 seconds
		Extend	72°C, 60 seconds
	d.	25 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	55°C, 30 seconds
		Extend	72°C, 60 seconds
10	e.	Hold	4°C

The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

Following the PCR, an aliquot of the reaction (5 µl) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook *et al.*, *supra*. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, CA).

#### EXAMPLE 3: Isolation of cDNA Clones Using Signal Algorithm Analysis

Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, CA) upon ESTs as well as clustered and assembled EST fragments from public (*e.g.*, GenBank) and/or private (LIFESEQ®, Incyte Pharmaceuticals, Inc., Palo Alto, CA) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

#### EXAMPLE 4: Isolation of cDNA clones Encoding Human PRO Polypeptides

Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, USA (ATCC) as shown in Table 7 below.

Table 7

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA16435-1208	209930	June 2, 1998
	DNA23318-1211	209787	April 21, 1998
	DNA23322-1393	203400	October 27, 1998
5	DNA23334-1392	209918	June 2, 1998
	DNA26843-1389	203099	August 4, 1998
	DNA 26844-1394	209926	June 2, 1998
	DNA30867-1335	209807	April 28, 1998
	DNA33470-1175	209398	October 17, 1997
10	DNA34436-1238	209523	December 10, 1997
	DNA35557-1137	209255	September 16, 1997
	DNA35599-1168	209373	October 16, 1997
	DNA35668-1171	209371	October 16, 1997
	DNA36992-1168	209382	October 16, 1997
15	DNA39423-1182	209387	October 17, 1997
	DNA39427-1179	209395	October 17, 1997
	DNA39510-1181	209392	October 17, 1997
	DNA39518-1247	209529	December 10, 1997
	DNA39975-1210	209783	April 21, 1998
20	DNA39976-1215	209524	December 10, 1997
	DNA39979-1213	209789	April 21, 1998
	DNA40594-1233	209617	February 5, 1998
	DNA40603-1232	209486	November 21, 1997
	DNA40604-1187	209394	October 17, 1997
25	DNA40625-1189	209788	April 21, 1998
	DNA41225-1217	209491	November 21, 1997
	DNA41379-1236	209488	November 21, 1997
	DNA41386-1316	209703	March 26, 1998
	DNA44161-1434	209907	May 27, 1998
30	DNA44179-1362	209851	May 6, 1998
	DNA44192-1246	209531	December 10, 1997
	DNA44694-1500	203114	August 11, 1998
	DNA45234-1277	209654	March 5, 1998
	DNA45409-2511	203579	January 12, 1999
35	DNA45415-1318	209810	April 28, 1998
	DNA45417-1432	209910	May 27, 1998
	DNA45493-1349	209805	April 28, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA46776-1284	209721	March 31, 1998
	DNA48296-1292	209668	March 11, 1998
	DNA48306-1291	209911	May 27, 1998
5	DNA48328-1355	209843	May 6, 1998
	DNA48329-1290	209785	April 21, 1998
	DNA48334-1435	209924	June 2, 1998
	DNA49141-1431	203003	June 23, 1998
	DNA49624-1279	209655	March 5, 1998
10	DNA49647-1398	209919	June 2, 1998
	DNA49819-1439	209931	June 2, 1998
	DNA50911-1288	209714	March 31, 1998
	DNA50914-1289	209722	March 31, 1998
	DNA50919-1361	209848	May 6, 1998
15	DNA50980-1286	209717	March 31, 1998
	DNA52185-1370	209861	May 14, 1998
	DNA53906-1368	209747	April 7, 1998
	DNA53912-1457	209870	May 14, 1998
	DNA53913-1490	203162	August 25, 1998
20	DNA53977-1371	209862	May 14, 1998
	DNA53978-1443	209983	June 16, 1998
	DNA53996-1442	209921	June 2, 1998
	DNA54002-1367	209754	April 7, 1998
	DNA55737-1345	209753	April 7, 1998
25	DNA56050-1455	203011	June 23, 1998
	DNA56052-1454	203026	June 23, 1998
	DNA56107-1415	203405	October 27, 1998
	DNA56110-1437	203113	August 11, 1998
	DNA56406-1704	203478	November 17, 1998
30	DNA56409-1377	209882	May 20, 1998
	DNA56410-1414	209923	June 2, 1998
	DNA56436-1448	209902	May 27, 1998
	DNA56529-1647	203293	September 29, 1998
	DNA56855-1447	203004	June 23, 1998
35	DNA56859-1445	203019	June 23, 1998
	DNA56860-1510	209952	June 9, 1998
	DNA56865-1491	203022	June 23, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA56868-1478	203024	June 23, 1998
	DNA56869-1545	203161	August 25, 1998
	DNA56870-1492	209925	June 2, 1998
5	DNA57039-1402	209777	April 14, 1998
	DNA57253-1382	209867	May 14, 1998
	DNA57254-1477	203289	September 29, 1998
	DNA57699-1412	203020	June 23, 1998
	DNA57704-1452	209953	June 9, 1998
10	DNA57710-1451	203048	July 1, 1998
	DNA57827-1493	203045	July 1, 1998
	DNA57844-1410	203010	June 23, 1998
	DNA58723-1588	203133	August 18, 1998
	DNA58727-1474	203171	September 1, 1998
15	DNA58730-1607	203221	September 15, 1998
	DNA58732-1650	203290	September 29, 1998
	DNA58737-1473	203136	August 18, 1998
	DNA58743-1609	203154	August 25, 1998
	DNA58747-1384	209868	May 14, 1998
20	DNA58828-1519	203172	September 1, 1998
	DNA58846-1409	209957	June 9, 1998
	DNA58848-1472	209955	June 9, 1998
	DNA58849-1494	209958	June 9, 1998
	DNA58850-1495	209956	June 9, 1998
25	DNA58852-1637	203271	September 22, 1998
	DNA58853-1423	203016	June 23, 1998
	DNA58855-1422	203018	June 23, 1998
	DNA59211-1450	209960	June 9, 1998
	DNA59212-1627	203245	September 9, 1998
30	DNA59213-1487	209959	June 9, 1998
	DNA59219-1613	203220	September 15, 1998
	DNA59497-1496	209941	June 4, 1998
	DNA59602-1436	203051	July 1, 1998
	DNA59603-1419	209944	June 9, 1998
35	DNA59605-1418	203005	June 23, 1998
	DNA59607-1497	209946	June 9, 1998
	DNA59610-1556	209990	June 16, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA59612-1466	209947	June 9, 1998
	DNA59613-1417	203007	June 23, 1998
	DNA59616-1465	209991	June 16, 1998
5	DNA59619-1464	203041	July 1, 1998
	DNA59625-1498	209992	June 16, 1998
	DNA59817-1703	203470	November 17, 1998
	DNA59827-1426	203089	August 4, 1998
	DNA59828-1608	203158	August 25, 1998
10	DNA59837-2545	203658	February 9, 1999
	DNA59844-2542	203650	February 9, 1999
	DNA59853-1505	209985	June 16, 1998
	DNA59854-1459	209974	June 16, 1998
	DNA59855-1485	209987	June 16, 1998
15	DNA60278-1530	203170	September 1, 1998
	DNA60283-1484	203043	July 1, 1998
	DNA60608-1577	203126	August 18, 1998
	DNA60611-1524	203175	September 1, 1998
	DNA60619-1482	209993	June 16, 1998
20	DNA60625-1507	209975	June 16, 1998
	DNA60629-1481	209979	June 16, 1998
	DNA60740-1615	203456	November 3, 1998
	DNA61608-1606	203239	September 9, 1998
	DNA61755-1554	203112	August 11, 1998
25	DNA62809-1531	203237	September 9, 1998
	DNA62812-1594	203248	September 9, 1998
	DNA62813-2544	203655	February 9, 1999
	DNA62845-1684	203361	October 20, 1998
	DNA64849-1604	203468	November 17, 1998
30	DNA64852-1589	203127	August 18, 1998
	DNA64863-1573	203251	September 9, 1998
	DNA64881-1602	203240	September 9, 1998
	DNA64902-1667	203317	October 6, 1998
	DNA64952-1568	203222	September 15, 1998
35	DNA65403-1565	203230	September 15, 1998
	DNA65413-1534	203234	September 15, 1998
	DNA65423-1595	203227	September 15, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA66304-1546	203321	October 6, 1998
	DNA66308-1537	203159	August 25, 1998
	DNA66511-1563	203228	September 15, 1998
5	DNA66512-1564	203218	September 15, 1998
	DNA66519-1535	203236	September 15, 1998
	DNA66521-1583	203225	September 15, 1998
	DNA66658-1584	203229	September 15, 1998
	DNA66660-1585	203279	September 22, 1998
10	DNA66669-1597	203272	September 22, 1998
	DNA66674-1599	203281	September 22, 1998
	DNA68836-1656	203455	November 3, 1998
	DNA68862-2546	203652	February 9, 1999
	DNA68866-1644	203283	September 22, 1998
15	DNA68869-1610	203164	August 25, 1998
	DNA68871-1638	203280	September 22, 1998
	DNA68879-1631	203274	September 22, 1998
	DNA68880-1676	203319	October 6, 1998
	DNA68882-1677	203318	October 6, 1998
20	DNA68883-1691	203535	December 15, 1998
	DNA68885-1678	203311	October 6, 1998
	DNA71180-1655	203403	October 27, 1998
	DNA71184-1634	203266	September 22, 1998
	DNA71213-1659	203401	October 27, 1998
25	DNA71234-1651	203402	October 27, 1998
	DNA71269-1621	203284	September 22, 1998
	DNA71277-1636	203285	September 22, 1998
	DNA71286-1687	203357	October 20, 1998
	DNA71883-1660	203475	November 17, 1998
30	DNA73401-1633	203273	September 22, 1998
	DNA73492-1671	203324	October 6, 1998
	DNA73730-1679	203320	October 6, 1998
	DNA73734-1680	203363	October 20, 1998
	DNA73735-1681	203356	October 20, 1998
35	DNA73742-1662	203316	October 6, 1998
	DNA73746-1654	203411	October 27, 1998
	DNA73760-1672	203314	October 6, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA76393-1664	203323	October 6, 1998
	DNA76398-1699	203474	November 17, 1998
	DNA76399-1700	203472	November 17, 1998
5	DNA76522-2500	203469	November 17, 1998
	DNA76533-1689	203410	October 27, 1998
	DNA77303-2502	203479	November 17, 1998
	DNA77626-1705	203536	December 15, 1998
	DNA77648-1688	203408	October 27, 1998
10	DNA81754-2532	203542	December 15, 1998
	DNA81757-2512	203543	December 15, 1998
	DNA82302-2529	203534	December 15, 1998
	DNA82340-2530	203547	December 22, 1998
	DNA87991-2540	203656	February 9, 1999
15	DNA92238-2539	203602	January 20, 1999
	DNA115291-2681	PTA-202	June 8, 1999
	DNA23336-2861	PTA-1673	April 11, 2000
	DNA30862-1396	209920	June 2, 1998
	DNA30871-1157	209380	October 16, 1997
20	DNA32279-1131	209259	September 16, 1997
	DNA33206-1165	209372	October 16, 1997
	DNA35673-1201	209418	October 28, 1997
	DNA47361-1154-2	209431	November 7, 1997
	DNA49631-1328	209806	April 28, 1998
25	DNA52594-1270	209679	March 17, 1998
	DNA55800-1263	209680	March 17, 1998
	DNA56531-1648	203286	September 29, 1998
	DNA56965-1356	209842	May 6, 1998
	DNA57037-1444	209903	May 27, 1998
30	DNA57695-1340	203006	June 23, 1998
	DNA57834-1339	209954	June 9, 1998
	DNA57841-1522	203458	November 3, 1998
	DNA58847-1383	209879	May 20, 1998
	DNA59493-1420	203050	July 1, 1998
35	DNA59586-1520	203288	September 29, 1998
	DNA59608-2577	203870	March 23, 1999
	DNA59849-1504	209986	June 16, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA60292-1506	203540	December 15, 1998
	DNA62377-1381-1	203552	December 22, 1998
	DNA62880-1513	203097	August 4, 1998
5	DNA66672-1586	203265	September 22, 1998
	DNA67962-1649	203291	September 29, 1998
	DNA69555-2867	PTA-1632	April 4, 2000
	DNA71162-2764	PTA-860	October 19, 1999
	DNA71290-1630	203275	September 22, 1998
10	DNA76401-1683	203360	October 20, 1998
	DNA76541-1675	203409	October 27, 1998
	DNA76788-2526	203551	December 22, 1998
	DNA77623-2524	203546	December 22, 1998
	DNA80136-2503	203541	December 15, 1998
15	DNA83568-2692	PTA-386	July 20, 1999
	DNA84210-2576	203818	March 2, 1999
	DNA86576-2595	203868	March 23, 1999
	DNA87976-2593	203888	March 30, 1999
	DNA92256-2596	203891	March 30, 1999
20	DNA92289-2598	PTA-131	May 25, 1999
	DNA96850-2705	PTA-479	August 3, 1999
	DNA96855-2629	PTA-18	May 4, 1999
	DNA96857-2636	PTA-17	May 4, 1999
	DNA96860-2700	PTA-478	August 3, 1999
25	DNA96861-2844	PTA-1436	March 2, 2000
	DNA96866-2698	PTA-491	August 3, 1999
	DNA96870-2676	PTA-254	June 22, 1999
	DNA96872-2674	PTA-550	August 17, 1999
	DNA96878-2626	PTA-23	May 4, 1999
30	DNA96879-2619	203967	April 27, 1999
	DNA96889-2641	PTA-119	May 25, 1999
	DNA96893-2621	PTA-12	May 4, 1999
	DNA96897-2688	PTA-379	July 20, 1999
	DNA98564-2643	PTA-125	May 25, 1999
35	DNA107443-2718	PTA-490	August 3, 1999
	DNA107786-2723	PTA-474	August 3, 1999
	DNA108682-2712	PTA-486	August 3, 1999



Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA108684-2761	PTA-653	September 14, 1999
	DNA108701-2749	PTA-554	August 17, 1999
	DNA108720-2717	PTA-511	August 10, 1999
5	DNA108726-2729	PTA-514	August 10, 1999
	DNA108728-2760	PTA-654	September 14, 1999
	DNA108738-2767	PTA-862	October 19, 1999
	DNA108743-2722	PTA-508	August 10, 1999
	DNA108758-2759	PTA-655	September 14, 1999
10	DNA108765-2758	PTA-657	September 14, 1999
	DNA108783-2747	PTA-616	August 31, 1999
	DNA108789-2748	PTA-547	August 17, 1999
	DNA108806-2724	PTA-610	August 31, 1999
	DNA108936-2719	PTA-519	August 10, 1999
15	DNA119510-2771	PTA-947	November 9, 1999
	DNA119517-2778	PTA-951	November 16, 1999
	DNA119535-2756	PTA-613	August 31, 1999
	DNA119537-2777	PTA-956	November 16, 1999
	DNA119714-2851	PTA-1537	March 21, 2000
20	DNA125170-2780	PTA-953	November 16, 1999
	DNA129594-2841	PTA-1481	March 14, 2000
	DNA129793-2857	PTA-1733	April 18, 2000
	DNA130809-2769	PTA-949	November 9, 1999
	DNA131639-2874	PTA-1784	April 25, 2000
25	DNA131649-2855	PTA-1482	March 14, 2000
	DNA131652-2876	PTA-1628	April 4, 2000
	DNA131658-2875	PTA-1671	April 11, 2000
	DNA132162-2770	PTA-950	November 9, 1999
	DNA136110-2763	PTA-652	September 14, 1999
30	DNA139592-2866	PTA-1587	March 28, 2000
	DNA139608-2856	PTA-1581	March 28, 2000
	DNA143292-2848	PTA-1778	April 25, 2000
	DNA144844-2843	PTA-1536	March 21, 2000
	DNA144857-2845	PTA-1589	March 28, 2000
35	DNA145841-2868	PTA-1678	April 11, 2000
	DNA148004-2882	PTA-1779	April 25, 2000
	DNA149893-2873	PTA-1672	April 11, 2000

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA149930-2884	PTA-1668	April 11, 2000
	DNA150157-2898	PTA-1777	April 25, 2000
	DNA150163-2842	PTA-1533	March 21, 2000
5	DNA153579-2894	PTA-1729	April 18, 2000
	DNA164625-2890	PTA-1535	March 21, 2000
	DNA57838-1337	203014	June 23, 1998
	DNA59777-1480	203111	August 11, 1998
	DNA66675-1587	203282	September 22, 1998
10	DNA76532-1702	203473	November 17, 1998
	DNA105849-2704	PTA-473	August 3, 1999
	DNA83500-2506	203391	October 29, 1998

These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

#### 30 EXAMPLE 5: Use of PRO as a hybridization probe

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

35 Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH

6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

5     EXAMPLE 6: Expression of PRO in *E. coli*

This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

10     The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

15     The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

20     Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

25     After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

30     PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq)). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 0.71 g sodium citrate•2H<sub>2</sub>O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO<sub>4</sub>) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify

expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

*E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 7: Expression of PRO in mammalian cells

This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-

## PRO.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10  $\mu$ g pRK5-PRO DNA is mixed with about 1  $\mu$ g DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500  $\mu$ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M  $\text{CaCl}_2$ . To this mixture is added, dropwise, 500  $\mu$ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM  $\text{NaPO}_4$ , and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200  $\mu\text{Ci/ml}$   $^{35}\text{S}$ -cysteine and 200  $\mu\text{Ci/ml}$   $^{35}\text{S}$ -methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700  $\mu$ g pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5  $\mu\text{g/ml}$  bovine insulin and 0.1  $\mu\text{g/ml}$  bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as  $\text{CaPO}_4$  or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as  $^{35}\text{S}$ -methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be

concentrated and purified by any selected method, such as by  $\text{Ni}^{2+}$ -chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

5 Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

10 Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

15 Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect<sup>®</sup> (Qiagen), Dosper<sup>®</sup> or Fugene<sup>®</sup> (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately  $3 \times 10^7$  cells are frozen in an ampule for further growth and production as described below.

20 The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2  $\mu\text{m}$  filtered PS20 with 5% 0.2  $\mu\text{m}$  diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with  $3 \times 10^5$  cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at  $1.2 \times 10^6$  cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22  $\mu\text{m}$  filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

35 For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional

equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275  $\mu$ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 8: Expression of PRO in Yeast

The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### EXAMPLE 9: Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then

digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al.,  
5 Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by Ni<sup>2+</sup>-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl<sub>2</sub>; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated  
10 twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 μm filter. A Ni<sup>2+</sup>-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded  
15 onto the column at 0.5 mL per minute. The column is washed to baseline A<sub>280</sub> with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A<sub>280</sub> baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni<sup>2+</sup>-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His<sub>10</sub>-tagged PRO are pooled and dialyzed  
20 against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

#### 25 EXAMPLE 10: Preparation of Antibodies that Bind PRO

This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled  
30 artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected  
into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional  
35 immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.



After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

#### EXAMPLE 11: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

**EXAMPLE 12: Drug Screening**

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

**EXAMPLE 13: Rational Drug Design**

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO

polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

#### EXAMPLE 14: Identification of PRO Polypeptides That Stimulate TNF- $\alpha$ Release In Human Blood (Assay 128)

This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF- $\alpha$  in human blood. PRO polypeptides testing positive in this assay are useful for, among other things, research purposes where stimulation of the release of TNF- $\alpha$  would be desired and for the therapeutic treatment of conditions wherein enhanced TNF- $\alpha$  release would be beneficial. Specifically, 200  $\mu$ l of human blood supplemented with 50mM Hepes buffer (pH 7.2) is aliquoted per well in a 96 well test plate. To each well is then added 300 $\mu$ l of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37°C for 6 hours. The samples are then centrifuged and 50 $\mu$ l of plasma is collected from each well and tested for the presence of TNF- $\alpha$  by ELISA assay. A positive in the assay is a higher amount of TNF- $\alpha$  in the PRO polypeptide treated samples as compared to the negative control samples.

The following PRO polypeptides tested positive in this assay:

PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567, and PRO4333.

#### EXAMPLE 15: Promotion of Chondrocyte Redifferentiation (Assay 129)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage

disorders such as, for example, sports injuries and arthritis.

Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100 µl of the same media without serum and 100 µl of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200 µl/well. After 5 days at 37°C, 22 µl of media containing 100 µg/ml Hoechst 33342 and 50 µg/ml 5-CFDA is added to each well and incubated for an additional 10 minutes at 37°C. A picture of the green fluorescence is taken for each well and the differentiation state of the chondrocytes is calculated by morphometric analysis. A positive result in the assay is obtained when the >50% of the PRO polypeptide treated cells are differentiated (compared to the background obtained by the negative control).

PRO6029 polypeptide tested positive in this assay.

**EXAMPLE 16: Microarray Analysis to Detect Overexpression of PRO Polypeptides in Cancerous Tumors**

Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (disease tissue) sample is greater than hybridization signal of a probe from a control (normal tissue) sample, the gene or genes overexpressed in the disease tissue are identified. The implication of this result is that an overexpressed protein in a diseased tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on March 31, 2000 and which is herein incorporated by reference.

In the present example, cancerous tumors derived from various human tissues were studied for PRO polypeptide-encoding gene expression relative to non-cancerous human tissue in an attempt to identify those PRO polypeptides which are overexpressed in cancerous tumors. Two sets of experimental data were generated. In one set, cancerous human colon tumor tissue and matched non-cancerous human colon tumor tissue from the same patient ("matched colon control") were obtained and analyzed for PRO polypeptide expression using the above described microarray technology. In the second set of data, cancerous human tumor tissue from any of a variety of different human tumors was obtained and compared to a "universal" epithelial control sample which was

prepared by pooling non-cancerous human tissues of epithelial origin, including liver, kidney, and lung. mRNA isolated from the pooled tissues represents a mixture of expressed gene products from these different tissues. Microarray hybridization experiments using the pooled control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the pooled "universal control" sample not only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from the tumor tissues listed above were used for the hybridization thereto. A value based upon the normalized ratio:experimental ratio was designated as a "cutoff ratio". Only values that were above this cutoff ratio were determined to be significant. Table 8 below shows the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly overexpressed in various human tumor tissues as compared to a non-cancerous human tissue control. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more cancerous tumors, but also serve as therapeutic targets for the treatment of those tumors.

Table 8

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
20	PRO276	lung tumor	universal normal control
	PRO284	colon tumor	universal normal control
	PRO284	lung tumor	universal normal control
	PRO284	breast tumor	universal normal control
	PRO193	colon tumor	universal normal control
	PRO193	lung tumor	universal normal control
25	PRO193	breast tumor	universal normal control
	PRO193	prostate tumor	universal normal control
	PRO190	colon tumor	universal normal control
	PRO190	lung tumor	universal normal control
	PRO190	breast tumor	universal normal control
30	PRO180	colon tumor	universal normal control
	PRO180	lung tumor	universal normal control
	PRO180	breast tumor	universal normal control
	PRO194	colon tumor	universal normal control
	PRO194	lung tumor	universal normal control
35	PRO194	breast tumor	universal normal control
	PRO194	cervical tumor	universal normal control
	PRO218	colon tumor	universal normal control
	PRO218	lung tumor	universal normal control
	PRO260	colon tumor	universal normal control
40	PRO260	lung tumor	universal normal control
	PRO260	breast tumor	universal normal control
	PRO260	rectal tumor	universal normal control
	PRO233	colon tumor	universal normal control
	PRO233	lung tumor	universal normal control
45	PRO233	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO234	colon tumor	universal normal control
	PRO234	lung tumor	universal normal control
	PRO234	breast tumor	universal normal control
5	PRO234	liver tumor	universal normal control
	PRO236	colon tumor	universal normal control
	PRO236	lung tumor	universal normal control
	PRO236	breast tumor	universal normal control
	PRO244	colon tumor	universal normal control
10	PRO244	lung tumor	universal normal control
	PRO262	colon tumor	universal normal control
	PRO262	lung tumor	universal normal control
	PRO262	breast tumor	universal normal control
	PRO271	colon tumor	universal normal control
15	PRO271	lung tumor	universal normal control
	PRO268	colon tumor	universal normal control
	PRO268	lung tumor	universal normal control
	PRO268	breast tumor	universal normal control
	PRO270	colon tumor	universal normal control
20	PRO270	lung tumor	universal normal control
	PRO270	breast tumor	universal normal control
	PRO270	liver tumor	universal normal control
	PRO355	lung tumor	universal normal control
	PRO355	breast tumor	universal normal control
25	PRO355	prostate tumor	universal normal control
	PRO298	colon tumor	universal normal control
	PRO298	lung tumor	universal normal control
	PRO298	breast tumor	universal normal control
	PRO299	colon tumor	universal normal control
30	PRO299	lung tumor	universal normal control
	PRO299	breast tumor	universal normal control
	PRO296	colon tumor	universal normal control
	PRO296	breast tumor	universal normal control
	PRO329	colon tumor	universal normal control
35	PRO329	lung tumor	universal normal control
	PRO329	breast tumor	universal normal control
	PRO330	colon tumor	universal normal control
	PRO330	lung tumor	universal normal control
	PRO294	lung tumor	universal normal control
40	PRO294	breast tumor	universal normal control
	PRO300	colon tumor	universal normal control
	PRO300	lung tumor	universal normal control
	PRO300	breast tumor	universal normal control
	PRO307	lung tumor	universal normal control
45	PRO334	colon tumor	universal normal control
	PRO334	lung tumor	universal normal control
	PRO334	breast tumor	universal normal control
	PRO334	prostate tumor	universal normal control
	PRO352	colon tumor	universal normal control
50	PRO352	lung tumor	universal normal control
	PRO352	breast tumor	universal normal control
	PRO352	liver tumor	universal normal control
	PRO710	breast tumor	universal normal control
	PRO873	colon tumor	universal normal control
55	PRO873	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO873	breast tumor	universal normal control
	PRO873	prostate tumor	universal normal control
	PRO354	colon tumor	universal normal control
5	PRO354	lung tumor	universal normal control
	PRO354	breast tumor	universal normal control
	PRO1151	lung tumor	universal normal control
	PRO1151	breast tumor	universal normal control
10	PRO382	colon tumor	universal normal control
	PRO382	lung tumor	universal normal control
	PRO382	breast tumor	universal normal control
	PRO1864	lung tumor	universal normal control
	PRO1864	breast tumor	universal normal control
	PRO1864	liver tumor	universal normal control
15	PRO386	colon tumor	universal normal control
	PRO386	lung tumor	universal normal control
	PRO386	prostate tumor	universal normal control
	PRO541	colon tumor	universal normal control
	PRO541	lung tumor	universal normal control
20	PRO541	breast tumor	universal normal control
	PRO852	breast tumor	universal normal control
	PRO700	colon tumor	universal normal control
	PRO700	lung tumor	universal normal control
	PRO700	breast tumor	universal normal control
25	PRO700	rectal tumor	universal normal control
	PRO708	colon tumor	universal normal control
	PRO708	lung tumor	universal normal control
	PRO708	breast tumor	universal normal control
	PRO707	colon tumor	universal normal control
30	PRO707	lung tumor	universal normal control
	PRO864	colon tumor	universal normal control
	PRO864	lung tumor	universal normal control
	PRO864	breast tumor	universal normal control
	PRO706	colon tumor	universal normal control
35	PRO706	lung tumor	universal normal control
	PRO706	breast tumor	universal normal control
	PRO706	liver tumor	universal normal control
	PRO732	lung tumor	universal normal control
	PRO732	breast tumor	universal normal control
40	PRO732	cervical tumor	universal normal control
	PRO537	colon tumor	universal normal control
	PRO537	lung tumor	universal normal control
	PRO537	breast tumor	universal normal control
	PRO545	lung tumor	universal normal control
45	PRO545	breast tumor	universal normal control
	PRO718	lung tumor	universal normal control
	PRO718	breast tumor	universal normal control
	PRO872	lung tumor	universal normal control
	PRO872	breast tumor	universal normal control
50	PRO872	liver tumor	universal normal control
	PRO704	colon tumor	universal normal control
	PRO704	lung tumor	universal normal control
	PRO704	breast tumor	universal normal control
	PRO705	lung tumor	universal normal control
55	PRO705	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO871	lung tumor	universal normal control
	PRO871	breast tumor	universal normal control
	PRO871	liver tumor	universal normal control
5	PRO702	lung tumor	universal normal control
	PRO944	colon tumor	universal normal control
	PRO944	lung tumor	universal normal control
	PRO944	rectal tumor	universal normal control
	PRO739	lung tumor	universal normal control
10	PRO739	breast tumor	universal normal control
	PRO739	prostate tumor	universal normal control
	PRO941	colon tumor	universal normal control
	PRO941	lung tumor	universal normal control
	PRO941	breast tumor	universal normal control
15	PRO941	rectal tumor	universal normal control
	PRO1082	lung tumor	universal normal control
	PRO1082	breast tumor	universal normal control
	PRO1133	colon tumor	universal normal control
	PRO1133	lung tumor	universal normal control
20	PRO983	colon tumor	universal normal control
	PRO983	lung tumor	universal normal control
	PRO983	breast tumor	universal normal control
	PRO784	colon tumor	universal normal control
	PRO784	lung tumor	universal normal control
25	PRO784	breast tumor	universal normal control
	PRO784	prostate tumor	universal normal control
	PRO783	colon tumor	universal normal control
	PRO783	lung tumor	universal normal control
	PRO783	breast tumor	universal normal control
30	PRO783	liver tumor	universal normal control
	PRO940	colon tumor	universal normal control
	PRO940	lung tumor	universal normal control
	PRO940	breast tumor	universal normal control
	PRO768	colon tumor	universal normal control
35	PRO768	lung tumor	universal normal control
	PRO768	breast tumor	universal normal control
	PRO1079	colon tumor	universal normal control
	PRO1079	lung tumor	universal normal control
	PRO1079	breast tumor	universal normal control
40	PRO1079	rectal tumor	universal normal control
	PRO1078	colon tumor	universal normal control
	PRO1078	lung tumor	universal normal control
	PRO1018	colon tumor	universal normal control
	PRO1018	lung tumor	universal normal control
45	PRO1018	breast tumor	universal normal control
	PRO793	colon tumor	universal normal control
	PRO793	lung tumor	universal normal control
	PRO793	breast tumor	universal normal control
	PRO793	rectal tumor	universal normal control
50	PRO1773	colon tumor	universal normal control
	PRO1773	lung tumor	universal normal control
	PRO1773	prostate tumor	universal normal control
	PRO1014	lung tumor	universal normal control
	PRO1014	breast tumor	universal normal control
55	PRO1013	colon tumor	universal normal control



Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1013	lung tumor	universal normal control
	PRO1013	breast tumor	universal normal control
	PRO1013	liver tumor	universal normal control
5	PRO937	colon tumor	universal normal control
	PRO937	lung tumor	universal normal control
	PRO937	breast tumor	universal normal control
	PRO937	cervical tumor	universal normal control
	PRO937	rectal tumor	universal normal control
10	PRO1477	lung tumor	universal normal control
	PRO1477	breast tumor	universal normal control
	PRO1477	rectal tumor	universal normal control
	PRO842	colon tumor	universal normal control
	PRO842	lung tumor	universal normal control
15	PRO842	breast tumor	universal normal control
	PRO839	colon tumor	universal normal control
	PRO1180	colon tumor	universal normal control
	PRO1180	lung tumor	universal normal control
	PRO1180	liver tumor	universal normal control
20	PRO1134	lung tumor	universal normal control
	PRO1134	breast tumor	universal normal control
	PRO1134	prostate tumor	universal normal control
	PRO1115	colon tumor	universal normal control
	PRO1115	lung tumor	universal normal control
25	PRO1115	breast tumor	universal normal control
	PRO1277	colon tumor	universal normal control
	PRO1277	lung tumor	universal normal control
	PRO1135	lung tumor	universal normal control
	PRO1135	breast tumor	universal normal control
30	PRO1135	cervical tumor	universal normal control
	PRO827	colon tumor	universal normal control
	PRO827	lung tumor	universal normal control
	PRO827	prostate tumor	universal normal control
	PRO827	cervical tumor	universal normal control
35	PRO1057	lung tumor	universal normal control
	PRO1057	breast tumor	universal normal control
	PRO1113	colon tumor	universal normal control
	PRO1113	lung tumor	universal normal control
	PRO1006	colon tumor	universal normal control
40	PRO1006	lung tumor	universal normal control
	PRO1006	breast tumor	universal normal control
	PRO1006	rectal tumor	universal normal control
	PRO1074	lung tumor	universal normal control
	PRO1074	rectal tumor	universal normal control
45	PRO1073	lung tumor	universal normal control
	PRO1073	breast tumor	universal normal control
	PRO1136	colon tumor	universal normal control
	PRO1136	lung tumor	universal normal control
	PRO1136	breast tumor	universal normal control
50	PRO1004	lung tumor	universal normal control
	PRO1344	colon tumor	universal normal control
	PRO1344	lung tumor	universal normal control
	PRO1344	breast tumor	universal normal control
	PRO1344	rectal tumor	universal normal control
55	PRO1110	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1110	lung tumor	universal normal control
	PRO1110	breast tumor	universal normal control
	PRO1378	colon tumor	universal normal control
5	PRO1378	lung tumor	universal normal control
	PRO1378	prostate tumor	universal normal control
	PRO1378	cervical tumor	universal normal control
	PRO1481	colon tumor	universal normal control
	PRO1481	lung tumor	universal normal control
10	PRO1109	lung tumor	universal normal control
	PRO1109	breast tumor	universal normal control
	PRO1383	colon tumor	universal normal control
	PRO1383	lung tumor	universal normal control
	PRO1383	breast tumor	universal normal control
15	PRO1072	lung tumor	universal normal control
	PRO1189	colon tumor	universal normal control
	PRO1189	lung tumor	universal normal control
	PRO1189	breast tumor	universal normal control
	PRO1189	prostate tumor	universal normal control
20	PRO1003	colon tumor	universal normal control
	PRO1003	lung tumor	universal normal control
	PRO1003	breast tumor	universal normal control
	PRO1003	liver tumor	universal normal control
	PRO1003	rectal tumor	universal normal control
25	PRO1108	colon tumor	universal normal control
	PRO1108	lung tumor	universal normal control
	PRO1108	breast tumor	universal normal control
	PRO1137	colon tumor	universal normal control
	PRO1137	lung tumor	universal normal control
30	PRO1137	breast tumor	universal normal control
	PRO1138	colon tumor	universal normal control
	PRO1138	lung tumor	universal normal control
	PRO1138	breast tumor	universal normal control
	PRO1415	colon tumor	universal normal control
35	PRO1415	lung tumor	universal normal control
	PRO1415	prostate tumor	universal normal control
	PRO1054	lung tumor	universal normal control
	PRO1054	breast tumor	universal normal control
	PRO994	colon tumor	universal normal control
40	PRO994	lung tumor	universal normal control
	PRO994	rectal tumor	universal normal control
	PRO1069	lung tumor	universal normal control
	PRO1069	breast tumor	universal normal control
	PRO1411	colon tumor	universal normal control
45	PRO1411	lung tumor	universal normal control
	PRO1129	lung tumor	universal normal control
	PRO1129	rectal tumor	universal normal control
	PRO1359	colon tumor	universal normal control
	PRO1359	lung tumor	universal normal control
50	PRO1359	breast tumor	universal normal control
	PRO1359	prostate tumor	universal normal control
	PRO1139	lung tumor	universal normal control
	PRO1065	lung tumor	universal normal control
	PRO1028	colon tumor	universal normal control
55	PRO1028	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1028	breast tumor	universal normal control
	PRO1028	cervical tumor	universal normal control
	PRO1027	colon tumor	universal normal control
5	PRO1027	lung tumor	universal normal control
	PRO1027	breast tumor	universal normal control
	PRO1140	colon tumor	universal normal control
	PRO1140	breast tumor	universal normal control
10	PRO1291	colon tumor	universal normal control
	PRO1291	breast tumor	universal normal control
	PRO1105	colon tumor	universal normal control
	PRO1105	lung tumor	universal normal control
	PRO1026	lung tumor	universal normal control
	PRO1026	prostate tumor	universal normal control
15	PRO1104	colon tumor	universal normal control
	PRO1104	lung tumor	universal normal control
	PRO1104	breast tumor	universal normal control
	PRO1100	colon tumor	universal normal control
	PRO1100	lung tumor	universal normal control
20	PRO1100	breast tumor	universal normal control
	PRO1100	rectal tumor	universal normal control
	PRO1141	lung tumor	universal normal control
	PRO1772	colon tumor	universal normal control
	PRO1772	lung tumor	universal normal control
25	PRO1772	breast tumor	universal normal control
	PRO1772	cervical tumor	universal normal control
	PRO1064	colon tumor	universal normal control
	PRO1064	lung tumor	universal normal control
	PRO1379	colon tumor	universal normal control
30	PRO1379	lung tumor	universal normal control
	PRO1379	cervical tumor	universal normal control
	PRO3573	lung tumor	universal normal control
	PRO3573	breast tumor	universal normal control
	PRO3566	colon tumor	universal normal control
35	PRO3566	lung tumor	universal normal control
	PRO1156	lung tumor	universal normal control
	PRO1156	breast tumor	universal normal control
	PRO1156	prostate tumor	universal normal control
	PRO1098	colon tumor	universal normal control
40	PRO1098	lung tumor	universal normal control
	PRO1098	rectal tumor	universal normal control
	PRO1128	colon tumor	universal normal control
	PRO1128	lung tumor	universal normal control
	PRO1128	breast tumor	universal normal control
45	PRO1248	lung tumor	universal normal control
	PRO1248	breast tumor	universal normal control
	PRO1127	colon tumor	universal normal control
	PRO1127	lung tumor	universal normal control
	PRO1127	breast tumor	universal normal control
50	PRO1316	colon tumor	universal normal control
	PRO1316	lung tumor	universal normal control
	PRO1316	breast tumor	universal normal control
	PRO1197	colon tumor	universal normal control
55	PRO1197	lung tumor	universal normal control
	PRO1197	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1125	lung tumor	universal normal control
	PRO1158	breast tumor	universal normal control
	PRO1124	colon tumor	universal normal control
5	PRO1124	lung tumor	universal normal control
	PRO1380	colon tumor	universal normal control
	PRO1380	lung tumor	universal normal control
	PRO1380	breast tumor	universal normal control
	PRO1380	liver tumor	universal normal control
10	PRO1377	colon tumor	universal normal control
	PRO1377	lung tumor	universal normal control
	PRO1287	lung tumor	universal normal control
	PRO1287	breast tumor	universal normal control
	PRO1249	lung tumor	universal normal control
15	PRO1249	breast tumor	universal normal control
	PRO1335	colon tumor	universal normal control
	PRO1335	lung tumor	universal normal control
	PRO1335	breast tumor	universal normal control
	PRO3572	lung tumor	universal normal control
20	PRO1599	colon tumor	universal normal control
	PRO1599	lung tumor	universal normal control
	PRO1599	breast tumor	universal normal control
	PRO1374	lung tumor	universal normal control
	PRO1374	breast tumor	universal normal control
25	PRO1345	lung tumor	universal normal control
	PRO1345	breast tumor	universal normal control
	PRO1311	lung tumor	universal normal control
	PRO1311	breast tumor	universal normal control
	PRO1357	colon tumor	universal normal control
30	PRO1357	lung tumor	universal normal control
	PRO1557	colon tumor	universal normal control
	PRO1557	lung tumor	universal normal control
	PRO1557	breast tumor	universal normal control
	PRO1305	colon tumor	universal normal control
35	PRO1305	lung tumor	universal normal control
	PRO1305	breast tumor	universal normal control
	PRO1302	colon tumor	universal normal control
	PRO1302	lung tumor	universal normal control
	PRO1302	breast tumor	universal normal control
40	PRO1302	rectal tumor	universal normal control
	PRO1266	colon tumor	universal normal control
	PRO1336	colon tumor	universal normal control
	PRO1336	lung tumor	universal normal control
	PRO1336	breast tumor	universal normal control
45	PRO1278	colon tumor	universal normal control
	PRO1278	lung tumor	universal normal control
	PRO1270	breast tumor	universal normal control
	PRO1298	colon tumor	universal normal control
	PRO1298	lung tumor	universal normal control
50	PRO1301	lung tumor	universal normal control
	PRO1301	breast tumor	universal normal control
	PRO1268	colon tumor	universal normal control
	PRO1268	breast tumor	universal normal control
	PRO1327	lung tumor	universal normal control
55	PRO1327	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1328	colon tumor	universal normal control
	PRO1328	lung tumor	universal normal control
	PRO1328	breast tumor	universal normal control
5	PRO1329	colon tumor	universal normal control
	PRO1329	lung tumor	universal normal control
	PRO1329	breast tumor	universal normal control
	PRO1339	colon tumor	universal normal control
	PRO1339	lung tumor	universal normal control
10	PRO1342	colon tumor	universal normal control
	PRO1342	lung tumor	universal normal control
	PRO1342	breast tumor	universal normal control
	PRO1342	rectal tumor	universal normal control
	PRO1487	colon tumor	universal normal control
15	PRO1487	breast tumor	universal normal control
	PRO3579	lung tumor	universal normal control
	PRO3579	breast tumor	universal normal control
	PRO1472	colon tumor	universal normal control
	PRO1472	lung tumor	universal normal control
20	PRO1385	lung tumor	universal normal control
	PRO1385	breast tumor	universal normal control
	PRO1461	colon tumor	universal normal control
	PRO1461	lung tumor	universal normal control
	PRO1461	breast tumor	universal normal control
25	PRO1429	colon tumor	universal normal control
	PRO1429	lung tumor	universal normal control
	PRO1429	breast tumor	universal normal control
	PRO1568	lung tumor	universal normal control
	PRO1568	breast tumor	universal normal control
30	PRO1569	colon tumor	universal normal control
	PRO1569	lung tumor	universal normal control
	PRO1569	breast tumor	universal normal control
	PRO1753	colon tumor	universal normal control
	PRO1753	lung tumor	universal normal control
35	PRO1570	colon tumor	universal normal control
	PRO1570	lung tumor	universal normal control
	PRO1570	breast tumor	universal normal control
	PRO1570	prostate tumor	universal normal control
	PRO1570	rectal tumor	universal normal control
40	PRO1559	colon tumor	universal normal control
	PRO1559	lung tumor	universal normal control
	PRO1559	breast tumor	universal normal control
	PRO1486	lung tumor	universal normal control
	PRO1486	breast tumor	universal normal control
45	PRO1433	colon tumor	universal normal control
	PRO1433	lung tumor	universal normal control
	PRO1433	breast tumor	universal normal control
	PRO1433	rectal tumor	universal normal control
	PRO1490	lung tumor	universal normal control
50	PRO1490	breast tumor	universal normal control
	PRO1482	lung tumor	universal normal control
	PRO1482	breast tumor	universal normal control
	PRO1409	colon tumor	universal normal control
	PRO1409	lung tumor	universal normal control
55	PRO1409	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1446	colon tumor	universal normal control
	PRO1446	lung tumor	universal normal control
	PRO1446	breast tumor	universal normal control
5	PRO1446	prostate tumor	universal normal control
	PRO1604	colon tumor	universal normal control
	PRO1604	lung tumor	universal normal control
	PRO1604	breast tumor	universal normal control
	PRO1491	colon tumor	universal normal control
10	PRO1491	lung tumor	universal normal control
	PRO1491	breast tumor	universal normal control
	PRO1431	colon tumor	universal normal control
	PRO1431	lung tumor	universal normal control
	PRO1563	colon tumor	universal normal control
15	PRO1563	lung tumor	universal normal control
	PRO1563	breast tumor	universal normal control
	PRO1571	colon tumor	universal normal control
	PRO1571	lung tumor	universal normal control
	PRO1571	breast tumor	universal normal control
20	PRO1572	lung tumor	universal normal control
	PRO1572	prostate tumor	universal normal control
	PRO1573	lung tumor	universal normal control
	PRO1573	breast tumor	universal normal control
	PRO1508	lung tumor	universal normal control
25	PRO1508	breast tumor	universal normal control
	PRO1485	colon tumor	universal normal control
	PRO1485	lung tumor	universal normal control
	PRO1564	colon tumor	universal normal control
	PRO1564	lung tumor	universal normal control
30	PRO1564	breast tumor	universal normal control
	PRO1550	colon tumor	universal normal control
	PRO1550	lung tumor	universal normal control
	PRO1550	breast tumor	universal normal control
	PRO1757	lung tumor	universal normal control
35	PRO1757	breast tumor	universal normal control
	PRO1757	prostate tumor	universal normal control
	PRO1758	lung tumor	universal normal control
	PRO1781	colon tumor	universal normal control
	PRO1781	lung tumor	universal normal control
40	PRO1781	breast tumor	universal normal control
	PRO1606	lung tumor	universal normal control
	PRO1606	breast tumor	universal normal control
	PRO1784	colon tumor	universal normal control
	PRO1784	lung tumor	universal normal control
45	PRO1784	breast tumor	universal normal control
	PRO1774	colon tumor	universal normal control
	PRO1774	lung tumor	universal normal control
	PRO1774	breast tumor	universal normal control
	PRO1605	colon tumor	universal normal control
50	PRO1605	lung tumor	universal normal control
	PRO1605	prostate tumor	universal normal control
	PRO1928	colon tumor	universal normal control
	PRO1928	lung tumor	universal normal control
	PRO1928	cervical tumor	universal normal control
55	PRO1865	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1865	liver tumor	universal normal control
	PRO1925	lung tumor	universal normal control
	PRO1926	liver tumor	universal normal control
5	PRO2630	colon tumor	universal normal control
	PRO2630	lung tumor	universal normal control
	PRO2630	breast tumor	universal normal control
	PRO2630	liver tumor	universal normal control
	PRO3443	colon tumor	universal normal control
10	PRO3443	lung tumor	universal normal control
	PRO3443	breast tumor	universal normal control
	PRO3301	colon tumor	universal normal control
	PRO3301	lung tumor	universal normal control
	PRO3301	breast tumor	universal normal control
15	PRO3301	rectal tumor	universal normal control
	PRO3442	colon tumor	universal normal control
	PRO3442	lung tumor	universal normal control
	PRO3442	rectal tumor	universal normal control
	PRO4978	colon tumor	universal normal control
20	PRO4978	lung tumor	universal normal control
	PRO4978	breast tumor	universal normal control
	PRO4978	rectal tumor	universal normal control
	PRO5801	colon tumor	universal normal control
	PRO5801	breast tumor	universal normal control
25	PRO19630	colon tumor	universal normal control
	PRO203	colon tumor	universal normal control
	PRO204	colon tumor	universal normal control
	PRO204	lung tumor	universal normal control
	PRO204	breast tumor	universal normal control
30	PRO204	prostate tumor	universal normal control
	PRO210	colon tumor	universal normal control
	PRO210	lung tumor	universal normal control
	PRO223	lung tumor	universal normal control
	PRO223	breast tumor	universal normal control
35	PRO247	colon tumor	universal normal control
	PRO247	lung tumor	universal normal control
	PRO247	breast	universal normal control
	PRO358	lung tumor	universal normal control
	PRO358	breast tumor	universal normal control
40	PRO358	prostate tumor	universal normal control
	PRO724	lung tumor	universal normal control
	PRO868	colon tumor	universal normal control
	PRO868	lung tumor	universal normal control
	PRO868	prostate tumor	universal normal control
45	PRO868	rectal tumor	universal normal control
	PRO740	colon tumor	universal normal control
	PRO1478	colon tumor	universal normal control
	PRO1478	lung tumor	universal normal control
	PRO162	colon tumor	universal normal control
50	PRO162	lung tumor	universal normal control
	PRO162	breast tumor	universal normal control
	PRO828	colon tumor	universal normal control
	PRO828	lung tumor	universal normal control
	PRO828	breast tumor	universal normal control
55	PRO828	cervical tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO828	liver tumor	universal normal control
	PRO819	lung tumor	universal normal control
	PRO819	breast tumor	universal normal control
5	PRO819	rectal tumor	universal normal control
	PRO813	colon tumor	universal normal control
	PRO813	lung tumor	universal normal control
	PRO813	breast tumor	universal normal control
	PRO813	prostate tumor	universal normal control
10	PRO1194	colon tumor	universal normal control
	PRO1194	lung tumor	universal normal control
	PRO1194	breast tumor	universal normal control
	PRO887	colon tumor	universal normal control
	PRO887	lung tumor	universal normal control
15	PRO887	rectal tumor	universal normal control
	PRO1071	colon tumor	universal normal control
	PRO1071	lung tumor	universal normal control
	PRO1071	breast tumor	universal normal control
	PRO1029	colon tumor	universal normal control
20	PRO1029	lung tumor	universal normal control
	PRO1029	breast tumor	universal normal control
	PRO1190	lung tumor	universal normal control
	PRO1190	breast tumor	universal normal control
	PRO4334	lung tumor	universal normal control
25	PRO1155	colon tumor	universal normal control
	PRO1155	lung tumor	universal normal control
	PRO1157	breast tumor	universal normal control
	PRO1157	cervical tumor	universal normal control
	PRO1122	lung tumor	universal normal control
30	PRO1122	breast tumor	universal normal control
	PRO1183	colon tumor	universal normal control
	PRO1183	lung tumor	universal normal control
	PRO1183	breast tumor	universal normal control
	PRO1337	colon tumor	universal normal control
35	PRO1337	lung tumor	universal normal control
	PRO1337	breast tumor	universal normal control
	PRO1480	colon tumor	universal normal control
	PRO1480	lung tumor	universal normal control
	PRO1480	breast tumor	universal normal control
40	PRO19645	colon tumor	universal normal control
	PRO9782	colon tumor	universal normal control
	PRO1419	colon tumor	universal normal control
	PRO1575	colon tumor	universal normal control
	PRO1575	lung tumor	universal normal control
45	PRO1567	colon tumor	universal normal control
	PRO1567	lung tumor	universal normal control
	PRO1567	breast tumor	universal normal control
	PRO1891	colon tumor	universal normal control
	PRO1889	colon tumor	universal normal control
50	PRO1889	lung tumor	universal normal control
	PRO1785	lung tumor	universal normal control
	PRO1785	prostate tumor	universal normal control
	PRO6003	colon tumor	universal normal control
	PRO4333	colon tumor	universal normal control
55	PRO4356	colon tumor	universal normal control



Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO4352	colon tumor	universal normal control
	PRO4354	colon tumor	universal normal control
	PRO4354	lung tumor	universal normal control
5	PRO4354	prostate tumor	universal normal control
	PRO4369	colon tumor	universal normal control
	PRO6030	colon tumor	universal normal control
	PRO4433	colon tumor	universal normal control
	PRO4424	colon tumor	universal normal control
10	PRO4424	breast tumor	universal normal control
	PRO6017	colon tumor	universal normal control
	PRO19563	colon tumor	universal normal control
	PRO6015	colon tumor	universal normal control
	PRO5779	colon tumor	universal normal control
15	PRO5776	colon tumor	universal normal control
	PRO4430	lung tumor	universal normal control
	PRO4421	colon tumor	universal normal control
	PRO4499	colon tumor	universal normal control
	PRO4423	colon tumor	universal normal control
20	PRO5998	colon tumor	universal normal control
	PRO5998	lung tumor	universal normal control
	PRO4501	colon tumor	universal normal control
	PRO6240	colon tumor	universal normal control
	PRO6245	colon tumor	universal normal control
25	PRO6175	colon tumor	universal normal control
	PRO9742	colon tumor	universal normal control
	PRO7179	colon tumor	universal normal control
	PRO6239	colon tumor	universal normal control
	PRO6493	colon tumor	universal normal control
30	PRO9741	colon tumor	universal normal control
	PRO9822	colon tumor	universal normal control
	PRO6244	colon tumor	universal normal control
	PRO9740	colon tumor	universal normal control
	PRO9739	colon tumor	universal normal control
35	PRO7177	colon tumor	universal normal control
	PRO7178	colon tumor	universal normal control
	PRO6246	colon tumor	universal normal control
	PRO6241	colon tumor	universal normal control
	PRO9835	colon tumor	universal normal control
40	PRO9857	colon tumor	universal normal control
	PRO7436	colon tumor	universal normal control
	PRO9856	colon tumor	universal normal control
	PRO19605	colon tumor	universal normal control
	PRO9859	colon tumor	universal normal control
45	PRO12970	colon tumor	universal normal control
	PRO19626	colon tumor	universal normal control
	PRO9883	colon tumor	universal normal control
	PRO19670	colon tumor	universal normal control
	PRO19624	colon tumor	universal normal control
50	PRO19680	colon tumor	universal normal control
	PRO19675	colon tumor	universal normal control
	PRO9834	colon tumor	universal normal control
	PRO9744	colon tumor	universal normal control
	PRO19644	colon tumor	universal normal control
55	PRO19625	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO19597	colon tumor	universal normal control
	PRO16090	colon tumor	universal normal control
	PRO19576	colon tumor	universal normal control
5	PRO19646	colon tumor	universal normal control
	PRO19814	colon tumor	universal normal control
	PRO19669	colon tumor	universal normal control
	PRO19818	colon tumor	universal normal control
	PRO20088	colon tumor	universal normal control
10	PRO16089	colon tumor	universal normal control
	PRO20025	colon tumor	universal normal control
	PRO20040	colon tumor	universal normal control
	PRO1760	adrenal tumor	universal normal control
	PRO1760	breast tumor	universal normal control
15	PRO1760	cervical tumor	universal normal control
	PRO1760	colon tumor	universal normal control
	PRO1760	liver tumor	universal normal control
	PRO1760	lung tumor	universal normal control
	PRO1760	prostate tumor	universal normal control
20	PRO1760	rectal tumor	universal normal control
	PRO6029	adrenal tumor	universal normal control
	PRO6029	colon tumor	universal normal control
	PRO6029	prostate tumor	universal normal control
	PRO1801	colon tumor	universal normal control
25	PRO1801	lung tumor	universal normal control

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16),  
5 Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54),  
10 Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92),  
15 Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID  
20 NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure  
25 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID  
30 NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure  
35 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID

[illegible]

NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), and Figure 610 (SEQ ID NO:610).

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figures 75A-75B (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID

NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 5 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 10 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID NO:249), Figure 251 (SEQ ID NO:251), Figure 253 (SEQ ID NO:253), Figure 255 (SEQ ID NO:255), Figure 257 (SEQ ID NO:257), Figure 259 (SEQ ID NO:259), Figure 261 (SEQ ID NO:261), Figure 263 (SEQ ID NO:263), Figure 265 (SEQ ID NO:265), Figure 267 (SEQ ID NO:267), Figure 269 (SEQ ID NO:269), Figure 15 271 (SEQ ID NO:271), Figure 273 (SEQ ID NO:273), Figure 275 (SEQ ID NO:275), Figure 277 (SEQ ID NO:277), Figure 279 (SEQ ID NO:279), Figure 281 (SEQ ID NO:281), Figure 283 (SEQ ID NO:283), Figure 285 (SEQ ID NO:285), Figure 287 (SEQ ID NO:287), Figures 289A-289B (SEQ ID NO:289), Figure 291 (SEQ ID NO:291), Figure 293 (SEQ ID NO:293), Figure 295 (SEQ ID NO:295), Figure 297 (SEQ ID NO:297), Figure 299 (SEQ ID NO:299), Figure 301 (SEQ ID NO:301), Figure 303 (SEQ ID NO:303), Figure 305 (SEQ ID NO:305), Figure 307 (SEQ ID NO:307), Figure 309 (SEQ ID NO:309), Figures 311A-311B (SEQ ID NO:311), 20 Figure 313 (SEQ ID NO:313), Figure 315 (SEQ ID NO:315), Figure 317 (SEQ ID NO:317), Figure 319 (SEQ ID NO:319), Figure 321 (SEQ ID NO:321), Figure 323 (SEQ ID NO:323), Figure 325 (SEQ ID NO:325), Figure 327 (SEQ ID NO:327), Figure 329 (SEQ ID NO:329), Figure 331 (SEQ ID NO:331), Figure 333 (SEQ ID NO:333), Figure 335 (SEQ ID NO:335), Figure 337 (SEQ ID NO:337), Figure 339 (SEQ ID NO:339), Figure 25 341 (SEQ ID NO:341), Figure 343 (SEQ ID NO:343), Figure 345 (SEQ ID NO:345), Figure 347 (SEQ ID NO:347), Figure 349 (SEQ ID NO:349), Figures 351A-351B (SEQ ID NO:351), Figure 353 (SEQ ID NO:353), Figure 355 (SEQ ID NO:355), Figure 357 (SEQ ID NO:357), Figure 359 (SEQ ID NO:359), Figure 361 (SEQ ID NO:361), Figure 363 (SEQ ID NO:363), Figure 365 (SEQ ID NO:365), Figure 367 (SEQ ID NO:367), Figure 369 (SEQ ID NO:369), Figure 371 (SEQ ID NO:371), Figure 373 (SEQ ID NO:373), Figure 375 (SEQ ID NO:375), Figure 377 (SEQ ID NO:377), Figure 379 (SEQ ID NO:379), Figure 381 (SEQ ID NO:381), Figure 30 383 (SEQ ID NO:383), Figure 385 (SEQ ID NO:385), Figure 387 (SEQ ID NO:387), Figure 389 (SEQ ID NO:389), Figure 391 (SEQ ID NO:391), Figure 393 (SEQ ID NO:393), Figure 395 (SEQ ID NO:395), Figure 397 (SEQ ID NO:397), Figure 399 (SEQ ID NO:399), Figure 401 (SEQ ID NO:401), Figure 403 (SEQ ID NO:403), Figure 405 (SEQ ID NO:405), Figure 407 (SEQ ID NO:407), Figure 409 (SEQ ID NO:409), Figure 35 411 (SEQ ID NO:411), Figure 413 (SEQ ID NO:413), Figure 415 (SEQ ID NO:415), Figure 417 (SEQ ID NO:417), Figure 419 (SEQ ID NO:419), Figure 421 (SEQ ID NO:421), Figure 423 (SEQ ID NO:423), Figure 425 (SEQ ID NO:425), Figure 427 (SEQ ID NO:427), Figure 429 (SEQ ID NO:429), Figure 431 (SEQ ID

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3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure

71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figures 75A-75B (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID NO:249), Figure 251 (SEQ ID NO:251), Figure 253 (SEQ ID NO:253), Figure 255 (SEQ ID NO:255), Figure 257 (SEQ ID NO:257), Figure 259 (SEQ ID NO:259), Figure 261 (SEQ ID NO:261), Figure 263 (SEQ ID NO:263), Figure 265 (SEQ ID NO:265), Figure 267 (SEQ ID NO:267), Figure 269 (SEQ ID NO:269), Figure 271 (SEQ ID NO:271), Figure 273 (SEQ ID NO:273), Figure 275 (SEQ ID NO:275), Figure 277 (SEQ ID NO:277), Figure 279 (SEQ ID NO:279), Figure 281 (SEQ ID NO:281), Figure 283 (SEQ ID NO:283), Figure 285 (SEQ ID NO:285), Figure 287 (SEQ ID NO:287), Figures 289A-289B (SEQ ID NO:289), Figure 291 (SEQ ID NO:291), Figure 293 (SEQ ID NO:293), Figure 295 (SEQ ID NO:295), Figure 297 (SEQ ID NO:297), Figure 299 (SEQ ID NO:299), Figure 301 (SEQ ID NO:301), Figure 303 (SEQ ID NO:303), Figure 305 (SEQ ID NO:305), Figure 307 (SEQ ID NO:307), Figure 309 (SEQ ID NO:309), Figures 311A-311B (SEQ ID NO:311), Figure 313 (SEQ ID NO:313), Figure 315 (SEQ ID NO:315), Figure 317 (SEQ ID NO:317), Figure 319 (SEQ ID NO:319), Figure 321 (SEQ ID NO:321), Figure 323 (SEQ ID NO:323), Figure 325 (SEQ ID NO:325), Figure 327 (SEQ ID NO:327), Figure 329 (SEQ ID NO:329), Figure 331 (SEQ ID NO:331), Figure 333 (SEQ ID NO:333), Figure 335 (SEQ ID NO:335), Figure 337 (SEQ ID NO:337), Figure



339 (SEQ ID NO:339), Figure 341 (SEQ ID NO:341), Figure 343 (SEQ ID NO:343), Figure 345 (SEQ ID NO:345), Figure 347 (SEQ ID NO:347), Figure 349 (SEQ ID NO:349), Figures 351A-351B (SEQ ID NO:351), Figure 353 (SEQ ID NO:353), Figure 355 (SEQ ID NO:355), Figure 357 (SEQ ID NO:357), Figure 359 (SEQ ID NO:359), Figure 361 (SEQ ID NO:361), Figure 363 (SEQ ID NO:363), Figure 365 (SEQ ID NO:365), Figure 367 (SEQ ID NO:367), Figure 369 (SEQ ID NO:369), Figure 371 (SEQ ID NO:371), Figure 373 (SEQ ID NO:373), Figure 375 (SEQ ID NO:375), Figure 377 (SEQ ID NO:377), Figure 379 (SEQ ID NO:379), Figure 381 (SEQ ID NO:381), Figure 383 (SEQ ID NO:383), Figure 385 (SEQ ID NO:385), Figure 387 (SEQ ID NO:387), Figure 389 (SEQ ID NO:389), Figure 391 (SEQ ID NO:391), Figure 393 (SEQ ID NO:393), Figure 395 (SEQ ID NO:395), Figure 397 (SEQ ID NO:397), Figure 399 (SEQ ID NO:399), Figure 401 (SEQ ID NO:401), Figure 403 (SEQ ID NO:403), Figure 405 (SEQ ID NO:405), Figure 407 (SEQ ID NO:407), Figure 409 (SEQ ID NO:409), Figure 411 (SEQ ID NO:411), Figure 413 (SEQ ID NO:413), Figure 415 (SEQ ID NO:415), Figure 417 (SEQ ID NO:417), Figure 419 (SEQ ID NO:419), Figure 421 (SEQ ID NO:421), Figure 423 (SEQ ID NO:423), Figure 425 (SEQ ID NO:425), Figure 427 (SEQ ID NO:427), Figure 429 (SEQ ID NO:429), Figure 431 (SEQ ID NO:431), Figure 433 (SEQ ID NO:433), Figure 435 (SEQ ID NO:435), Figure 437 (SEQ ID NO:437), Figure 439 (SEQ ID NO:439), Figure 441 (SEQ ID NO:441), Figure 443 (SEQ ID NO:443), Figure 445 (SEQ ID NO:445), Figure 447 (SEQ ID NO:447), Figure 449 (SEQ ID NO:449), Figure 451 (SEQ ID NO:451), Figure 453 (SEQ ID NO:453), Figure 455 (SEQ ID NO:455), Figure 457 (SEQ ID NO:457), Figure 459 (SEQ ID NO:459), Figure 461 (SEQ ID NO:461), Figure 463 (SEQ ID NO:463), Figure 465 (SEQ ID NO:465), Figure 467 (SEQ ID NO:467), Figure 469 (SEQ ID NO:469), Figure 471 (SEQ ID NO:471), Figure 473 (SEQ ID NO:473), Figure 475 (SEQ ID NO:475), Figure 477 (SEQ ID NO:477), Figure 479 (SEQ ID NO:479), Figure 481 (SEQ ID NO:481), Figure 483 (SEQ ID NO:483), Figure 485 (SEQ ID NO:485), Figure 487 (SEQ ID NO:487), Figure 489 (SEQ ID NO:489), Figure 491 (SEQ ID NO:491), Figure 493 (SEQ ID NO:493), Figure 495 (SEQ ID NO:495), Figure 497 (SEQ ID NO:497), Figure 499 (SEQ ID NO:499), Figure 501 (SEQ ID NO:501), Figure 503 (SEQ ID NO:503), Figure 505 (SEQ ID NO:505), Figure 507 (SEQ ID NO:507), Figure 509 (SEQ ID NO:509), Figure 511 (SEQ ID NO:511), Figure 513 (SEQ ID NO:513), Figure 515 (SEQ ID NO:515), Figure 517 (SEQ ID NO:517), Figure 519 (SEQ ID NO:519), Figure 521 (SEQ ID NO:521), Figure 523 (SEQ ID NO:523), Figures 525A-525B (SEQ ID NO:525), Figure 527 (SEQ ID NO:527), Figure 529 (SEQ ID NO:529), Figure 531 (SEQ ID NO:531), Figure 533 (SEQ ID NO:533), Figure 535 (SEQ ID NO:535), Figure 537 (SEQ ID NO:537), Figure 539 (SEQ ID NO:539), Figure 541 (SEQ ID NO:541), Figure 543 (SEQ ID NO:543), Figure 545 (SEQ ID NO:545), Figure 547 (SEQ ID NO:547), Figure 549 (SEQ ID NO:549), Figure 551 (SEQ ID NO:551), Figure 553 (SEQ ID NO:553), Figure 555 (SEQ ID NO:555), Figure 557 (SEQ ID NO:557), Figure 559 (SEQ ID NO:559), Figure 561 (SEQ ID NO:561), Figure 563 (SEQ ID NO:563), Figure 565 (SEQ ID NO:565), Figure 567 (SEQ ID NO:567), Figure 569 (SEQ ID NO:569), Figure 571 (SEQ ID NO:571), Figure 573 (SEQ ID NO:573), Figure 575 (SEQ ID NO:575), Figure 577 (SEQ ID NO:577), Figure 579 (SEQ ID NO:579), Figure 581 (SEQ ID NO:581), Figure 583 (SEQ ID NO:583), Figure 585 (SEQ ID NO:585), Figure 587 (SEQ ID NO:587), Figure 589 (SEQ ID NO:589), Figure 591 (SEQ ID NO:591), Figure 593 (SEQ ID NO:593), Figure 595 (SEQ ID NO:595), Figure 597 (SEQ ID NO:597), Figure 599 (SEQ ID NO:599), Figure 601 (SEQ ID NO:601), Figure 603 (SEQ ID NO:603), Figure

605 (SEQ ID NO:605), Figure 607 (SEQ ID NO:607), and Figure 609 (SEQ ID NO:609).

4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

5            5.        A vector comprising the nucleic acid of Claim 1.

6. A host cell comprising the vector of Claim 5.

7. The host cell of Claim 6, wherein said cell is a CHO cell.

10

8. The host cell of Claim 6, wherein said cell is an *E. coli*.

9. The host cell of Claim 6, wherein said cell is a yeast cell.

15            10.        A process for producing a PRO polypeptide comprising culturing the host cell of Claim 6 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.

11. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid  
sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2),  
Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10),  
Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID  
NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ  
ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34  
(SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure  
42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48),  
Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID  
NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ  
ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72  
(SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure  
80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86),  
Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID  
NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102  
(SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108),  
Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ  
ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure  
124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID

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NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), and Figure 610 (SEQ ID NO:610).

12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

13. A chimeric molecule comprising a polypeptide according to Claim 11 fused to a heterologous amino acid sequence.

14. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is an epitope tag sequence.

15. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

5

16. An antibody which specifically binds to a polypeptide according to Claim 11.

17. The antibody of Claim 16, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

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18. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure

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188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure

454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), lacking its associated signal peptide;

(b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ

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- NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), with its associated signal peptide; or
- (c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18

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- 10           19.     An isolated polypeptide having at least 80% amino acid sequence identity to:
  - (a)     an amino acid sequence of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194),

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(b) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ

ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 5 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 10 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 15 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 20 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 25 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 30 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 35 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID

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(c) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure



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292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID  
NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure

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572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), lacking its associated signal peptide.

20. A method for stimulating the release of TNF- $\alpha$  from human blood, said method comprising contacting said blood with a PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or PRO4333 polypeptide, wherein the release of TNF- $\alpha$  from said blood is stimulated.

10

21. A method for stimulating the proliferation or differentiation of chondrocyte cells, said method comprising contacting said cells with a PRO6029 polypeptide, wherein the proliferation or differentiation of said cells is stimulated.

15

22. A method for detecting the presence of tumor in an mammal, said method comprising comparing the level of expression of any PRO polypeptide shown in Table 8 in (a) a test sample of cells taken from said mammal and (b) a control sample of normal cells of the same cell type, wherein a higher level of expression of said PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of tumor in said mammal.

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23. The method of Claim 22, wherein said tumor is adrenal tumor, lung tumor, colon tumor, breast tumor, prostate tumor, rectal tumor, cervical tumor or liver tumor.

24. An oligonucleotide probe derived from any of the nucleotide sequences shown in the accompanying figures.

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1/615

**FIGURE 1**

GAAGGCTGCCTCGCTGGTCCGAATTCCGGTGGCGCCACGTCGGCCCCGTCTCCGCCTTCTGCATCGCGGCTTCGGCG  
GCTTCCACCTAGACACCTAACAGTCGCGGAGCCGCGCGCTCGTGAGGGGGTCGGGCACGGGGAGTCGGGCGGTCT  
TGTGCATCTTGGCTACCTGTGGGTCTGAAGATGTCGGACATCGGAGACTGGTTTCAAGAGCATCCCGGCGATCACGC  
GCTATTGGTTTCGCCGCCACCGTCGCGGTGCCCTTGGTTCGGCAAACCTCGGCCTCATCAGCCCCGCTACCTCTTCC  
TCTGGCCCCGAAGCCTTCCCTTTATCGCTTTTTCAGATTGGAGGCCAATCACTGCCACCTTTTATTTCCTGTGGGTC  
CAGGAACTGGATTTCTTTATTTGGTCAATTTATATTCTTATATCAGTATTCTACGCGACTTGAAACAGGAGCTT  
TTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTGGATTGTCATCGTGATTACTGGCTTAGCAA  
TGGATATGCAGTTGCTGATGATTCTCTGATCATGTGAGTACTTTATGTCTGGGCCCAGCTGAACAGAGACATGA  
TTGTATCATTTTGGTTTGGAAACACGATTTAAGGCGCTGCTATTTACCCTGGGTTATCCTTGGATTCAACTATATCA  
TCGGAGGCTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTTTCCCTAATGTTTTCAGATACC  
CAATGGACTTGGGAGGAAGAAATTTTCTATCCACACCTCAGTTTTTTGTACCCTGGCTGCCAGTAGGAGAGGAG  
GAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGCTGCTGATCAGAATGGCGGAGGCGGGAGACACA  
ACTGGGGCCAGGGCTTTCGACTTGGAGACCAGTGAAGGGGCGGCTCGGGCAGCCGCTCCTCTCAAGCCACATTT  
CCTCCAGTGTGGGTGCACTTAACAACGCTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTC  
TTTCAGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTCCACAAGTTTTCAGATTCTCATTCA  
AGTCCCTTACTGCTGTGAAGAACAATAACAACTGTGCAAACTGCAAACTGACTACATTTTTTGGTGTCTTCTCT  
TCTCCCTTTCCGTCTGAATAATGGGTTTTAGCGGGTCTTAATCTGCTGGCATTGAGCTGGGGCTGGGTACCAA  
ACCCTTCCCAAAAGGACCTTATCTCTTCTTGCACACATGCCTCTCTCCACTTTTCCCAACCCCCACATTTGCA  
ACTAGAAAAAGTTGCCATAAAATTGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGGT  
CACAACAATCATATTCACGTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAGAGACAGCCACG  
GATGAAGCGTTTCTCAGCTTTTGGAAATGCTTCGACTGACATCCGTTGTTAACGTTTGCCACTCTTCAGATATT  
TTTTATAAAAAAGTACCCTGAGTTTATGAGGGCCACAGATTGGTTATTAATGAGATACGAGGTTGGTGCTGG  
GTGTTTGTCTTCTGAGCTAAGTGATCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGG  
GGATGCACCCCTTTGCGTTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGTTA  
GGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTGATTCCCATTTCAATC  
TCATTCTGGATATGTGTTTATTGAGTAAAGGAGGAGAGACCCCTCATACGCTATTTAAATGTCATTTTTTGCCTA  
TCCCCCGTTTTTTGGTCATGTTTCAATTAATTGTGAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTTA  
AAGCTAATGTAAGCACATCTAAGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGGG  
GTGTGTTATTTTGTGATCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTTTCGTA  
GGTGGGCTTTTTCTATCAGAGCTTGGCTCATAACCAATAAAGTTTTTTGAAGGCCATGGCTTTTCAACAGTTA  
TTTTATTTTATGACGTTATCTGAAAGCAGACTGTAGGAGCAGTATTGAGTGGCTGTACACTTTTGAGGCAACTA  
AAAAGGCTTCAAACGTTTTGATCAGTTTCTTTTTCAGGAAACATTGTGCTCTAACAGTATGACTATTTCTTTCCCC  
ACTCTTAAACAGTGTGATGTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACCTTCTCATTTTGAATAGAGTTT  
GTGTGTAATTTCTCCATATTTAATTTATATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACTGTCATGTTTTGT  
TGTTTCATCTGTGGCCACAATAAAGTTTACTTGTAAATTTTAGAGGCCATTACTCCAATTATGTTGCACGTACAC  
TCATTGTACAGGCGTGGAGACTCATTGTATGTATAAGAATATTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGT  
ACCCTCTTACCAGTCAGCTGCCTGCGAGCAGTCATTTTTTCTTAAAGGTTTACAAGTATTTAGAACTTTTCAGTT  
CAGGGCAAATGTTTCATGAAGTTATTCCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGA  
TTATGTTTCTGGAATAATTTTACCAAAACAAGCTATTTGAGTTTGTACTTGACAAGGCAAAACATGACAGTGGAT  
TCTCTTTACAAATGGAATAAAAAAATCCTTATTTTGTATAAAGGACTTCCCTTTTTGTAAACTAATCCTTTTTAT  
TGGTAAAAATGTAATTAATAATGTGCAACTTG

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**FIGURE 2**

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGKISPAYLFLWPEAFLYRFQIWRPITATFYFPVGP GTGFLYLVN  
LYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIPLIMSVLYVWAQLNRDMIVSFWFGTRF  
KACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFLMFRYPMDLGGRNFLSTPQFLYRWLPSSRRGGVSGFGVPPA  
SMRRAADQNGGGGRHNWGQGFRLGDQ

**Transmembrane domain:**

amino acids 98-116, 152-172

**N-myristoylation site.**

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

**Glycosaminoglycan attachment site.**

amino acids 218-222

**FIGURE 3**

GAGCGAGGCCCGGGGACTGAAGGTGTGGGTGTCTGAGCCCTCTGGCAGAGGGTTAACTGGGTCAAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCGCGCAGGACTTGAAGTCCTGAGCGCTCAAGTTTTGTCCGTAGGTGAGAGAAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCGGAGCTTTTGCTGCCGAAGCTGTGACTGCCGATTTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCAGAGAGCCCTATTACCGGAAATCTGATGAGGACCGCTCCGGAGCTGTTTGGCAAAGATGACACAGCAGAGAATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGAATACAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTGTGTGACTATATTCAACACAGTGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATGTCAGGAGCTGTACGGGAAGTCTTTTTAGGATAAACCGTAGGCCCTGCGTGGCTCTGGTGGCTGGTGGCATAATTGGAGCCTTGCTGGGCACTCCTGTAGGAGCCCTGCTGATGGCAATTCAGAAGTACGCTGGTGAGACTGTTCCAGGAAGAAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACCTGGAAGAGTGGAAAGGCAGACTACAAGTTACTGAGCACTCCCTGAGAAAATTGAAAGTAGTTTACGGGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACCCTTCAGTATAGATAAACACAGACAAGGACTGGAAGTGCCTCTGAACCTGAAACTCACTGGAGAGCTGAAGGGAGCTGCCATGTCTCCGATGAATGCCACAGACAGGCCACTCTTTTGGTCAGCCTGCTGACAAATTTAAGTCTGGTAGCTGTGTGGTGAGCAGTGGCTTGCTCTTGCTCTTTTCTTTTAACTAAGAATGGGCTGTTGTACTCTCACTTTACTTATCTTAAATTTAAATACATACTTATGTTTGTATTAACTCATCAATATATGGCATAATGGATATATCCACCCACCTAGATTTTAAAGCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

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**FIGURE 4**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELFQKDEQQRISKDLA
NICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEYHNRFDAVQSAHRAATRGFIRYGWRWGWRTAVEVTIFN
TVNTSLNVYRNKDLSHFVIAGAVTGSLFRINVGLRGLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDR
KALHELKLEEWKGRQLQVTEHLPEKIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD
```

**Important Features:****Signal Peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 76-96 and 171-195

**N-glycosylation site:**

amino acids 153-156

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**FIGURE 5**

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGCGCCTGAAGTCGGC  
GTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGCTTAAGAAGTAAAAATGGCAGGCTTCC  
TAGATAATTTTCGTTGGCCAGAATGTGAATGTATTGACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCG  
CAGGTATATTGTTTTTACAGGCTGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGA  
ACCATGCCTTTCACACATGTGGTGTATTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTCAGG  
TGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTTTTCATTGGTTTCATGT  
TGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTGGTGCATATGTTACCCAAAATACTGATGTTTATC  
CGGGACTAGCTGTGTTTTTCAAATGCACTTATATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAG  
AGCTATGGACCTGAGATCACTTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATC  
TCTCAGTACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTGTTCCTTACATTTTATGTTCTGAGTT  
TTGAAATAGTTTATGAAATTTCTTATTTTTTCATTGCATAGACTGTTAATATGTATATAATACAAGACTATATG  
AATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAACTTGATCTACTCCCTGAGCCAGGGTTACATCA  
TCTTGTCATTTTAGAAGTAACCACTCTTGTCTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTT  
TGGGAGGCCGAGGCGGGCCGATTGCTTGAGGTCAAGTGTTTGAAGCCAGCCTGGCCAACATGGCGAAACCCCATC  
TACTAAAAATACAAAAATTAGCCAGGCATGGTGGTGGTGCCTGTAATCCCAGCTACCTGGGAGGCTGAGGCAGG  
AGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCACTGCACTCTAGCCTGGGGGAGAA  
AGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATCTCTGATTTCTGAAGATGTACAAAAAATATAGCTT  
CATATATCTGGAATGAGCACTGAGCCATAAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGT  
TTTTTTGGTAAAGAAAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCC  
CAAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA



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## **FIGURE 6**

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCGVFSTLAFMINAV  
SNAQVRGDSYESGCLGRTGARVWLFIFGMLMFGSLIASMWILFGAYVTQNTDVYPGLAVFFQNALIFFSTLIYKF  
GRTEELWT

**Important features:**

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

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**FIGURE 7**

GGGTGGTTTTTTGTTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTTCGCCTATACCTACTGTAGCTTCTCCACG  
TATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAGGATGTGCGTTCTTC  
CACTAGAAGCTCTTCTGAGGGAGGTAATTAACCAACAGTGGAATGGAAAAACAGTGCTGTAGTCATCCTGTAATA  
TGCTCCTTGTCAACAATGTATACATTCTCTGCTAGGTGCCATATTGCTTTAAGCTCAAGTCGCATCTTACTA  
GTGAAGTATTCTGCCAATGAAGAAAAACAAGTATGATTATCTTCCAACTACTGTGAATGTGTGCTCAGAACTGGTG  
AAGCTAGTTTTCTGTGTGCTTGTGTCTTCTGTGTTATAAGAAAGATCATCAAAGTAGAAATTTGAAATATGCT  
TCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCTGGATAACTTGATTGTC  
TTCTATGTCCTGTCTCTATCTTCAACCAGCCATGGCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTT  
CTATTCAAGGATAGTGCTGAAGAGGCGTCTAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATT  
GTGGCCTTGACTGCCGGGACTAAAACCTTTACAGCACAACTTGGCAGGACGTGGATTTCATCACGATGCCTTTTTTC  
AGCCCTTCCAATTCTGCCTTCTTTTTCAGAAGTGAGTGTCCCAGAAAAGACAATTGTACAGCAAAGGAATGGACT  
TTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTCACATCCGTCTTGGCATGGGCCATGTTCTTATT  
ATAGTCCAGTGTTTTATTTCTTCAATGGCTAATATCTATAATGAAAGATACTGAAGGAGGGGAACAGCTCACT  
GAAAGCATCTTCATACAGAACAGCAAACCTCTATTCTTTGGCATTCTGTTAATGGGCTGACTCTGGGCCTTCAG  
AGGAGTAACCGTGATCAGATTAAGAACTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCCCTTATTTTT  
GTAAGTCGATTTCCAGGGCCTTTCAGTGGCTTTTCATTCTGAAGTTCTGGATAACATGTTCCATGTCTTGATGGCC  
CAGGTTACCCTGTCTATCACAACAGTGTCTGTCTGCTGCTTGTGACTTCAGGCCCTCCCTGGAATTTTTCTTG  
GAAGCCCCATCAGTCTTCTCTCTATATTTATTTATAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGG  
CAAGAAAGGATCCGAGATCTAAGTGGCAATCTTTGGGAGCGTCCAGTGGGGATGGAGAAGAACTAGAAAGACTT  
ACCAAACCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCAGCTCTCTTGAAC  
CTTATTTTTACATTTTTCAGTGTGTGTAATATTTATCTTTTCAGTTTGATAAACAGAAATGTTTCTAAATCCTAA  
TATTCTTTGCATATATCTAGCTACTCCCTAAATGGTTCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTC  
TAAAGAACTGATACAGGAGTAACAATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATAT  
GTGCAGATTATTTTCCCTTGGCCTTCAAGCTTCCAAAAAAGCTTGAATAATCATGTTAGCTATAGCTTGTATATAC  
ACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGTCTTCCCTTTTTAACA  
TTATAAAAGCTAGGTTGTCTCTTGAATTTTGAGGCCCTAGAGATAGTCATTTTGCAAGTAAGAGCAACGGGACC  
CTTTCTAAAAACGTTGGTTGAAGGACCTAAATACCTGGCCATACCATAGATTGGGATGATGTAGTCTGTGCTAA  
ATATTTTGCTGAAGAAGCAGTTTCTCAGACACAACATCTCAGAATTTTAATTTTGAAGAAATTCATGGGAAATTGG  
ATTTTTGTAATAATCTTTTGATGTTTTAAACATGGTTCCCTAGTACCATAGTTACCCTTGTATTTTAAGTCA  
TTTAAACAAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGATGTCTATTCTCCTGAATTA  
TTACATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTTACTAATTCAGCTGTGACTATTGTATATCTTTCC  
AAGAGTTGAAATGCTGGCTTCAGAATCATACCAGATTGTGAGTGAAGCTGATGCCTAGGAACCTTTAAAGGGATC  
CTTTCAAAGGATCACTTAGCAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAA  
AGACCAGTAATATATAAGTCACTTTACAGTGTACTTCACACTTAAAGTGCATGGTATTTTTCATGGTATTTTG  
CATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAATAATTAGCAAACAAAAGTGAC  
TTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGGCTTTAACTGGCAGGCCTGTATGTTTACAGACTAC  
CATACTGTAATATAGAGCTTTATGGTGTCTATTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTC  
ATGCAGATGAATATAAGGTAATATACTATTATATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAAT  
TGGTGGAATTTGTAATTAATAATTATTAACCT

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**FIGURE 8**

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSSELVKLVFCVLVSFCVIK  
KDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAVIFS NFSIITTALLFRIVLKRRLNWIQ  
WASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFFSPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFS  
HIRLGMGHVLIIVQCFISSMANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFY  
GHSAFSVALIFVTAFOGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNA  
SKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLT KPKSDEDEDTF

**Transmembrane domains:**

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293, 298-318,  
328-368

**N-glycosylation sites.**

amino acids 128-132, 204-208, 218-222, 374-378

**Glycosaminoglycan attachment site.**

amino acids 402-406

**N-myristoylation sites.**

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

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**FIGURE 9**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATGAGCAGGTCTG  
AAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGTTGGTGGTTTCAGCAAGGCCTCAGTTTC  
CTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACTCCACCAT  
ATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTA  
AATATTGCGGCAGTTTATGCATTGCTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAG  
AACGTTATCATCAAATTAACAAGGCTGGCCTTGTACTTGGAACTACTGAGTTGTTTAGGACTTCTATTGTGGCA  
AACTTCCAGAAAACAACCCCTTTTGTGTCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCATTATAT  
ATGTTTGTTCAGACCATCCTTTCCTACCAAATGCAGCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTG  
TTGTTGGTTATCTGGTGTGGAGTAAGTGCACTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTT  
GGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACTACTGCA  
GCAGAATGGTCTATGTCATTTTCTTCTTTGGTTTTTTCCTGACTTACATTTCGTGATTTTCAGAAAATTTCTTTA  
CGGGTGGAAGCCAATTTACATGGATTAACCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGG  
CTACTTTCAGAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG  
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCT  
GATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTATTAAAAACA  
CCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

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**FIGURE 10**

MWWFQQGLSFLPSALVIWTSAAFI FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATYVRY  
KQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFGMGSLYMFVQTILSYQMOPKI  
HGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLT  
YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTRLLSRDI

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**FIGURE 11**

CCCACGCGTCCGCCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGGCCGGGGTGC GGAG  
CCGACATGCGCCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCACCTTCGCCTTGCTACTTGCTGTGACGC  
GACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGGAGGCTGGAGGCAGGTGCGTGTGGTTCCTTCCGACCTGG  
CAGAGCTGCGGGAGCTCTCTGAGGTCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTCTGCTCTTCT  
GCGGCGCTACCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCTTGT  
TTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGCTGCTACCTGCTCTCCA  
GTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGTGGCCCTGCTGCAGAGAAAGGTGGAGGAGA  
ACAGAAACAGCTTGTTTTTTTTCTTATTGTTTTTGAGACTTTTCCCCATGACACCAAACCTGGTTCTTGAACCTCT  
CGGCCCCAATTCTGAACATTCCCATCGTGCAGTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAATTTCA  
TCTGTGTGCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTCTCCTGGGACACTGTCTTTA  
AGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCCTCATTAAAAAATTTAGTCAGAAACATCTGCAAT  
TGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGACACATTGATCTGGATTTTTCTGTTTGCCACATCC  
CTGGACTCAGTTGCTTATTTGTGTAATGGATGTGGTCTCTAAAGCCCCCTCATTGTTTTTGATGCTTCTATAG  
GTGATGTGGACACTGTGCATCAATGTGCAGTGTCTTTTCAAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATC  
AGGTTTTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGTGGCCGGGCG  
CGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGATTCAACAAGGTGAGGAGTTCAAGACC  
AGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAATACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGT  
AATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGAT  
CACACCACTGCACTCCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

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**FIGURE 12**

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYRKEHQAYVFLFCG  
AYLYKQGFAIPGSSFLNVLAGALFGPWLGLLCCVLTSVGATCCYLLSSIFGKQLVVSYPFDKVALLRKVEENR  
NSLFFFLFLRLFPMTPNWFLNLSAPILNIPIVQFFFSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKL  
LAIAMVALIPGTLIKKSQKHLQLNETSTANHIHSRKDT

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 101-123, 189-211

**N-glycosylation sites.**

amino acids 172-176, 250-254

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 240-244, 261-265

**N-myristoylation site.**

amino acids 13-19, 104-110, 115-121, 204-210

**Amidation site.**

amino acids 27-31

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 4-15

**Protein splicing proteins.**

amino acids 25-31

**Sugar transport proteins.**

amino acids 162-172

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**FIGURE 13**

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACCGTGTGAG  
GGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTCCTTACACTTCGCCA  
TGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCA  
TGCGCCAATTGTTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTT  
CTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACTGGA  
AAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTACATTGGCTATTTTATTGTGAGCA  
ATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGCTCTTATGGCTGACCTTTATGTATTTCTTCTGGA  
AACTAGGAGATCCCTTTCCCATTTCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTG  
GTGTGATTGGAGTGACTCTCATGGCTCTTCTTCTGGATTTGGTGCTGTCAACTGCCCATACACTTACATGTCTT  
ACTTCTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGATCA  
TAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACAAACCATCAG  
GTTTCTGGGGAATGATAAAAAGTGTACCACTTCAGCATCAGGAAGTGAAAATCTTACTCTTATTCAACAGGAAG  
TGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAG  
AATACTCCAAAACCTTCAAGGGGAAATATTTTAATTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAA  
TTTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGCATTGAGATCA  
CTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATTTCTTTCATTCTTGTGGAATAA  
TCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCT  
CCAATGTCAATTGTCTGCTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGA  
GTATGCCTTTAGAATACCGCACCATAATCACTGAAGTCCTTGGAGAAGTGCAGTTCAACTTCTATCACCGTTGGT  
TTGATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACAGAGA  
AGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTAGATATAAGAGG  
GGGGAATAATGGAACAGGGCCTGACATTTTATAAACAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGC  
ATACTCCTTCCCCGTAGGTGATACTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAATACTCAA  
GACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGCCAAGAACTAAAG  
GTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTA  
AGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATTTAAATCAGAGACTGTAACAAAAA  
AAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCATGGCCCACTTGTTTATTG  
CAGCTTATAATG



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**FIGURE 14**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGVLNSSSRYPFW  
KMNLGVILLILVFMVFPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFFWKLGDPPILSPKHGILSIEQLISRV  
GVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPS  
GFWGMIKSVTTSASGSENLTLLIQQEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFGLGYFFSIYCVWK  
IFMATINIVFDRVGKTDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKS  
SNVIVLLLAQIMGMVFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSAALSSILFLYLAKHQAPE  
KQMAP

**Important features:****Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398, 425-444

**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160

**FIGURE 15**

CACGGAAGAAGACAGCGCTCCCGAGGCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCGGGACATGCGGCC  
 CAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGCTGCTGCTGCCGCCGCCGCCGTGCCCTGCC  
 CACAGCGCCACGCGCTTCCGACCCCCACCTGGGAGATCCCTGGAGCSCCGCCAGCTGCCCGCGTGGTTTGACCAAGGCC  
 AAGTTCCGGCATCTTCACTCACTGGGAGTGTTCCTCGGCCAGCTTCGGTAGCAGTGGTTCTGGTGGTATTGG  
 CAAAAGGAAAAAGATACCGAAGTATGTGAATTTTGAAGATAATACCCTCCTAGTTTCAAAATATGAAGATTTT  
 GGACCACTATTTACAGCAAAATTTTTTAATGCCAACCACTGGGCAGATATTTTTCAGGCCTCTGGTGCCAAATAC  
 ATTGCTTAACTTCAAACATCATGAAGGCTTTACCTTGTTGGGGGTGAGAATATTCGTGGAAGTGAATGCCATA  
 GATGAGGGGCCCCAAGAGGGACATTGTC AAGGAACCTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTGGA  
 CTGTACTATTCCCTTTTTGAATGGTTTTCATCCGCTCTTCCTTGAGGATGAATCAGCTTCATTCCATAAGCGGCAA  
 TTTCCAGTTTCTAAGACATTGCCAGACTCTATGAGTTAGTGAACAACTACAGCTAGGTTCTGTGGTCCGAT  
 GGTGACGGAGGAGCACCCGATCAATACTGGAACAGCACAGGCTTCTTGGCTGGTTATATAATGAAAGCCCGATT  
 CGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCATCTGTAAGCATGGTGGCTTCTATACCTGCAGT  
 GATCGTTATAACCCAGGACATCTTTGCCACATAAATGGGAAACTGCATGACAATAGACAAACTGTCCTGGGGC  
 TATAGGAGGGAAGCTGGAATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTATAGACAGTTTCA  
 TGTGGAGGAATCTTTTGATGAATATTGGGCCCACATAGATGGCACCATTCTGTAGTTTTGAGGAGCGACTG  
 AGGCAAGTGGGGTCTTGCTATAAAGTCAATGGAGAAGCTATTTTATGAAACCTATACCTGGCGATCCCGAATGAC  
 ACTGTCAACCCAGATGTGTGGTACATCATCCAAGCCTAAAGAAAAATTAGTCTATGCCATTTTTCTTAAATGGCCC  
 ACATCAGGACAGCTGTTTCCTTGCCATCCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGA  
 CAGGCACTTAACTGGATTTCTTTGGAGCAAAATGGCATTATGGTAGAAGTGCCACAGCTAACCATTCATCAGATG  
 CCGTGTAATGGGGCTGGGCTCTAGGCCCTAACTAATGTGATCTAAGAGTGCAGCAGAGTGGCTGATGCTGCAGTT  
 ATGTCTAAGGCTAGGAATCATCAGGTGCTATAATTGTAGCATCATGGAGAAAGCAATGAAACTGGATAAGAAAA  
 TTATTTTGGCAGTTTCCAGCCTTTCCCTTTTTCCCACTGAAATTTTTCTTAAATTACCCATGTAACCATTTTTAACTCT  
 CCAGTGCACTTTGCCATTAAAGTCTCTTACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTCA  
 CATATAGTAGCAAGGAATTGGTGGTATTATGGACCGAAGTAAAAATTTATGTTGAAGCCATATCCCCCATGAT  
 TATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGCTAGTCAATTTTTTTTTGTGCCAA  
 CATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACACACCTAATGTGTATGGTATAGACTGTG  
 CTCCTAGGCTACAGACATATACAGCATGTTACTGAATCTAGTAGGCAATAGTAAACGTGGTATTGTATATCGAA  
 ACATATGGAACATAGAGAAGGTACAGTAAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCAC  
 GAATGGAGCTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTATTGAA  
 CACTGCCAGACGTTATAAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAGTTTTTCTTCTTCAATT  
 ATAAATTAACATAAGTGTACTGTAACTTTACAAACGTTTTAATTTTTTAAACCTTTTTGGCTCTTTTGTAAATAAC  
 ACTTAGCTTAAACATAAACTCATTGTGCAAAATGTA

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**FIGURE 16**

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDEPTWESLDARQLPAWFDQAKFGIFIHWGVSFVSFGSEWFW  
WYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQASGAKYIVLTSKHHEGFTLWGSEYSWNW  
NAIDEGPKRDIVKELEVAIRNRDRLRFGLYSLFEWFHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVL  
WSDGDGGAPDQYWNSTGFLAWLYNESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKL  
SWGyrREAGISDYLTIIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYTWRS  
QNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWISLEQNGIMVELPQITI  
HQMPCCKGWALALTNI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319, 375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

**FIGURE 17**

[illegible]

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**FIGURE 18**

MKFLLDIILLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSKL  
VLWDINKHGLEETAACKCKGLGAKVHTFVVDSCNREDIYSSAKKVKAIEIGDVSILVNNAGVVYT  
SDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYCSSK  
FAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMHGILT  
EQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

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**FIGURE 19**

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGAT  
GCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCTCTGCCCGCCAGCCCGCTCCACCGCCGTAG  
CGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGGCC**ATG**AGGCCGGGAACCGCGCTACAGGCCG  
TGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCCTCGG  
ATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTATAAAG  
TCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCTGCAGGA  
GGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAAAAGTTCA  
TTGAAAACCTCTTGCCATCTGATGGTGA CTCTGGATTGGGCTCAGGAGGCGTGAGGAGAAAC  
AAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATATCACAATTTA  
GGAAGTGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATGTACCATCAGC  
CATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGACCGGTGCAACA  
TGAAGAACAATTTCAATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTTCTAGAGAAGCTG  
AAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAGGAAGAAGATGCCA  
AAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACATCCTAATCCCCAGCA  
TTCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTTGGATCTGTAGAAAAA  
GAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATCTGGCCCTCTCCTCACC  
AGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACAAAGCGAAGCTGACTTAG  
CTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTTGCGGGAGAAGCCACTCCCG  
ATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCAGAAAGTGGGTTTGTGACTC  
TGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGAGTTCTCCCCAGACCAAATGG  
GGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATGGTTAT**TAG**GACATATAAAAAA  
CTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATCCTCTTATTTTCTATAAGGAAAA  
TACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCTGTGGATGAGCATGTGGTCCCCACGA  
CCTCCTGTTGGACCCCCACGTTTTTGGCTGTATCCTTTATCCCAGCCAGTCATCCAGCTCGACC  
TTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTAGAGTCTCAATAAATGTCACCTGGTT  
GGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTGGCAGTGATAAAGATGGGCTGTGGAGC  
TTGGAACACACCTCTGTTTTCTTGTCTATACAGCAGCACATATTATCATAACAGACAGAAA  
ATCCAGAATCTTTTCAAAGCCCACATATGGTAGCACAGGTGGCCTGTGCATCGGCAATTCTC  
ATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGAGCAGGAAAAAAAAA

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**FIGURE 20**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQRPCYKVIYFHDTSRRLN  
FEEAKEACRRDGGQLVSI ESEDEQKLIKFIENLLPSDGD F WIGLRRREEKQSNSTACQDLYA  
WTDGSISQFRN WYVDEPSCGSEYCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE  
KPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLLLVVTTV  
VCWVWICRKRKREQPD PSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDLKNISF  
RVCSGEATPD DMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKESGWVENE  
IYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

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**FIGURE 21**

AGGCTCCCGCGCGGGCTGAGTGCGGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAACACGCG**ATG**ACCA  
CGTGGAGCCTCCGGCGGAGGCCGGCCCGCACGCTGGGACTCCTGCTGCTGGTCTGCTTGGGCTTCCTGGTGCTCC  
GCAGGCTGGACTGGAGCACCTTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA  
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT  
GGAGGGACCGCCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCCCTCACCACCTATGTTCCGTGGAACCTGCATG  
AGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCTGATGGCCGCAGAGATCG  
GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGCCAGCTGGCTAC  
TCCAAGACCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTCACCGAAGCAGTGGACCTTATTTTGACCACC  
TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG  
GTTCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGACCGTGGCATTGTGGAACCTGC  
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCAGT  
CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT  
ACTGGACGGGGTGGTTTGACTCGTGGGGAGGCCCTCACAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGT  
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG  
GAGCCATGCACTTCCATGACTACAAGTCAGATGTCAACAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG  
ATTACACGGCCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTTCCCTCCCCACCTG  
ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC  
TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCCT  
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG  
TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTTGGTGGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG  
GCTTAATTGGAATCTCTATCTGAATGATTACCCCTGAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA  
GCTTCTTTTCAAGGTTTCGGCCTGGACAAATGNGTTCCCTCCGAGAAACACCCACATTACCTGCTTTCTTCTTGG  
GTAGCTTGTCCATCAGCTCCACGCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA  
TCAATGGCCAGAACCTTGACGTTACTGGAACATTGGACCCAGAGACGCTTTACCTCCCAGGTCCCTGGTTGA  
GCAGCGGAATCAACCAGGTCACTGTTTTTGGAGAGACGATGGCGGGCCCTGCATTACAGTTACGGAAACCCCC  
ACCTGGGCAGGAACCACTACATTAAG**TG**AGCGGTGGCACCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCTC  
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG  
ACTGGGGGCTACAGTCTGCCCTGTCTCAGCTCAAAACCCCTAAGCTGCAGGGAAAGGTGGGATGGCTCTGGGCC  
TGGCTTTGTTGATGATGGCTTTCCTACAGCCCTGCTCTTGTGCCGAGGCTGTCTGGGCTGTCTTAGGGTGGGAGC  
AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGCTGAAACGTGCCCTTGACCCGGACGTACAGCCC  
TGCGAGCATCTGCTGGACTCAGGCGTGCTCTTTGCTGGTTTCTGGGAGGCTTGGCCACATCCCTCATGGCCCCAT  
TTTATCCCCGAAATCCTGGGTGTGTACCAAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT  
CTTCCTTCAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGACTTCCCTT  
TCCCTTCCACTCGCTGCTTCCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCTCACCTGCGTCTTCC  
CAAGTTAGCAGGTGTCTGCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCC  
AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGGA  
GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGG  
ACAGAAGGCCAGCTCAGTGGCCCCCGCTCCCCACCCCCACGCCGAACAGCAGGGGAGAGCAGCCCTCCTTC  
GAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCTGTA  
GTTGCAGTAAAGCTATAACCTTGAATCACA



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**FIGURE 22**

MTTWSLRRRPARTLGLLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFWI  
FGGSIHYFRVPREYWRDRLKMKACGLNTLTITYVPWNLHEPERGKFDFSGNLDLEAFVLMMAE  
IGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMSRVVPLQYKR  
GGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLLTSDNKDGLSKGIVQGVLATINLQ  
STHELQLLTTFLEFNVQGTQPKVMMEYWTGWFDWGGPHNILDSEVLKTVSAIVDAGSSINLY  
MFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIPLPPPPD  
LLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFYIYETSITSSG  
ILSGHVHVRGQVFVNTVSIQFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGENIDDQRKGL  
IGNLYLNDSPKFNRIYSLDMKKSFFQRFGLDKWXSLETPETLPAFFLGSLSSSTPCDTFLK  
LEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPALQFTETPHLG  
RNQYIK

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

**FIGURE 23**

[illegible]

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**FIGURE 24**

MNSSKSSETQCTERGCFSQMFLLWTVAGIPILFLSACFITRCVVTFRI FQTCDEKKFQLPENF  
TELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQEF  
LSYKKPKMREFFIGLSDQVVEGQWQWVDGTP LTKSLSFWDVGEPNNIATLED CATMRDSSNPR  
QNWNDVTCFLNYFRICEMVGINPLNKGKSL

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

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**FIGURE 25**

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACCC  
TGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGGGG  
AGCAAAGCCGGGCTCGGCCCCGAGGCCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATCCGA  
CACGTGACGCTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCC**ATG**GCTCCCAAGA  
AGCTGTCTTGCCTTCGTTCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCAGGCAG  
AACTCGGTGCTTCGTAGTGGATAGGGGTGATGACCGGTTTCTCCTAGACGGGGCCCCGTTCC  
GCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCGGACCGGCTTT  
TGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTATGTGCCCTGGAACACCACGAGC  
CACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGAATGAGGCAG  
CTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAGTGGGAGATGG  
GGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTCAGATCCAGACT  
TCCTTGCCGCACTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATCCATGGCTTTATC  
ACAATGGGGGCAACATCATTAGCATTGAGGTGGAGAATGAATATGGTAGCTACAGAGCCTGTG  
ACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCGTGCACTGCTAGGAGAAAAGATCTTGC  
TCTTACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGGGACTCTATACCACTG  
TAGATTTTGGCCCAGCTGACAACATGACCAAAATCTTTACCCTGCTTCGGAAGTATGAACCCC  
ATGGGCCATTTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTACTGGGGCCAGAATCACT  
CCACACGGTCTGTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGCTCAAGTTGGGAGCCAGTG  
TGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGGAATGGTGCCGATAAGAAGG  
GACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACCTATATCTGAAGCAGGGGACC  
CCACACCTAAGCTTTTGTCTCTTCGAGATGTCATCAGCAAGTTCCAGGAAGTTCTTTGGGAC  
CTTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTGACTCTGCACCTGGTTGGGCATT  
TACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCATTCATTCAATCTTGCCAATGACCT  
TTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACCGAACCTATATGACCCATACCATTT  
TTGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTCCATGACCGTGCCTATGTGATGGTGG  
ATGGGGTGTTCCAGGGTGTTGTGGAGCGAAATATGAGAGACAAACTATTTTGGACGGGGAAAC  
TGGGGTCCAAACTGGATATCTTGGTGGAGAACATGGGGAGGCTCAGCTTTGGGTCTAACAGCA  
GTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTGGGGCAAACAATCCTTACCCAGTGGATGA  
TGTTCCCTCTGAAAATTGATAACCTTGTGAAGTGGTGGTTTCCCCCTCCAGTTGCCAAAATGGC  
CATATCCTCAAGCTCCTTCTGGCCCCACATTCTACTCCAAAACATTTCCAATTTTAGGCTCAG  
TTGGGGACACATTTCTATATCTACCTGGATGGACCAAGGGCCAAGTCTGGATCAATGGGTTTA  
ACTTGGGCCGGTACTGGACAAAGCAGGGGCCACAACAGACCCTCTACGTGCCAAGATTCTGC  
TGTTTCCCTAGGGGAGCCCTCAACAAAATTACATTGCTGGAACTAGAAGATGTACCTCTCCAGC  
CCCAAGTCCAATTTTGGATAAGCCTATCCTCAATAGCACTAGTACTTTGCACAGGACACATA  
TCAATTCCCTTTCAGCTGATACACTGAGTGCCTCTGAACCAATGGAGTTAAGTGGGCAC**TGAA**  
AGGTAGGCCGGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTG  
GATTACCTGAGGTGAGGACTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTA  
AAAATACAAAATTAGCCGGGCGTGATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTG  
AGGGCAGGAGAATTGCTTGAATCCAGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTG  
CACTCCAGCCTGGCTGACAGTGAGACACTCCATCTCAAAAAAAAAAAAA

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**FIGURE 26**

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDGRGHDRFLLDGAPFRYVSGSLHYFRVPRVLW  
ADRLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYICA  
EWEMGGPLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENEYGS  
YRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIFTLLR  
KYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMYMFHGGTNFGYWNG  
ADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMMLGPVTLH  
LVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPNNGVHDRA  
YVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKPPILGQTIL  
TQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFYLPGWTKGQVW  
INGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLDKPILNSTSTL  
HRTHINSLSADTLSASEPMELSGH

**Signal sequence:**  
amino acids 1-27

**N-glycosylation site.**  
amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 4-8

**Casein kinase II phosphorylation site.**  
amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**  
amino acids 191-198

**N-myristoylation site.**  
amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

**FIGURE 27**

[illegible]

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**FIGURE 28**

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYQG  
ASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQDKE  
HDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQVCA  
EQAAVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPRHRRL  
HRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDRCDAGW  
LADGSVRYFPVVHHPNCGPPEPGVRSFGFPDQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**amino acids 36-42, 184-190, 208-214, 237-243, 297-303,  
307-313

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**FIGURE 29**

GCAAGCGGCGAAATGCGGCCCTCCGGGAGTCTTGACGTTCCCCTGGCAGTCCTGGTGCTGTTG  
CTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTCCGCGTCATCACGGACGAGAAC  
TGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCTTGT  
CAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAATATT  
GCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTCTTCCT  
ACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAGAAGGAC  
TTCATAAACTTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCGTTTCATCATGGTTTGGT  
CCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGATCAGGACG  
TGCCATAACTACTTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACTGTTTTTGCT  
TTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGCAGATTGCCTT  
TGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAATTATTATCAGAA  
TCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAAGATGTTTCAGAA  
GAAGAAGCTGAAAGTAAAGAAGGAACAACAAGACTTTCCACAGAATGCCATAAGACAACGC  
TCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAGTTATCTTAATATTA  
TGATTTTGATAAAAACAGAAGATTGATCATTTTGTGGTTTGAAGTGAAGTGTGACTTTTTT  
GAATATTGCAGGGTTCAGTCTAGATTGTCAATTAATTGAAGAGTCTACATTCAGAACATAAAA  
GCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATGGTTTAAATAGTTCTCTA  
ATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGTTTAATAATAACCTATTTT  
AAGTCTGAGTTTTGAAAATTTACATTTCCCAAGTATTGCATTATTGAGGTATTTAAGAAGATT  
ATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTTCTCTGTTTCACTGTGTGAAAAAAG  
AAGATATTTCCCATATAATGGGAAGTTTGGCCATTGTCTCAAGAAATGTGTATTTTCAAGTACAA  
TTTCGTGGTCTTTTTTAGAGGTATATTCCAAAATTTCTTGTATTTTTAGGTTATGCAACTAAT  
AAAACTACCTTACATTAATTAATTACAGTTTTCTACACATGGTAATACAGGATATGCTACTG  
ATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTCCAACAAAGTTTGATTTTCTCTTGT  
ATTTTTCTTACTTACTATGGGTACATTTTTTATTTTTCAAATTTGGATGATAATTTCTTGGAA  
ACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGTTGTTTCAAAGTGAAGTTTACTGAGAGA  
TCCATCAAATGAACAATCTGTTGTAATTTAAAATTTTGGCCACTTTTTTTCAGATTTTACATC  
ATTCTTGCTGAAGTTCAAGTTGAAATGTTTTTTTTTCTTTTTGGATGTGAAGGTGAACATT  
CCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTATTTTACATTTGAAAATTCAAAGAAGCTT  
AATATAAAAGTTTGCATTCTACTCAGGAAAAAGCATCTTCTGTATATGTCTTAAATGTATTT  
TTGTCCTCATATACAGAAAGTTCTTAATTGATTTTACAGTCTGTAATGCTTGATGTTTTAAAA  
TAATAACATTTTTATATTTTTTAAAAGACAACTTCATATTATCCTGTGTTCTTTCCTGACTG  
GTAATATTGTGTGGGATTTACAGGTAAAAGTCAGTAGGATGGAACATTTTAGTGTATTTTA  
CTCCTTAAAGAGCTAGAATACATAGTTTTACCTTAAAAGAAGGGGGAAAATCATAAATACAA  
TGAATCAACTGACCATTACGTAGTAGACAATTTCTGTAATGTCCCCTTCTTCTAGGCTCTGT  
TGCTGTGTGAATCCATTAGATTTACAGTATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCC  
TTTAGAATTTAAATATTTGTACCATTAAAGAGTTTGGATGTGTAAGTGTGATGCCTTAGAAA  
AATATCCTAAGCACAAAATAAACCTTTCTAACCCTTCATTAAAGCTGAAAAAAAAAAAAAA  
AAA



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**FIGURE 30**

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNLO  
PEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFINF  
ISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFALATL  
FSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEAEDEEDVSEEEAE  
SKEGTNKDFPQNAIQRSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

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**FIGURE 31**

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGATTTCGGTGCCGCGACTTTCACGATGGC  
TCGCCCCAACCTTACTACCTTCTGTGCGGCCCTGCTCTCTGCTGCCCTTCCTACTCGTGAGGAAAC  
TGCCGCGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTGACT  
GGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGATCCA  
TCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAATTCTTT  
TCTTCCGCTTGATATTTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTCTCTGATGA  
CGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAAACCATTG  
ATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAATTGGTCTA  
ATGACTGCCAATCATTTGCCCCCTATCTATGCTGACCTCTCCCTTAAATACAACGTGTACAGGGC  
TAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTACAAAGTGAGCA  
CATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAAGGAGGCAATGC  
GGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTGAGGAGAATGTGA  
TCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCAAAGGCTGGAGACA  
ATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGATGGGGAAAACAAGA  
AGGATAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATTCCAGGCTCTTTCCAT  
AACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGGCTGNGACTGGNTGGGG  
CAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAGGCACCCTACAGGAAGGC  
CTGCCATGCTGTGGCCAACGTGTTTCACTGGAGCAAGAAAGAGATCTCATAGGACGGAGGGGGA  
AATGGTTTTCCCTCCAAGCTTGGGTCAGTGTGTTAACTGCTTATCAGCTATTCAGACATCTCCA  
TGGTTTTCTCCATGAACTCTGTGGTTTCATCATTCTTCTTAGTTGACCTGCACAGCTTGGTT  
AGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAACGCTAAGAATTTTCCCCCAAG  
GACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTCTTCATTAAGTATAAGCCTAA  
CTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAGTTTTTATCATTGAAGACAATATT  
GAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAATAGAGGCTTGAGACTTTCCTTTGT  
GTGGTAGGACTTGAGGAGAAATCCCCTGGACTTTCACTAACCTCTGACATACTCCCCACAC  
CCAGTTGATGGCTTTCCGTAATAAAAAGATTGGGATTTTCCTTTTG

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**FIGURE 32**

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFDW  
REVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFLMT  
CKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPYADLSLKYNCTGL  
NFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSEENV  
REFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

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**FIGURE 33**

CGGACGCGTGGGGTGCCCGAC**ATG**GCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGCG  
GCAGCGGCGGCGGCGGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGGCA  
CTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGAGAG  
GTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTGAGTACTGAATCCC  
AACAGGCAGACCATTTATTTAGGGACTTCAGGCCCTTTGAAGGACAGCAGGTTTCAGTTGCTG  
AATTTTTCTAGCAGTGAATCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAAGGAAGA  
TACTTTTGCCAGCTCTATACCGATCCCCCACAGGAAAGTTACACCACCATCACAGTCCTGGTC  
CCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGGAGATTGAA  
GTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAAGGGAACACA  
GAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGACCAGTCAGCTG  
ATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGGAGCACCTGCG  
GTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCTCAAGTGCACATT  
CAGATGACTTATCCTCTACAAGGCTTAACCCGGAAGGGGACGCGCTTGAGTTAACATGTGAA  
GCCATCGGGAAGCCCCAGCCTGTGATGGTAACCTGGGTGAGAGTCGATGATGAAATGCCTCAA  
CACGCCGTACTGTCTGGGCCCAACCTGTTTCATCAATAACCTAAACAAAACAGATAATGGTACA  
TACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTATATGCTGTATGTATAC  
GATCCCCCCCACAACTATCCCTCCTCCCACAACAACCACCACCACCACCACCACCACCACC  
ACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGCTCGATCAGGGCAGTGGAT  
CATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCATGCTGTGCTTGCTCATCATT  
CTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTCATGAAGCCAAAGGAGCCGAT  
GACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGAGGACAGAACAACCTCCGAAGAA  
AAGAAAGAGTACTTCATC**TAG**ATCAGCCTTTTTGTTTCAATGAGGTGTCCAACCTGGCCCTATT  
TAGATGATAAAGAGACAGTGATATTGG

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**FIGURE 34**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCO
VNSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVSISDEGRYFCQLYT
DPPQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTTELKGKSE
VEEWSDMYTVTSQMLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLO
GLTREGDALELTCEAIGKPQPMVMTWVRVDDEMPQHAVLSGPNLFINNLNKT DNGTYRCEASN
IVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGV
VAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
```

**Signal sequence.**

amino acids 1-36

**Transmembrane domain.**

amino acids 372-393

**N-glycosylation sites.**amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,  
430-434**Tyrosine kinase phosphorylation sites.**

amino acids 233-240, 319-328

**N-myristoylation sites.**amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,  
411-417, 427-433, 428-432

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**FIGURE 35**

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTTGTCTCAGGAGGAGACAGCCTCCCGGCCCGGGGAG  
GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCCGTTTCTGCCGTCTAGCTGCCCGGCCG  
AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCTGCTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGG  
AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT  
TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCTGTAATCGCAAAACCCATTTTGGAGCAGGAATTCCAATCA  
**TG**TCTGTGATGGTGGTGAGAAAGAAGTGACACGGAATGGGAGAACTCCCAGGCAGGAACACCTTTTGCTGTG  
ATGGCCCGCTCATGATGGCCCGGCAAAAGGGCATTCTTCTACCTGACCTTTTCTCATCTCTGGGGACATGTACAC  
TCTTCTTCGCCCTTTGAGTGCCGCTACCTGGCTGTTCTGAGCTGTCTCTGCCATCCCTGTATTTGCTGCCATGCTCT  
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCTGGAGTGATTCTCGGGCGCTACCAGATG  
AAGCAGCTTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCGAGGGCCAGCGACCAACCGCCTCGTA  
TCAAGAATTTCCAGATAAACAACCAGATTGTGAACTGAAATACTGTTACACATGCAAGATCTTCCGGCCTCCCC  
GGGCCTCCCATTGCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCTGGGTGGGGAATTGTG  
TTGGAAAGAGGAATACCGCTACTTCTACCTCTTCATCTTTCTCTCTCCCTCCTCACAATCTATGTCTTCGCCT  
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAAATTGGCTTCTTGGAGACATTGAAAGAACTCCTGGAAGT  
TTCTAGAAGTCTCATTGCTTCTTTACACTCTGGTCCGTCGTGGGACTGACTGGATTTCATACTTTCTCTGCTG  
CTCTCAACCAGCAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC  
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGTGTGTGGCCCTTGCCCCCAGTGCTGCTGGATCGAAGGGGTA  
TTTTGCCACTGGAGGAAAGTGAAGTCGACCTCCCAGTACTCAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC  
CAGCCCCACAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG  
AGCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAG**TAG**CCTATCTATGGAAGAGACTTTTGTGTTGTGTT  
TAATTAGGGCTATGAGAGATTTTCAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT  
GTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTGGCATTCTTCTGCTGCAAGCTTTTTTAAATTTCTGA  
CAAGGCAGTGGCAGAAAGATGTGAGTCACTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCT  
CCATGGCCTCAGCCACAGGGTCCCCTTGGACCCCTCTCTTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTCTC  
TGGTCTCATTTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA  
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG  
TGGGGTCAAGAAATTCTCCTGGCCACCAAGTGCCAGCATTGCCACAAATCCTTTAGGAATGGGACAGGTACCT  
TCCACTTGTTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTTCTTTGACTCCTGCTCCCATTAGGAG  
CAGGAATGGCAGTAATAAAAGTCTGCACTTTGGTCATTTCTTTTCTCAGAGGAAGCCCGAGTGCTCACTTAAAC  
ACTATCCCCCTCAGACTCCCTGTGTGAGGCCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG  
GCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAAAAATGCTAACCAGTTCTTCCATTAAAGCCT  
CGGCTGAGTGAGGGAAAGCCAGCACTGCTGCCCTCTCGGTAAGTCAACCTAAGGCCTCGGCCACCTCTGGCT  
ATGGTAACCACACTGGGGCTTCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTT  
CACCTGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTAGGGAAGAAGATTTATGT  
ATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGATGACTTAT  
CGGGTGGGGGAGTGTAACCGGAACTTTCATCTATTTGAAGGCGATTAACTGTGTCTAATGCA

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**FIGURE 36**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTFLFLILGTCTLFFAFECRYLAVQ  
LSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPPRI  
KNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGKRNYRYFYLFIL  
SLSLLTIYVFAFNIVYVALKSLKIGFLETCLKETPGTVLEVLI CFFTLWSVVGLTGFHTFLVAL  
NQT TNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSRPPSTQ  
ETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPPEPPQEAAEAEK

**Putative transmembrane domains:**

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

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**FIGURE 37**

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCGCGTCACTGCG  
TCCTGGCTCCGGCTCCCGCGCCCTCCCGGCCGCGCCATGCGAGCCCCGCGCGCCAGGCGCCGGTGCGCAGCTGC  
TGCCCCGCGCTGGCCCTGCTGCTGCTGCTGCTCGGAGCGGGGCCCCGAGGCAGCTCCCTGGCCAACCCGGTGCCCG  
CCGCGCCCTTGTCTGCGCCCGGGCCGTGCGCCGCGCAGCCCTGCCGGAATGGGGGTGTGTGCACCTCGCGCCCTG  
AGCCGGACCCGCGACACCCGGCCCCCGCGCGAGCCTGGCTACAGCTGCACCTGCCCGCGGGGATCTCCGGCG  
CCAACTGCCAGCTTGTGTCAGATCCTTGTGCCAGCAACCCCTGTCAACATGGCAACTGCAGCAGCAGCAGCAGCA  
GCAGCAGCGATGGCTACCTCTGCATTTGCAATGAAGGCTATGAAGGTCCCAACTGTGAACAGGCACCTTCCAGTC  
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCCGACAGCTTCAGCCTGTTCCCTGCTACTCAGGAGCCTGACA  
AAATCCTGCCTCGCTCTCAGGCAACGGTGACACTGCCTACCTGGCAGCCGAAAACAGGGCAGAAAAGTTGTAGAAA  
TGAAATGGGATCAAGTGGAGGTGATCCAGATATTGCCTGTGGGAATGCCAGTTCTAACAGCTCTGCGGGTGGCC  
GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTCCGCAAGATGCCACTGCCCTCACTGATTTTGC  
TCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTTCAGGCTT  
CAGGGGGACTGGTCCCTCCTGGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATTGGTTTTGTGAATGATTCTG  
TGACTAAGTCTATTGTGGCTTTGCGCTTAACTCTGGTGGTGAAGGTGAGCACCTGTGTGCCGGGGGAGAGTCACG  
CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGCACCACGAAGCCGTGAGAGGCAACTTTTTCTGTACCTGTG  
AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATAACGATGCTTGCCAGAGGAAAACCTTGCCAAAACAACGCGAGCT  
GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCTGGTTATACTGGAGAGCTTT  
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT  
TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTCGCCTCGTCTCCGT  
GCCAGAACAACGGCACCTGCTATGTGGACGGGTACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGA  
CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCCCTGTGCTCATGGCACGTGCCGACGGTGGGCACACAGCT  
ACAAATGCCTCTGTGATCCAGGTTACCATGGCCTCTACTGTGAGGAGGAATATAATGAGTGCCCTCTCCGCTCCAT  
GCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTGTGCCTGGCAGAATACAAAGGAACAC  
ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTGAGTGTCTGAACGGAGCCACCTGTGACAGCGACGGCCTGA  
ATGGCACGTGCATCTGTGCACCCGGGTTTACAGGTGAAGAGTGGCAGATTGACATAAATGAATGTGACAGTAACC  
CCTGCCACCATGGTGGGAGCTGCCCTGGACCGCCCAATGGTTATAACTGCCACTGCCCGCATGGTTGGGTGGGAG  
CAAATGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCACATGCCACGGCCTCCC  
TCTACATCATCATTGGAGCCCTCTGCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGGATTTGCCGCA  
TCAGCCGCATTGAATACCAGGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAACCTGCCCGCAGCATCGACAGCG  
AGTTCAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTTGGAAAGAAATCCCGGCCCTGCAATGTATGATGTGA  
GCCCCATCGCCTATGAAGATTACAGTCTGATGACAAACCTTGGTCACTGATTAAACTAAAGATTTGTAAT  
CTTTTTTTGGATTATTTTTTCAAAAAGATGAGATACTACACTCATTTAAATATTTTTTAAGAAAATAAAAAGCTTAA  
GAAATTTAAATGCTAGCTGCTCAAGAGTTTTTCAGTAGAATATTTAAGAATAATTTTCTGCAGCTTTTAGTTTG  
GAAAAATATTTTAAAAACAAAATTTGTGAAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAACTGT  
GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCACGAGACCCAGATTAATTTCTGTGGTTGTTACA  
GAATAAGTCTAATCAAGGAGAAGTTTCTGTTGACGTTTGTAGTGCCGGCTTCTGAGTAGAGTTAGGAAAACCAC  
GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAAGTCTGAAATGTTGTTTTGTGAAA  
AGAACTAGTTAAATTTACTATTCCTAACCGAATGAAATTAGCCTTTGCCTTATTCTGTGCATGGGTAAGTAAC  
TTATTTCTGCATGTTTTGTTGAACCTTGTGGAACATTTCTTCGAGTTTGTTTTTGTCAATTTTCGTAACAGTCG  
TCGAACTAGGCCCTAAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAATTCGATTGATTTGAATCTATATTT  
TTCTTTAAAAAGTCAAGGGTTCTATATTGTGAGTAAATTAATTTACATTTGAGTTGTTTGTGCTAAGAGGTAG  
TAAATGTAAGAGAGTACTGGTTCCTTCAGTAGTGAGTATTTCTCATAGTGCAGCTTTATTTATCTCCAGGATGTT  
TTTGTGGCTGATTTTGATTGATATGTGCTTCTTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC  
AAGTCA



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**FIGURE 38**

><subunit 1 of 1, 737 aa, 1 stop  
><MW: 78475, pI: 5.09, NX(S/T): 11  
MQPRRAQAPGAQLLPALALLLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSRP  
EPDPQHPAPAGEPGYSCTCPAGISGANQQLVADPCASNPCHHGNCSSSSSSSSSDGYLCICNEG  
YEGPNCEQALPSLPATGWTESMAPRQLQVPATQEPDKILPRSQATVTLPTWQPKTGQKVVEM  
KWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQQCSL  
IDGRSVTPLQASGGLVLLLEMLALGNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPGESHAN  
DLECSGKGKCTTKPSEATFSCCTCEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQDGSNFTC  
VCLPGYTGELCQSKIDYCIDLPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPCASSPCQN  
NGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPGYHGLYCEE  
EYNECLSAFCLNAATCRDLVNGYECVCLAELYKGTCELKDPKANVSCNLGATCDSDGLNGTC  
ICAPGFTGEECDIDINECDSNPCHHGGSCLDQPNGYNCHCPHGWVGANCEIHLQWKS GHMAES  
LTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYNCRSIDSEFSNA  
IASIRHARFGKKS RPAMYDVSP IAYEDYSPDDKPLVTLIKTKDL

**Signal sequence.**

amino acids 1-28

**Transmembrane domain.**

amino acids 641-660

**N-glycosylation sites.**amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,  
375-379, 442-446, 549-553, 564-568**Glycosaminoglycan attachment site.**

amino acids 320-324

**Tyrosine kinase phosphorylation sites.**

amino acids 490-498, 674-682

**N-myristoylation sites.**amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,  
373-379, 449-455, 480-486, 562-568, 565-571**Amidation site.**

amino acids 702-706

**Aspartic acid and asparagine hydroxylation site.**

amino acids 520-532, 596-608

**EGF-like domain cysteine pattern signatures.**amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,  
491-503, 529-541, 567-579, 605-617

**FIGURE 39**

[illegible]

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**FIGURE 40**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979
><subunit 1 of 1, 204 aa, 1 stop
><MW: 22147, pI: 8.37, NX(S/T): 3
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NCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLR FVGGIGLFFSFTEILGVWLTyr
YRNQKDPRANPSAFL
```

**Signal Peptide:**  
amino acids 1-34

**Transmembrane domains:**  
amino acids 47-63, 72-95 and 162-182

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**FIGURE 41**

CAGTCACCA**ATGA**AGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTGC  
TCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGTCT  
GCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCTTCC  
AGGTCAAGGCCTACACTTTCAGTGAACCTTCCACCTGATTGTGTCCTATGACTGGCTGATCC  
TCCAAGGTCCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTCTGCGCTGCCAGGCCTGGC  
AAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCCCGGGC  
CTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCACTGCAGTG  
GCATCTTCCAGAGCCCTGGTCCTGGGATCCCAGAAACAGCATCTGTTGTGGCTATCACAGTCC  
AAGAAGTGTTCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAGCAGGAAGCC  
CCATGACCCTGAGTTGTCAGACAAAGTTGCCCTGCAGAGGTCAGCTGCCCGCCTCCTCTTCT  
CCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATTCAGATCCCCA  
CAGCTTCAGAAGATCACTCCGGGTCACTACTGGTGTGAGGCAGCCACTGAGGACAACCAAGTTT  
GGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCTGCTGCACCTCCA  
CATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACTGCTCCTGAGGAGGCCCTGGGC  
CTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTTCTCCTCTGGGGATGC  
CAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATGCAGGATGTGAGAGTCC  
TCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCAGAAGCCTGGGACCACAA  
AGGCTACTGCTGAAT**AGA**AGTAAACAGTTCATCCATGATCTCACTTAACCACCCCAATAAATC  
TGATTCTTTATTTTCTCTTCTCCTGTCTGCACATATGCATAAGTACTTTTACAAGTTGTCCAG  
TGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTTATATAAAGTGAGAATTAGAG  
TTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTCTGCTGTCTAGATCAGGAATTT  
CTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAACTAATGGAAGTGGATTGAATAC  
AGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACATTGGGCAATGTTTGGAGACATTT  
TGGTCATTATACTTGGGGGGTTGGGGGATGGTGGGATGTGTGTCTACTGGCATCCAGTAAATA  
GAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAGGGCAGTACCCACACGAAAAATAA  
TCTGGCCCCAAATGTCAGTTGTACTGAGTTTGAGAAACCCAGCCTAATGAAACCCTAGGTGT  
TGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTATTATCTCTTCCAGCCTCATTTCAGCTAT  
TCTTACTGACATACCAGTCTTTAGCTGGTGCTATGGTCTGTTCTTTAGTTCTAGTTTGTATCC  
CCTCAAAGCCATTATGTTGAAATCCTAATCCCCAAGGTGATGGCATTAGAAGTGGGCCTTT  
GGGAAGTGATTAGATCAGGAGTGCAGAGCCCTCATGATTAGGATTAGTGCCCTTATTTAAAAA  
GGCCCCAGAGAGCTAACTCACCTTCCACCATATGAGGACGTGGCAAGAAGATGACATGTATG  
AGAACCAAAAAACAGCTGTCGCCAACACCGACTCTGTCGTTGCCTTGATCTTGAAGTTCCAG  
CCTCCAGAACTATGAGAAATAAAATTCTGGTTGTTTGTAGCCTAA

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**FIGURE 42**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359.aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMAWALYLSLGVWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQVK
AYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGPNR
EFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMT
LSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVWKQ
SPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSSEDPGFSSPLGMPDP
HLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE
```

**Signal sequence:**

amino acids 1-17

**Leucine zipper pattern sequence:**

amino acids 12-33

**Protein kinase C phosphorylation site:**

amino acids 353-355

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**FIGURE 43**

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTTAACTAATTCAACAAACGGGACCCTTC  
TGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGGAA  
GGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGCATT  
GCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCTTCACCTCTATTGGGCA  
CATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATCCTTGT  
GGAGGAAGCCAAGCTTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGACTAGCAA  
GTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAACTGGTGAAGCG  
GCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCAGGTTTTAT  
CGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGGAGCTGCCAA  
AGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCAGAGGGGAACT  
TCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATGGGCCGCTCGGC  
CTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCTAAAGCAGCTTGA  
TGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCAGCTATGCTGTCTT  
CCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCTGCTCTCCCTTGACCCAAG  
CCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGAGGAAGAGAGAGAAAA  
AACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAAGGCATCTATGAGAGGCCTGT  
GGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGTTGGGAGGGGTGTCAAACCTGAC  
ACCCCGTAGACAGAAGAGGGCTTTTTCTGTAGGTACCACCATGGCAACAGGGCCCCACAGCTGCT  
CATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACATCGTCAGGTACTACGATGT  
CATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAACCTAAACTTGCACGAGCCAC  
CGTTCGTGATCCCAAGACAGGAGTCTCACTGTGCGCCAGCTACCGGGTTTTCCAAAAGCTCCTG  
GCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATCGTCGGATGCAGCATATCACAGG  
GTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAATTATGGAGTGGGAGGACAGTATGA  
ACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGGCCTCAAAACAGAGGGGAATAGGTT  
AGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTGGTGGTGCCACCGTCTTCCCTGATCT  
GGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTGTTCTGGTACAACCTCTTGCGGAGCGG  
GGAAGGTGACTACCGAACAAGACATGCTGCCTGCCCTGTGCTTGTGGGCTGCAAGTGGGTCTC  
CAATAAGTGGTTCCATGAACGAGGACAGGAGTTCTTGAGACCTTGTGGATCAACAGAAGTTGA  
CTGACATCCTTTTCTGTCTTCCCCCTTCCTGGTCTTCAGCCCATGTCAACGTGACAGACACC  
TTTGTATGTTCTTTGTATGTTCTATCAGGCTGATTTTTGGAGAAATGAATGTTTGTCTGGA  
GCAGAGGGAGACCATACTAGGGCGACTCCTGTGTGACTGAAGTCCAGCCCTTCCATTACAGCC  
TGTGCCATCCCTGGCCCCAAGGCTAGGATCAAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGC  
CTAGCAAGGTGCCTTTGTACCTCAGGTGTTTTAGGTGTGAGATGTTTCAGTGAACCAAAGTTC  
TGATACCTTGTTTACATGTTTGTTTTTATGGCATTCTATCTATTGTGGCTTTACCAAAAAAT  
AAAATGTCCCTACCAGAAAAA

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**FIGURE 44**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWAN  
KMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFPTD  
EDEIGAALKMRLQDQTYRLDPGTISRGEIPGTYQAMLSVDDCFGMGRSAYNEGDDYYHTVLWM  
EQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRLLSLDPSHERAGGNLRYFEQ  
LLEEEREKTLTNQTEAELATPEGIYERPVDYLPERDVYESLCRGEVVKLTTPRRQKRLFCRYHH  
GNRAPQLLIAPFKEEDEWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTGVLTVAS  
YRVSKSSWLEEDDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFSRRPFDSG  
LKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYRTRHAACPV  
LVGCKWVSNKWFHERGQEFRLPCGSTVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

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**FIGURE 45**

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGGG  
CGGCGGGCGCGGGTGCGAGGGATCCCTGACGCCCTCTGTCCCTGTTTCTTTGTCGCTCCCAGCC  
TGTCTGTCTGTCGTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTGCGACACCGATCCTGGGC  
TTCGCTCGATTTGCCGCCGAGGCGCCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAGCGGG  
TCGTCTGTGTCCTCTCTCCTCTGCGCCGCGCCCCGGGGATCCGAAGGGTGCGGGGCTCTGAGGA  
GGTGACGCGCGGGGCTCCCGCACCCCTGGCCTTGCCCGCATTCTCCCTCTCTCCAGGTGTGA  
GCAGCCTATCAGTCACCA**ATG**TCCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTGTGTCTGC  
TGCTGTGCGCGGGGCGCGGGCAGCGAGGGAGCCGCTCCCATTTGCTATCACATGTTTTACCA  
GAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGGCTGCCCTCTTGAGG  
AATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGGGCTGCTGTCC  
ACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACCTGGTCGAGAAA  
ACTATTCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGATGGTCTGCTTCTT  
TCACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCAGTGTCCACAGCAC  
ATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGGCAATAAAGATTGTA  
AAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGCGCCGATTTAATTTAC  
AGAAGAATTTTGTGGGAAAGTGGCTCTAATGTTGGGAATTGGAACAGAAGGACCACATGTGG  
GCCTT**G**TTCAAGCCAGTGAACATCCCAAATAGAATTTTACTTGAAAACTTTACATCAGCCA  
AAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTAATCCAATACAGGAAAAG  
CCTTGAAGCATACTGCTCAGAAATCTTCACGGTAGATGCTGGAGTAAGAAAAGGATCCCCA  
AAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACATCGAGGAAGCAGGCATTGTGG  
CCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCAAGCCTATCCCTGAAGAACTGG  
GGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGTGCGGAATAATGGCTTCTTCTCTT  
ACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAAGCCTCTGGTACAGAAGCTGTGCA  
CTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACTCAGTGAACATTGCCTTTCTAATTG  
ATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTCATGCTTGAATTTGTTTCCAACATAG  
CCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGATAGCTGCTGTACAGTTTACTTATGATC  
AGCGCACGGAGTTTCACTTCACTGACTATAGCACCAAAGAGAATGTCCTAGCTGTATCAGAA  
ACATCCGCTATATGAGTGGTGGAAACAGCTACTGGTGATGCCATTTCTTCACTGTTAGAAATG  
TGTTTGGCCCTATAAAGGGAGAGCCCCAACAAAGAACTTCTAGTAATTGTCACAGATGGGCAGT  
CCTATGATGATGTCCAAGGCCCTGCAGCTGCTGCACATGATGCAGGAATCACTATCTTCTCTG  
TTGGTGTGGCTTGGGCACCTCTGGATGACCTGAAAGATATGGCTTCTAAACCGAAGGAGTCTC  
ACGCTTTCTTCACAAGAGAGTTTACAGGATTAGAACCAATTGTTTCTGATGTCATCAGAGGCA  
TTTGTAGAGATTTCTTAGAATCCCAGCAA**TAAT**GGTAACATTTTGACAACTGAAAGAAAAAGT  
ACAAGGGGATCCAGTGTGTAAATTGTATTCTCATAATACTGAAATGCTTTAGCATACTAGAAT  
CAGATACAAAACCTATTAAGTATGTCAACAGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCG  
CTGCCTTCTGGTTACAATTTACAGTGTACTTTGTTAAAAACACTGCTGAGGCTTCATAATCAT  
GGCTCTTAGAACTCAGGAAAGAGGAGATAATGTGGATTAAACCTTAAGAGTTCTAACCATG  
CCTACTAAATGTACAGATATGCAAATTCATAGCTCAATAAAAGAATCTGATACTTAGACCAA  
AAAAAAA



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**FIGURE 46**

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEF SVYG  
NIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVTKG  
KSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDKADIAFLIDGSFNIGQRRFNLQKNFVG  
KVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLEFAIKEVGFRGGNSNTGKALKHTA  
QKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELGMVQDV  
TFVDKAVCRNNGFFSYHMPNWF GTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLIDGSSSV  
GDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTFESFTDYSTKENVLAVIRNIRYMS  
GGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITIFSVGVAWA  
PLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532**N-myristoylation site.**amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449**Amidation site.**

amino acids 145-149

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**FIGURE 47**

GCCCCGCGCCCGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCC**ATG**GGGGCCTGCCTGGGAG  
CCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCT  
GCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCTCTTCCTGG  
GGGTGCTGGTGTCCATCATTATGCTGAGCCCCGGGCGTGGAGAGTCAGCTCTACAAGCTGCCCT  
GGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGGCTCCC  
TGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCTTCTTTT  
TCACCCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAGAATGGGT  
TTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTCATCCCTGACG  
GCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCTTCTCATCCCTCATCC  
AGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCGGTCGGTGGCTGGGCAAGGCCGAGG  
AGTGCGATTCCCGTGCCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTTCTCTGTGT  
CGATCGCGGCGCTGGCGCTGATGTTTCACTACTGAGCCAGCGGCTGCCACGAGGGCA  
AGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGTCTGCCCCA  
AGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTTCATCACCCTCTACACCA  
TGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTTGCCAA  
CCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCGAGGGCTATGAGACCCAGTGGTGGGATG  
CCCCGAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTTCATCAGTCTGCGCTCCT  
CAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCA  
CACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCCTTTGACAACGAGCAGGACG  
GCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGTGGCCTCACTGCACGTCATGA  
TGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGATGATCAGCACGTGGACCGCCG  
TGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTCTACCTGTGGACCCTGGTAGCCC  
CACTCCTCCTGCGCAACCGCGACTTCAGCT**TGA**GGCAGCCTCACAGCCTGCCATCTGGTGCCTC  
CTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTCCCCACACCAATCAGCC  
AGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTGCCCCCTGAGCCGGGCCTTCTAGTCGT  
AGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCACACCCAC  
ACGGTGGAGCTGCCTCTTCCTTCCCCTCCTCCCTGTTGCCCATCTCAGCATCTCGGATGAAA  
GGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACTCCCACC  
ACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCACGTCCCCCAGGGGACCCCTGCC  
CCCTTCCTGGACTTCGTGCCTTACTGAGTCTCTAAGACTTTTCTAATAAACAAGCCAGTGCG  
TGTAATAAAAAA

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**FIGURE 48**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVES  
QLYKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPR  
AAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSWNQR  
WLKAEECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVCS  
IAAVLPKVQDAQPNSSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGY  
ETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRA  
FDNEQDGVITYSYSFFHFCLVLASLHVMMTLTNWYKPGETRMISTWTAVVWKICASWAGLLLY  
LWTLVAPLLLNRNDFS

**Signal sequence:**

amino acids 1-20

**Transmembrane domains:**amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

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**FIGURE 49**

[illegible]

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**FIGURE 50**

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSS  
SCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKSRR  
KRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKGTQK  
LRVGFLKPKFKDGGRGANDSTSAMPEQMKEQWIRVKRTHVPKGWIKGNANDIGMDYDYALLEL  
KKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGA  
SGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNYL  
DCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

**FIGURE 51**

GGGAGGGGGCTCCGGGGCCCGCGCAGACAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCTCCGGGAGCGGCAG  
CAGTAGCCCGGGCGGCAGAGGGCTGGGGGTTCTCTCGAGACTCTCAGAGGGGCGCCTCCCATCGGCGCCCACCACCC  
CAACCTGTTTCTCTCGCGCGCCACTGCGCTGCGCCCCCAGGACCCCGCTGCCCAACATGGATTTTCTCTGGCGCTGGT  
TGCTGTATCTCGCTCTACCTGCAGGCGGCCCGGAGTTCGACGGGAGGTGGCCCAAGGCAATAGTGTATCATCGAT  
GCGCTATGTGCGTTATGTGTGGGAGGATTACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTCAAGCC  
TGTGTGCCAACACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTATCCTGGTTATGCTGG  
AAAAACCTGTAATCAAGATCTAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTA  
CGGCAGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCTGTCTCAAGTGCCCTGACCTG  
CTCCATGGCAAACTGTCAGTATGGCTGTGATGTTTATAAGGACAAATACGGTGCCAGTGGCCATCCCCTGCCCT  
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCTGGCCCTAGATT  
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTATAAAGGCTTCGATCTCATGTATATTGGAGG  
CAAATATCAATGTATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTTGCTCGATGTTATAA  
CGTACGTGGGTCCTACAAGTGCAAATGTAAAGAAGGATACCAGGGTGATGGACTGACTTGTGTGTATATCCCAA  
AGTTATGATTGAACCTTCAGGTCCAATTGATGTACCAAAGGGAATGGTACCATTATAAGAGGTGACACAGGAAA  
TAATAATTTGGATTCTCTGATGTTGGAAGTACTTGGTGGCTCCGAAGACCATATATATCTCCTCATATTACCA  
CAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATTCTACTCCACCACCACCACCACC  
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACACCACCGGACTGACAACTATAGC  
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACCCCTCAGAAACCCAGAGG  
AGATGTGTTTCAGTGTTCTGGTACACAGTTGTAATTTTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA  
TGACTTGCACCTGGGAACCAATCAGGAGACCCAGCGAGGTGGACAATATCTGCAGTGTGGCAGCAAAGGCCGAG  
GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCTCATGCATTACAGGGGACCTGTGCCTGTCAATCAGGCA  
CAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTGTTTGTGAGAAAACAGGTGCCACGGAGCAGCCCTGTG  
GGGAAGAAATGGTGCCCATGGCTGGAGGCAACACAGATCACCTTTCGAGGGGGCTGACATCAAGAGCGAATCACA  
AAGATGATTAAGGGTTGAAAAAAGATCTATGATGAAAAATTAAGGAACCTGGGATTATTGAGCCTGGAGAAG  
AGAAGACTGAGGGGCAACCATGATGTTTTCAAGTATTAAGGGTTGGCAGAGAGGGTGGCCAGCAGCTG  
TTCTCCATATGCACTAAGAATAGAACAAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGCAGG  
GGCCATTGTTAGAACTCTCATAAAAAAAGAGTGTGAAAATCTCAGTATCTCTCTCTTTCTAAAAAATTAGA  
TAAAAAATTGTCTAATTTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAATAAACAAATTATAGAAATTTCCCAA  
AGATGTTTTGATCCTACTAGTAGTACGTGAAATCTTTAGAACTAAATAAATTTGGACAAAGGCTTAATTTAGG  
CATTCCCTCTTGACCTCCTAATGGAGGGGATTGAAAGGGGAAGAGCCCAACATGCTGAGCTCACTGAAATA  
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGATGGAC  
AGATATTTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCC  
TTTCATTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTTAAAGAGATCCTTCAAGGAACACAGTTCAGAGAG  
ATTTTCATCGGGTGCAATCTCTCTGCTCGTGTGACAAGTTATCTTGCTGCTGAGAAGAGTGCCTGCCCGCC  
ACACCGGCAGACCTTTCCTTCACTCATCAGTATGATTCAGTTTTCTCTTATCAATTGGACTCTCCGAGGTTCCAC  
AGAACAGTAATATTTTTTGAACAATAGGTACAATAGAAGGTCTTCTGTCAATTAACCTGGTAAAGGCAGGGCTGG  
AGGGGGAAAAATAATATATAAGCCTTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTTTTTAATGGTTCATT  
TCCTTTATGGTCATATAACTGCACAGCTGAAGATGAAGAGGGGAAAAATAAATGAAATTTTTACTTTTCGATGCCAA  
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAGTACTGTATAACATCTTGTTTATTATTATGTTT  
CTAAAAATAAAAAATGTTAGTGGTTTTCCAATGGCCTAATAAAAAACAATTTATTGTAAATAAAAAACTTGTAGTAAT

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**FIGURE 52**

MDFLLALVLVSSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQPR  
CKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGS  
CSSALTCSMANCQYGCDVVKGQIRCQCPSPLHLAPDGRTCVDVDECATGRASCPRFRQCVNT  
FGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQGDGLT  
CVYIPKVMIEPSGPIHVPKNGTILKGD TGNNNWIPDVGSTWWPPKTPYIPPIITNRPTSKPT  
TRPTPKPTPIPTPPPPPLPTELRTPLPPTTTERPTTGLTTIAPAASTPPGGITVDNRVQTD  
QKPRGDFVSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLVL  
PLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIK  
SESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

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**FIGURE 53**

CGGGCCGCCCCCGGCCCCCATTCGGGCGGGCCTCGCTGCGGGCGGCGACTGAGCCAGGCTGGG  
CCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAGCC  
CAGCTGTCAGCCGCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGTGCA  
TGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGGTCCC  
TGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCCCTGA  
GCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACAGCTGGT  
GCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCCTCTTCCC  
GGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCTGCGTGTGGCGGACGAGGG  
CAGCTTCACCTGCTTCGTGAGCATCCGGGATTTTCGGCAGCGCTGCCGTGAGCCTGCAGGTGGC  
CGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGCCAGGGGACAC  
GGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTCTGGCAGGATGG  
GCAGGGTGTGCCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGAGCAGGGCTTGTT  
TGATGTGCACAGCGTCTGCGGGTGGTGTGGGTGCGAATGGCACCTACAGCTGCCTGGTGGC  
CAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCCACCATCACAGGGCAGCCTATGACATT  
CCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCATTGCACTGCTGGTGGC  
CCTGGCTTTCGTGTGCTGGAGAAAAGATCAAACAGAGCTGTGAGGAGGAGAATGCAGGAGCTGA  
GGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCTCTGAAACACTCTGACAG  
CAAAGAAGATGATGGACAAGAAATAGCCTGACCCATGAGGACCAGGGAGCTGCTACCCCTCCCT  
ACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCCTGCCCCAACAGATGCATC  
CTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACACAGACCACTGTGCAGCCTTAT  
TTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTTTTCTTATAGACACAATGAACA  
GACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCTGCCTTATTTTACAGTACATACA  
TTTCTTAGGGACACAGTACACTGACCACATCACCACCCTCTTCTTCCAGTGCTGCGTGGACCA  
TCTGGCTGCCTTTTTTCTCCAAAGATGCAATATTCAGACTGACTGACCCCTGCCTTATTTT  
ACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTTCTCCAATGGCCGTGATACACTAGTGA  
TCATGTTTACGCCCTGCTTCCACCTGCATAGAATCTTTTCTTCTCAGACAGGGACAGTGCGGCC  
TCAACATCTCCTGGAGTCTAGAAGCTGTTTCCTTTCCCTCCTTCCCTCCCTGCCCCAAGTGAA  
GACAGGGCAGGGCCAGGAATGCTTTGGGGACACCGAGGGGACTGCCCCCACCCTACCATGG  
TGCTATTCTGGGGCTGGGGCAGTCTTTTCCTGGCTTGCTTCTGGCCAGCTCCTGGCCTCTGGT  
AGAGTGAGACTTCAGACGTTCTGATGCCTTCCGGATGTCATCTCTCCCTGCCCCAGGAATGGA  
AGATGTGAGGACTTCTAATTTAAATGTGGGACTCGGAGGGATTTTGTAAGTGGGGGTATATT  
TTGGGGAAAATAAATGTCTTTGTAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 54**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQL
NLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQVRVVADEGSFTCFVSI
RDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGGQVPLTGN
VTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVARNPVLQQDAHXSVTITGQPMTFPPEALWVT
VGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGEKSTALQPLKHSKEDDGQEI
```

**Important features:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 251-270

**N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

**Homologous region to Immunoglobulins and MHC**

amino acids 217-234

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**FIGURE 55**

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTG  
GCT**ATG**TTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTT  
CTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAG  
TGTGACCACGTGCAATATACGCTGGTTCAGTTTCTGGGTGGCAAGAACTTGAAACTGCATTT  
CTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTA  
TTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGGCCAGTC  
AATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAACAAGATGATGACCTT  
GAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATTCAGGAAAT  
GACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATAGTGGAGCAA  
ACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCTCTTTGACTAC  
GAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGGCTTGGATGCTG  
TCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGACCAGTGGGTGCAA  
GACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCAGCGCCACGTTTCCCGC  
CACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCACACGGATCTCCTTT  
GAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGACAGCCTGTGCAACACC  
AGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAAGCGGCTCCAGGAGTTC  
CTTGACAGCATGGGTCTTCCCCTGAAGCAGGTGAAGCAGAAGTTCCAGGCCATGGACATCTCC  
TTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAATAAATTTGGGATGAAGGACATG  
CGCGTGACAGACTTTCAGCATTCATTTTGGGTTCAAGCACAAGTTTCTGGCCAGCGACGTGGTC  
TTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCTCAGGGACAGATCACTTCATC  
CAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTGTACCATGGCCTGGAACTCGCC  
AAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGCCTTTGCACCAACCTCGTCATC  
TCCCAGGGGCCTTTCTGTACTGCTCTCTCATGGAGGGCACTCCAGATGTCATGCTGTTCTCT  
AGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCAAGTCCTTTGTGTGTTGACAAAG  
AACCGGCGCTGCAAACCTGCTGCCCCTGGTGATGGCTGCCCCCTGAGCATGGAGCATGGCACA  
GTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTCGGACAGGAAGAACTTTTGGGAGG  
GCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGATGCTGCACAACCATTTGACCTCTCA  
GTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTTCTGGACGCACTTATTTCCCTCCTGTCC  
**TAGGA**ATTTGATTCTTCCAGAATGACCTTCTATTTATGTAAGTGGCTTTCATTTAGATTGTA  
AGTTATGGACATGATTTGAGATGTAGAAGCCATTTTTTATTAAATAAAATGCTTATTTTAGGAAA

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**FIGURE 56**

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELET AFL  
EHKEQFHYFILINCGANVDLLDILQPDEDTIFFVCDSHRPVNVNVYNDTQIKLLIKQDDDL E  
VPAYEDIFRDEEEDEEHSGNDS DGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILFDYE  
QYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRHVSRH  
NHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKRLQEFL  
ADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFLASDVVF  
ATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQT IASCLCTNLVIS  
QGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAPLSMEHGT V  
TVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNFHDL SVIELKAEDRSKFLDALISLLS

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**FIGURE 57**

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGGC  
CCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTGCGCTTGCTGACGGCGTCGAG  
CCCTGGCCAGAC**ATG**TCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACCGTG  
GCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAACCCCT  
TCTGTGGGGCTCAATTTTGGAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTGCTCCT  
TCAAGTGGTTTTGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTAGGAGGA  
ACAAATACAGGTGCCTTGACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCCTGCAA  
GGAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTAGGAGTCCCCTTCTCCAGA  
CCTCCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAAGGAATCAGA  
GATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCGCAGGCTGGAGTGCAGTGGCA  
CGATCTCGGCTCACTGCAACCTCCGCCTCCGGGTTCAAGCGAGTCTCCTGCCTCAGCCTCTG  
AGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCGATGTACGTACGC  
ACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCTGAACGTGTACGCG  
CCGGCGCGCGCGCCCGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCCTCGGGAGGCGCCTTC  
ATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCGCGAGAAAGTGGTGCTG  
GTGTTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGACGACAGCCACGCGCGC  
GGAACTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGCAGGAGAACATCGCAGCC  
TTCGGGGGAGACCCAGGAAATGTGACCTGTTTCGGCCAGTCGGCGGGGGCCATGAGCATCTCA  
GGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCAGAGTGGCACC  
GCGTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGGTTGCCACCTG  
GCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGCCTGAGGGCACTATCAGGGACC  
AAGGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCAAGTGAACCTCCAGAGAGACCCGGAA  
GAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGGTGTATCCAGATGACCCCTTTGGTG  
CTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTTCTAGGTGTCAACAACCTGGAATTC  
AATTGGCTCTTGCCTTATAATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGAGTACCTG  
GACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGGACATAGTTCAAGAT  
GCCACTTTCGTGTATGCCCACTGCAGACTGCTCACTACCACCGAGAAACCCCAATGATGGGA  
ATCTGCCCTGCTGGCCACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAA  
GAGTGGGCAT**TGA**AGCTCAAGGAGAAGAAGATGGCTTTTGGATGAGTCTGTACCAGTCTCAA  
GACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCAGGAAGGAGCCAAAGAGGGGTTTGC  
CCCCACCATCCAGGCCCTGGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA  
CCCCAGTTTAGAAGTGCAGGAGCTCCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGT  
TGTGTGGGACCTGCAGTCCCCTTTCCAGCCTGACATCCCATGATGCCCCTCTACTTCACTGTT  
GACATCCAGTTAGGCCAGGCCCTGTCAACACCACACTGTGCTCAGCTCTCCAGCCTCAGGACA  
ACCTCTTTTTTTCCCTTCTTCAAATCCTCCCACCTTCAATGTCTCCTTGTGACTCCTTCTTA  
TGGGAGGTGACCCAGACTGCCACTGCCCCCTGTCACTGCACCCAGCTTGGCATTATACCATCCA  
TCCTGCTCAACCTTGTTCCTGTCTGTTCCACATTGGCCTGGAGGCCCTAGGGCAGGTTGTGACAT  
GGAGCAAACCTTTTGGTAGTTTGGGATCTTCTCTCCACCCACACTTATCTCCCCAGGGCCAC  
TCCAAAGTCTATACACAGGGGTGGTCTCTTCAATAAAGAAGTGTTGATTAGAAAAA

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**FIGURE 58**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPSSGF
GTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVPFSRPPLG
ILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLSVWG
YRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAFIVGA
ASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGD
PGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVAHLACGN
HNSTQILVNCRLRALSCTKVMRVSNKMRFLQLNFQRPDEEI IWSMSPVVDGVVIPDDPLVLLTQ
GKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDATEFV
YATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA
```

**Important features:****Signal peptide:**

amino acids 1-29

**Carboxylesterases type-B serine active site.**

amino acids 312-327

**Carboxylesterases type-B signature 2.**

amino acids 218-228

**N-glycosylation sites.**

amino acids 318-321, 380-383 and 465-468

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**FIGURE 59**

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGGTCCCCGAGCGTCCCGCGCCCTC  
GCCCCGCC**ATG**CTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTTCGCAGG  
AAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAGTCA  
GACTGTTGCAGAGGCTGAAAACCAAACCTTTGATGACAGAATTCTCAGTGAAGTCTACCATCA  
TTTCCCGTTATGCCTTCACTACGGTTTCCTGCAGAATGCTGAACAGAGCTTCTGAAGACCAGG  
ACATTGAGTTCCAGATGCAGATTCCAGCTGCAGCTTTCATCACCAACTTCACTATGCTTATTG  
GAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGGGTAAAAG  
AGAAAAGGAATAAAACACAGAAAGAAAATGGAGAGAAGGGGACTGAAATATTCAGAGCTTCTG  
CAGTGATTCCCAGCAAGGACAAAGCCGCCTTTTTCCTGAGTTATGAGGAGCTTCTGCAGAGGC  
GCCTGGGCAAGTACGAGCACAGCATCAGCGTGC GGCCCCAGCAGCTGTCCGGGAGGCTGAGCG  
TGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCCGCTTCACAACA  
GCAGGCAGAGGGGCGAGTGGGCGCGGGGAAGATGATTCTGGGCCTCCCCATCTACTGTCTATTA  
ACCAAAATGAAACATTTGCCAACATAATTTTTTAAACCTACTGTAGTACAACAAGCCAGGATTG  
CCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAGAGAACAGAGCATTG  
GGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTAAAGACCTTCCTCCTT  
TACCCAAGAATGTGGTATTCGTGCTTGACAGCAGTGCTTCTATGGTGGGAACCAAACCTCCGGC  
AGACCAAGGATGCCCTCTTCACAATTCTCCATGACCTCCGACCCAGGACCGTTTTCAGTATCA  
TTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACTTGATATCAGTCACTCCAGACAGCA  
TCAGGGATGGGAAAGTGTACATTACCATATGTCACCCACTGGAGGCACAGACATCAACGGGG  
CCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCACAGTGGCATTTGGAGACCGGA  
GCGTGTCCCTCATCGTCTTCTGACGGATGGGAAGCCCACGGTCGGGGAGACGCACACCCCTCA  
AGATCCTCAACAACACCCGAGAGGGCCGCCGAGGCCAAGTCTGCATCTTACCATTGGCATCG  
GCAACGACGTGGACTTCAGGCTGCTGGAGAACTGTCGCTGGAGAACTGTGGCCTCACACGGC  
GCGTGCACGAGGAGGAGGACGCAGGCTCGCAGCTCATCGGGTCTACGATGAAATCAGGACCC  
CGCTCCTCTCTGACATCCGCATCGATTATCCCCCAGCTCAGTGGTGCAGGCCACCAAGACCC  
TGTTCCCCAACTACTTCAACGGCTCGGAGATCATCATTGCGGGGAAGCTGGTGGACAGGAAGC  
TGGATCACCTGCACGTGGAGGTCACCGCCAGCAACAGTAAGAAATTCATCATCCTGAAGACAG  
ATGTGCCTGTGCGGCCTCAGAAGGCAGGGAAGATGTCACAGGAAGCCCCAGGCCTGGAGGCG  
ATGGAGAGGGGGACACCAACCACATCGAGCGTCTCTGGAGCTACCTACCCACAAAGGAGCTGC  
TGAGCTCCTGGCTGCAAAGTGACGATGAACCGGAGAAGGAGCGGCTGCGGCAGCGGGCCCAGG  
CCCTGGCTGTGAGCTACCGCTTCCTCACTCCCTTACCTCCATGAAGCTGAGGGGGCCGGTCC  
CACGCATGGATGGCCTGGAGGAGGCCACGGCATGTCGGCTGCCATGGGACCCGAACCGGTGG  
TGCAGAGCGTGCAGGAGCTGGCACGCAGCCAGGACCTTTGCTCAAGAAGCCAAACTCCGTCA  
AAAAAAAAACAAACAAAACAAAAAAAAAGACATGGGAGAGATGGTGTTTTTTCTCTCCACCACC  
TGGGGATACGAT**TG**AGAAGATGGCCACCTGCAAGCCAGGAAGACGGCCCTCACCAGACACCATG  
TCTGCTGGCACCTTGATCTTGACCTCCAGCCTCCAGAAGTGTGAGAAATAAATGTGTTTTG  
TTTAAGCTAAA

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**FIGURE 60**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

&lt;subunit 1 of 1, 694 aa, 1 stop

&lt;MW: 77400, pI: 9.54, NX(S/T): 6

MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQRLKTKPLMTEFSVKSTIISR  
YAFTTVSCRMLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKEKR  
NKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLSVDV  
NILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQARIAQN  
GILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMVGTKLRQTK  
DALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVYIHHMSPTGGTDINGALQ  
RAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNTREAARGQVCIFTIGIGND  
VDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVVQATKTLFP  
NYFNGSEIIAGKLVDRKLDHLHVEVTASNSKKFIILKTDVPVVRPQKAGKDVGTGSPRPGGDGE  
GDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTSMKLRGPVPRM  
DGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPPLLKKPNVKKKQNKTKKRHGRDGVFPLHHLGIR

**Signal sequence.**

amino acids 1-14

**N-glycosylation sites.**

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

**Glycosaminoglycan attachment sites.**

amino acids 213-217, 391-395

**N-myristoylation sites.**

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

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**FIGURE 61**

CAGGAACCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAACC  
ACGAAGGGGACGATACCAGAAAAACACCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTGGC  
TGACTTTTGGCTATAGAAAAAGAAAGGAACGAAAAGAGACAGTTTTTTTTTGGAAAGCTAAGTC  
TTCCCTTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAAACAATTGAGT  
AAAGTACGCTCCGGTCACCAATGGTGACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTCCTGCT  
CTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGCCAGCGG  
CTGCCAACGGTGCTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAGCCTCTTC  
CTCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCTACATTAATATCACCATCCTGAAGGG  
TGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGGTCCCCAAGG  
GGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCGGCGCCCCGTG  
CCAGAAGCGCTTCTTCGCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGCGCGAGGACTT  
CCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGACATGGCGACCGG  
CAAGTTTGTCTCTCCCTGCGTGGCATCTACTTCTTACGCCTCAATGTGCACAGCTGGAATTA  
CAAGGAGACGTACGTGCACATTATGCATAACCAAGAGAGGCTGTCATCCTGTACGCGCAGCC  
CAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGCCTACGGGGACCGCGT  
CTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAACGCCATCTACAGCAACGACTTCGACACCTA  
CATCACCTTACGCGGCCACCTCATCAAGGCCGAGGACGACTGAGGGCCTCTGGGCCACCCTCC  
CGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCCTGCAGGGCTCAGTTTGACTGCTGTGAAGC  
AGGAAGGCCAGGGAGGTCCCCGGGGACCTGGCATTCTGGGGAGACCCTGCTTCTATCTTGGCT  
GCCATCATCCCTCCAGCCTATTTCTGCTCCTCTCTTCTCTCTTGGACCTATTTTAAAGAGCT  
TGCTAACCTAAATATTCTAGAACTTTCCAGCCTCGTAGCCACGACTTCTCAAACCTTGGAAA  
TGCATGCGAATCACCCGGGGTTCGTGTTAAATGCAGATTCTGACTCAGCAGGTCTGAGTGGGT  
CCAGGATTCTGTGTTTCTCATATGTTCCCTGGGTGATGCTGATGGGGTCAGTCTATGAACCACA  
CTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAGTACTTTCTGAACATTCTGGAATCC  
TCCCCACATTCTAGAATTCTCCCAACATTTTTTTTTTCTTGAGACAGAGTCTTGCTCTGTTGCC  
CAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCAGTGAACCTCTGCCTCCCGGGTTCAAGCGA  
TTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTACAGGCGCCTGCTACCATTGCCTGGCTAAT  
TTTTGTATTTTTTAGTAGAGATGGGGTTTTACCATATTGGCCAGGCTGGTCTTGAACCTCTGAC  
TTCAGGTGACCCACCCGCTCGGCCTCTCAAAATGCTGGGATTACAGGTGTGAGCCACCGTGC  
CTGGCCAATTCCAACATTCTTAAATTCTCTCATCCCTCCAGGGCTCCCCGTGCTATGTTCTCT  
TTACCCCTTCCCCCTCTTCTCTTGCTCAGGCCTGCACCCTGCAGCCACCGTTTCAATTTATTCA  
TTCATTAAACACTGAGCACTCACTCTGTGCTGGGTCCCGGGAAGGGTGAGGGGGTCAGACACA  
GGCCCTGCCCTGCCCTCAGTGACTGGCCAGTCCAGCCCAGGCGGGGAGAGATGTGTACATAG  
GTTTTAAAGCAGACCCAGAGCTCATGGGGGCTGTGTTCTGGGTGTTTCAAGGTGCTGCTGGTCC  
TCCATTACCCACTGCTCCCCAAGGCTGGTGGGACGGGGTCCCGGTGGCAGGGGCGAGGTATCTC  
CTTCCCGTTCCCTCATCCACCTGCCAGTGCTCATCGTTACAGCAAACCCAGGGGGCCTTGGC  
CAGGTCAAGGGTTCTGTGAGGAGAGGACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGGC  
CCCCGAAGAATGGAACCCACACCCATAGCTCTCCCCACAGCTGATACGGCATCCTGCGAGAAG  
ACCTGCCCTCCTCACTGGGATCCCTTTCCTGCCTCCTCCAGGGCTCTGCCAGGGCCTTGCTC  
AGTCCCTTCCACCAAGTCATCTGAACCTCCGTTTCCCCAGGGCCTCCAGCTGCCCTCAGACA  
CTGATGTCTGTCCCCAGGTGCTCTCTGCCCTCATGCCCTCTCACCGGCCAGTGCCCCGAC  
TCTCCAGGCTTTATCAAGGTGCTAAGGCCGGGTGGGCAGCTCCTCGTCTCAGAGCCCTCCTC  
CGGCCTGGTGCTGCCTTTACAAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGA  
GCCCTCAGCAGGTCTGGGGAGCTAGAGCAAAGGAGGGACCTCAGGCCTTCCGTTTCTTCTTCC  
AGGGTGGGGTGGCCTGGTGTTCCTTAGCCTTCCAAACCCAGGTGGCCTGCCCTTCTCCCCAG  
AGGGAGGCGGCCTCCGCCCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCGGGGGGT  
GATCTCTGGTGCTCACAGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAACAGGGTCT  
GACCAAGTGCCAGGAAGACCTGTGCTATAAACCACCCTGCCTGATCCTGCCCTGCCTGACCC  
CGCCACGCCCTGCCGTCCAGCATGATTAAAGAATGCTGTCTCTTGGAAAAA



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**FIGURE 62**

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPHA  
LPEIRPYINITILKGDGDPGPMGLPGYMGREGPGQEPGPQSGKDGKMGEMGSPGAPCQKRFFA  
FSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKETIVH  
IMHNQKEAVILYAQPSEERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITFSGH  
LIKAEDD

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 72-75

**Clq domain proteins.**

amino acids 144-178, 78-111 and 84-117

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**FIGURE 63**

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGAC  
TCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCACCA  
**T**GGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTTGGCCTTG  
ATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTGTCAC  
TGCTGCCATTGAAGTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGCACTGG  
CCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCTTTAAGT  
GTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGACGAGTACC  
GCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTCGTGGAAGA  
CCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCCCAACTGGGTTC  
CAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCAGTTCGGGGAGGAGT  
TTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCACTCAGTATATG  
TGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAGTGCACAGCCTGTGGTCATAGAA  
GGGGCTACAGCTCACGCATCGTGGGTGGAACATGTCCTTGCTCTCGCAGTGGCCCTGGCAGG  
CCAGCCTTCAGTTCAGGGCTACCACCTGTGCGGGGGCTCTGTCATCACGCCCCTGTGGATCA  
TCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGACCATCCAGGTGGGTC  
TAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAGATTGTCTACCACAGCA  
AGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCTGGCCGGGGCCACTCACGT  
TCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGAACTTCCCCGATGGAAAAG  
TGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGACGCCTCCCCTGTCTGAACC  
ACGCGGCCCTCCCTTTGATTTCCAACAAGATCTGCAACCACAGGGACGTGTACGGTGGCATCA  
TCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCGTGGACAGCTGCCAGGGGGACA  
GCGGGGGGGCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAGTTAGTGGGAGCGACCAGCTTTG  
GCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACACCCGTGTCACCTCCTTCCTGGACT  
GGATCCACGAGCAGATGGAGAGAGACCTAAAAACCT**TGA**AGAGGAAGGGGACAAGTAGCCACCT  
GAGTTCCCTGAGGTGATGAAGACAGCCCGATCCTCCCCCTGGACTCCCGTGTAGGAACCTGCACA  
CGAGCAGACACCCTTGGAGCTCTGAGTTCGGGCACCAGTAGCAGGCCCCGAAAGAGGCACCCTT  
CCATCTGATTCCAGCACAACTTCAAGCTGCTTTTTTGTGTTTTTGTGTTTTTGTAGGTGGAGTCT  
CGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAATCCCTGCTCACTGCAGCCTCCGCTTCCC  
TGGTTCAAGCGATTCTCTTGCCTCAGCTTCCCCAGTAGCTGGGACCACAGGTGCCCGCCACCA  
CACCCAACTAATTTTTGTATTTTAGTAGAGACAGGGTTTTACCATGTTGGCCAGGCTGCTCT  
CAAACCCCTGACCTCAAATGATGTGCCTGCTTCAGCCTCCACAGTGCTGGGATTACAGGCAT  
GGGCCACCACGCCTAGCCTCACGCTCCTTTCTGATCTTCACTAAGAACAAAAGAAGCAGCAAC  
TTGCAAGGGCGGCCTTTCCCACTGGTCCATCTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCT  
GACGAGATAAGCAGTTATGTGACCTCACGTGCAAAGCCACCAACAGCCACTCAGAAAAGACGC  
ACCAGCCCAGAAGTGCAGAACTGCAGTCACTGCACGTTTTTCATCTCTAGGGACCAGAACCAAA  
CCCACCCTTTCTACTTCCAAGACTTATTTTACATGTGGGGAGGTAAATCTAGGAATGACTCG  
TTTAAGGCCTATTTTCATGATTTCTTTGTAGCATTTGGTGCTTGACGTATTATTGTCCTTTGA  
TTCCAAATAATATGTTTCCTTCCTCATTTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAAT  
CAAAATCATCCACTGAAA

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**FIGURE 64**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234
><subunit 1 of 1, 453 aa, 1 stop
><MW: 49334, pI: 6.32, NX(S/T): 1
MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILAL
AIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAASWK
TMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKVTALHHSVY
VREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWI
ITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLT
FNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPPLISNKICNHRDVYGGI
ISPSMLCAGYLTGGVDSCQGDSSGGPLVCQERRLWKLVGATSFQIGCAEVNKPQVYTRVTSFLD
WIHEQMERDLKT
```

**Signal Peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 240-284

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**FIGURE 65**

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCAACCCGTTAAGGTGTCTTCTCTTTAGGGATGGT  
GAGGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAG  
AACGCTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCC  
ACACAACCTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTC  
AGGAGGACTTTCTGTTTGTGTTGTCACCTTTGACCTCTTATTTCGTAACATTACTGTGGATAATA  
GAGTTAAATGTGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTAC  
TATTCTTCATATTTTGATATATTTCTTCTGGCAGTTTTTTCGATTTAAAGTGTTAATACTTGCA  
TATGCTGTGTGCAGACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCC  
TTTTTACTAGCAAAAGTGATCCTTTTCGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTG  
CCCATCATTTTCATTCATCCTTGCCCTGGATTGAGACGTGGTTCCTGGATTTCAAAGTGTTACCT  
CAAGAAGCAGAAGAAGAAAACAGACTCCTGATAGTTCAGGATGCTTCAGAGAGGGCAGCACTT  
ATACCTGGTGGTCTTTCTGATGGTCAGTTTTATTCCCCTCCTGAATCCGAAGCAGGATCTGAA  
GAAGCTGAAGAAAAACAGGACAGTGAGAAACCACTTTTAGAACTATTGAGTACTACTTTTGTTA  
AATGTGAAAAACCCTCACAGAAAGTCATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTG  
TCGACAGTAAAGTTGAAATGGTGACGTCCACTGCTGGCTTTATTGAACAGCTAATAAAGATTT  
ATTTATTGTAATACCTCACAAACGTTGTACCATATCCATGCACATTTAGTTGCCTGCCTGTGG  
CTGGTAAGGTAATGTCATGATTCATCCTCTCTTCAGTGAGACTGAGCCTGATGTGTAAACAAA  
TAGGTGAAGAAAGTCTTGCTGTATTCCTAATCAAAAGACTTAATATATTGAAGTAACACTT  
TTTTAGTAAGCAAGATACCTTTTTTATTTCATTCACAGAATGGAATTTTTTTGTTTCATGTCT  
CAGATTTATTTTGTATTTCTTTTTTAACACTCTACATTTCCCTTGTTTTTAACTCATGCACA  
TGTGCTCTTTGTACAGTTTTAAAAAGTGTAATAAAATCTGACATGTCAATGTGGCTAGTTTTA  
TTTTCTTGTTTTGCATTATGTGTATGGCCTGAAGTGTTGGACTTGCAAAAGGGGAAGAAAGG  
AATTGCGAATACATGTAAAATGTCACCAGACATTTGTATTATTTTATCATGAAATCATGTTT  
TTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGCACAAAATGACTTAAACC  
ATTCATATCATGTTTCCTTTGCGTTTCAGCCAATTTCAATTAAAATGAACTAAATTAAAAA

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**FIGURE 66**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDL  
LFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAI  
ALTTAVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQAEENRLLIV  
QDASERAALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

**Important features of the protein:****Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

**N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

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**FIGURE 67**

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCATC  
CAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCCTCTCCCGTAGCCACCCGACT  
AACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCAC  
GGGGCTCAGTCTCTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTACCTGC  
CACCTCAACGTCCTCAATGGCTCTGACGCCCCGCTGCCCTGCACCTTCAACTCCTGCTACAC  
AGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGA  
GATGTTCTCAGTTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGT  
GGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGGTGATGCTGAGAAACGTGCAGCCGGA  
GGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGGCCATGGCAA  
GATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGGCCGTGATTGT  
GGGTGCCTCCGTGCGGGGCTTCTGGCTGTGGTTCATCTTGGTGCTGATGGTGGTCAAGTGTGT  
GAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGAGGAGGGCAAGAC  
GGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCCCTGCAGCCTCCCG  
TGTCCCGTCTCCTCCCTCTCGCCCTGTACAGTGACCCTGCCTGCTCGCTCTTGGTGTGCTT  
CCCGTGACCTAGGACCCAGGGCCACCTGGGGCTCCTGAACCCCCGACTTCGTATCTCCCA  
CCCTGCACCAAGAGTGACCCACTCTCTCCATCCGAGAAACCTGCCATGCTCTGGGACGTGTG  
GGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGGGGGGAGGCAGGAGGCAC  
ATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGAGGAGGGGCCGCTGTCACC  
TGCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGGGGAGGGAGGGCTTTCTCTGT  
GCTGACAGCGCTCCCTCAGGAGGGCTTGGCCTGGCACGGCTGTGCTCCTCCCTGCTCCCA  
CCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTGAAACTTGGAGGGGCATGTTAAA  
GGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGGCTGCAGGCAAAGCTGGACATGT  
GCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATTGCTAGTGGCCTCCTTGGGGCTCC  
TGTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAGACTGGAAGAGCAGCTCCAGGTAGG  
GGGCCATGTTCCCAGCGGGGACCCACCAACAGAGGCCAGTTTCAAAGTCAGCTGAGGGGCTG  
AGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAGGCTCTGCCTTCTCCATGGGGTAACCA  
CCCTCGCTGGGCAGGGGCAGCCAAGGCTGGGAAATGAGGAGGCCATGCACAGGGTGGGGCAG  
CTTTCTTTGGGGCTTCAGTGAGAACTCTCCAGTTGCCCTTGGTGGGGTTTCCACCTGGCTTT  
TGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCGGCATAAGGGGAGGCCTTGGAACTGAGCT  
GCCAATGCCAGCCCTGTCCATCTGCGGCCACGCTACTCGCTCCTCTCCCAACAACTCCCTTC  
GTGGGGACAAAAGTGACAATTGTAGGCCAGGCACAGTGGCTCACGCCTGTAATCCAGCACTT  
TGGGAGGCCAAGGCGGGTGGATTACCTCCATCTGTTTAGTAGAAATGGGCAAAACCCATCTC  
TACTAAAAATACAAGAATTAGCTGGGCGTGGTGGCGTGTGCCTGTAATCCAGCTATTTGGGA  
GGCTGAGGCAGGAGAATCGCTTGAGCCCCGGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGAT  
AGTGCCACTGCAATTACGCCTGGGTGACATAGAGAGACTCCATCTCAAAAAA

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**FIGURE 68**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415  
<subunit 1 of 1, 215 aa, 1 stop  
<MW: 24326, pI: 6.32, NX(S/T): 4  
MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQF  
SLNWTYQECNNCSEEMFLQFRMKIINLKLRFQDRVEFSGNPSKYDVSVMRLRVQPEDEGIYN  
CYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRKKEQ  
KLSTDDLKTEEEGKTDGEGNPDDGAK

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 161-179

**Immunoglobulin-like fold:**

amino acids 83-127

**N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77

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**FIGURE 69**

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTCGCCGCCAGCCTCCGCCGCCGAGCCTC  
GTTTCGTGTCCCCGCCCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCCCACCCTGGCAGACTAACGAA  
GCAGCTCCCTTCCCACCCCAACTGCAGGTCTAATTTTGGACGCTTTGCCTGCCATTTCTTCCAGGTTGAGGGAGC  
CGCAGAGGCGGAGGCTCGCGTATTCTTGCAGTCAGCACCCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTC  
GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGCCGCTCCGGTTTGGCT  
CACCTCTCCAGGAACTTCACACTGGAGAGCCAAAAGGAGTGGAAGAGCCTGTCTTGAGATTTTCTGGGGAA  
ATCCTGAGGTCATTCAATATGAAGTGTACCGCGCGGAGTGGCTCAGAGTAACCACAGTGCTGTTTCATGGCTAGA  
GCAATTCAGCCATGGTGGTTCCCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT  
GAGTGGTGGATAGCCAAACAACGAGGGAAAAGGGCCATCACAGACAATGACATGGGATGTAGAGCTGGAAGA  
AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAGA  
TCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT  
TTGGGAGCACACTGGGGAAGATATAGGCCCCGACGTTTCATGTACAATCGTGGTATGATGAAGTGAAGACTTT  
AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTCAGGTGTTCTGGCCCTGTATGTACACATTATACA  
CAGGTCGTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTACATAACATGAACATCTGGGGGAC  
ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAACTGGTGGGGCCATGCCCTTACAAA  
CATGGGCGGCCCTGTTCTGCTTGCCACCTAGTTTTTGGAGGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGG  
TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC  
CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAATTTGTTCT  
TGTGAAGTAAGATTAAGAGATCAGTGCAAAGGAACAACCTGCAATAGGTACGAATGTCCTGCTGGCTGTTTGGAT  
AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT  
ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTCATCAAGTCCAATAGA  
AATGGTATTCAAACAATTGGCAAATATCAGTCTGCTAATTCCTTCACAGTCTCTAAAGTAACAGTTTCAGGCTGTG  
ACTTGTGAAACAACCTGTGGAACAGCTCTGTCCATTTTCATAAGCCTGCTTCACATTGCCCAAGAGTATACTGTCT  
CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAAATTGGAACCTCAGTATTATTCTGATCTGTCCAGTATC  
TGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA  
AAGACCTACATTGCTTCTTTTCAGAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATTC  
AGAGTGTTTGTCTGTTGTGTGAAGTGAATACTTGAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA  
ATTTTGTATAAACTGTAACTTACTGTACAGAGTACATCAACTATTTTCAGCCCCAAAAGGTGCCAAATGCATA  
TAAATCTTGATAAACAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG  
TTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT  
GTTCTACGTTTTCATATATTATGTTGCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG  
GCCCTCAGAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAAACCTGAAAGAAACCTTATCACATTTTCCCC  
AGTTCAATGCTATGCCATTACCAACTCCAATAATCTCAAATAATTTTCCACTTAATACTGTAAGTTTTTTTTT  
TGTTAATTTAGGCATATAGAATATTAATTTCTGATATTGCACTTCTTATTTTATATAAAATAATCCTTTAATATC  
CAAATGAATCTGTTAAATGTTTGATTCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT  
ATGAAAACATTCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTCTATGTACTGTTA  
AAATTGAGGTCACATATTTTCTTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT  
GAACAAAGATGAACATAATGTATTACATTACCATTGCCACTGATTTTTTTTTTAAATGGTAAATGACCTTGTATATA  
ATATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTTCTATGAAAAATGTATTGTGCTTTGATACTAAA  
AATCTGTAAATGTTAGTTTTGGTAATTTTTTTTCTGCTGGTGGATTACATATTAATTTTTTCTGCTGGTGA  
TAAACATTAATAATTAATCATGTTTCAAAAAAAAAAAAA



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**FIGURE 70**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417
<subunit 1 of 1, 500 aa, 1 stop
<MW: 56888, pI: 8.53, NX(S/T): 2
MKCTAREWLRVTTVLFMARAI PAMVVPNATLLEKLEKYMDDEDGEWWIAKQRGKRAITDNDMQ
SILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHWGR
YRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQV VWATSNRIGCAINLCHNM
NIWGQIWPKAVYLV CNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENLCYKEGSDRY YPPR
EEETNEIERQQSQVHDTHV RTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNRYECPA
GCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKH YFIKSNRNGIQTIGKY
QSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIGTRVYSDL
SSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKA FRVFAVV
```

**Important features:****Signal peptide:**

amino acids 1-20

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein**

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

**N-glycosylation site**

amino acids 28-31

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**FIGURE 71**

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGGC  
TGGGCGCGCCCCCGGGCCCCGCGTGGGC**ATG**GGCGCACTGGCCCCGGGCGCTGCTGCTGCCT  
CTGCTGGCCCAGTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCGCGCCCTTCACGCTGCC  
CTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCC  
GAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCC  
GCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAG  
ATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTT  
GCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACA  
TACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTT  
GGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACT  
ATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  
TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAA  
GCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCT  
GGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATC  
TGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGA  
GGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGC  
ACCACGCTGCTGCGCCTGCCCCAGAAAGTGTTTTGATGCGGTGGTGGAAAGCTGTGGCCCCGCGCA  
TCTCTGATTCCAGAATTCTCTGATGGTTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAAT  
TCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGC  
AGGTCATTCCGTATCACAACTCTGCCTCAGCTTTACATTACAGCCCATGATGGGGGCCGGCCTG  
AATTATGAATGTTACCGATTTCGGCATTTCCTCCATCCACAAATGCGCTGGTGATCGGTGCCACG  
GTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC  
CCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGAT  
GTAGCCAGCAACTGTGTCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTAT  
GCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTT  
CGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTGCTCAATGATGAGTCCTCTCTGGTCAGACAT  
CGCTGGAAA**TGA**ATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCA  
CATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTCTCCTGTGCCACCCGTCTTCAAT  
CTCTGTTCTGCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTT  
CAAATCCTCCCTACTTCCAAGAAAAATAATTAACAAAAAACTTCATTCTAA

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**FIGURE 72**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493
><subunit 1 of 1, 518 aa, 1 stop
><MW: 56180, pI: 5.08, NX(S/T): 2
MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GPTPAERHADGLALA
LEPALASPAGAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYI
DTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENFFLP
GIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLG
GIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTLLRLPQKV
FDAVVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKISYLRDENSRSFRITILPQ
LYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA EIAGAAV
SEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLV LIVLLLLPFR CQRRPRDPE
VVNDESSLVRHRWK
```

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 466-494

**N-glycosylation sites.**

amino acids 170-173 and 366-369

**Leucine zipper pattern.**

amino acids 10-31 and 197-118

**Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310

**FIGURE 73**

CCGCGCGGCGAGAGCGCGCCACGCCCGCCGCGATGCCCGCGCGCCAGGACGCCTCCTCCCGCTGCTGGCCCCGGC  
CGCGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGCGGCGGGCGCTGGGGCGCCCGGGCCAGG  
AGCGCGGCGGCGGCGGCGCGGAGCGGGCCCGCCCGCGCGAGACGGCGAGGACGGACAGGACCCGCACAGAGCAACC  
TGTATACGCCCGCATGTTCTACGCAAGGATCCAGAGCGCCGCGCATCTTCGTATGTTCTTCGCGCCCTGGTGTG  
GACACTGCGACGGCTGCAGCCGACTTGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT  
ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCCAGGGGTGCGAGGATAACCCACCTTAA  
AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCTCGGGACTTCCAGACACTGGAAGAACTGGATGC  
TGCAGACACTGAACGAGGAGCGAGTGACACAGAGCGGGAAGTGAACCGCCCACTGCCCCCGAGCTCAAGCAAG  
GGCTGTATGAGCTCTCAGCAAGCAACTTTGACCTGCACGTTGCACAGCGGACCACCTTTATCAAGTCTCTCGCTC  
CTGGTGTGGTCACTGCAAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCCGAAACTG  
TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACCTGCTCTCGGAAACCAGGTTCTGGCTATCCCACTC  
TTCTCTGGTTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGAAAGCGGGATTGGAGTCACTGAGGGAGTACG  
TGGAGTCGCAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTACGCCCCAGAGGCCCCGGTGTGGCAG  
TACGCCCCGAGGCTGACAAGGCGCACTGTGTTGGCACTCACTGAAATAAATCTTCGATGACACATTGCAGAAGGAA  
CTAGCTTTCATCAAGTTTTATGCTCCATGGTGTGGTCACTGTAAGACTCTGGCTCTACTTGGGAGGAACCTCTTA  
AAAAAGAAATTCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCAGTCTGTAACGGAATATCTGCAGCA  
AGTATTCGGTACGAGGCTACCCACGTTATTGCTTTTCCGAGGAGGGAAGAAAGTCACTGAGCACAGTGGAGGCA  
GAGACCTTGACTCGTTACACCGCTTTGTCTGAGCCAAGCGAAAGACGAACCTTAGGAAACACAGTTGGAGGTCAC  
CTCTCTCGCCAGCTCCCGCACCCCTGCTTTAGGAGTTCAGTCCCACAGAGGCCACCTGGGTCCCAGTGGTGGCT  
GTTCAGAAAGCAGAACATACTAAGCGTGAAGGTATCTCTTTGTGTGTGTTTCCAAGCCAACACACTCTACAG  
ATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACCTCATGGTCACTGTGTAACATTTTCACTGGCGATA  
TATCCCTTTTGACCTTCTCTTGATGAAATTTACATGGTTTCTTTGAGACTAAAATAGCGTTGAGGGAATGAA  
TTGCTGGACTATTTGTGGCTCTGAGTTGAGTGATTTTGGTGAAAGAAAGCACATCCAAGCATAGTTTACCTGC  
CCACGAGTCTGGAAGAGGTGGCCCTGTGGCAGTATTGACGTTTCTCTGATCTTAAGTCAAGTTGACTCAATAC  
TGTGTTGGTCCGTAGCATGAGCAGATGTAATGACAAAACCCACACCTTGAAGATACCTTACGCGCCGTGC  
TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC  
TGCTGTAGTAAGAGAATGCTGATGCATAACTTTATGTGTGATACTTGTCAAATCAGTTACTGTTCAAGGGAT  
CCTTCTGTTTCTCACGGGGTGAACATGTCTTTAGTTCCTCATGTTAACACGAAGCCAGAGCCACATGAACCTGT  
TGATGTCTTCTCTAGAAAAGGTTAGGCATGGAATTTCCAGAGGCTCATTCTCAGTATCTCATTAATCACTTGA  
AAGATTCCAGTTGTATTGTTCACTGGGGTGACAAGACAGACAGGCTTTCCAGGCGCTGGGTATCCAGGAGGC  
TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCCTTTAGAGG  
CTTGCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGAC  
CAAAGACAGATGTCAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTTA  
ACTCATGCTGTCTTGTGATTAACACCTCTATCTCCCTTGGAATAAGCACATCAGGCTTAAGCTTAAGATA  
GATAGGTGTTTGTCTTATTTACCATCGAGCTACTTCCCATAATAACCACCTTTCATCCAACACTCTTCAACCACT  
CCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAGACCACTTATA  
CTGTCTGTCTGAGGCAGAAGATACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCAG  
TATGGTTACAGATAAATCTTTTTTTAAAAAAACCCAACTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTA  
CAACAACCTCAGCTTTGCATCAGAGTCTGTGATTCCAAGAAAATCAAAGTGGTACAATTTGTTTGTTTACACTAT  
GATACTTTCTAAATAAATCTTTTTTTTTTAA

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**FIGURE 74**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLP LLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHSK
HLYTADMFTHTGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAHS
VCSAQGVRGYPTLKLFPKPGQEAVKYQGPRDFQTLNWMLQTLNEEPVTPEPEVEPPSAPELKQ
GLYELASNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCTQHYE
LCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLEYVESQLQRTETGATETVTPSEAPVLAA
EPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLAGVKIAE
VDCTAERNICKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHFRVLSQAKDEL
```

**Signal sequence:**  
amino acids 1-32

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**FIGURE 75A**

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG  
CAGTTTGCAGCGCTTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGC  
TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT  
GGAGGGAGATCAGGAAACGGCTTCTTCTCACTTCGCCCGCTGGTGAGTGTGCGGGGAGATTGGCAAACGCCTAGG  
AAAGGACTGGGAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGCTCCACTACGGCAGTTTATCTG  
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGCGCGA  
TCCCGCCGCCCTCCGTACCAGCACTCCCAGGAGAGTCAGCCTCGCTCCCCAACGTCGAGGGCGCTCTGGCCACGA  
AAAGTTCCTGTCCACTGTGATTCTCAATTCTTGTGTTGGTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTA  
ACTTTTTTCTTTTTTTTTTCTTGGTGGAGCTGCTCTAGGGAGGGGGGAGGAGGAGGAGAAAGTGAAATGTGC  
TGGAGAAGAGCGAGCCCTCCTTGTCTTCCGGAGTCCCATCCATTAAAGCCATCACTTCTGGAAGATTAAAGTTGT  
CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTACCCTGTGTTGGGTGCATG  
TGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTCTCCGCGTGGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA  
GGGGCTGTGCGGGGCATCCGCTCCGCTTCTCCACAGGCCTGTGTCTGTCTGGAAGATGCTAGCAATGGGGG  
CGCTGGCAGGATTCGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGGGGCCAGGCCTTAGAAGAGGAGG  
AAGAAGGGGCCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACCTCCACCTCCCAGCCCCATCTCA  
TTTTCATCTAGCGGATGATCAGGGATTTAGAGATGTGGGTACCACGGATCTGAGATTAAACACCTACTCTTG  
ACAAGCTCGTCCGGAAGGAGTTAACTGGAGAATACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT  
TTATTACTGGAAATATCAGATACACACCGGACTTCAACATTCTATCATAAGACCTACCCAACCAACTGTTTAC  
CTCTGGACAATGCCACCCTACCTCAGAACTGAAGGAGGTGGATATTCAACGCATATGGTCGAAAAATGGCACT  
TGGGTTTTTAACAGAAAAGAAATGCATGCCACCAGAGAGGATTTGATACCTTTTTTGGTTCCTTTTGGGAAGTG  
GGGATTACTATACACACTACAAATGTGACAGTCTGGGATGTTGGCTATGACTTGTATGAAAACGACAATGCTG  
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCATA  
ACCCACAAAGCCTATATTTTTATATACTGCCTATCAAGCTGTTTCACTCACCCTGCAAGCTCCTGGCAGGTATT  
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCTGCTTAGATGAAGCAA  
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTACTCTTCAGATAATG  
GTGGCCAGCCTACGGCAGGAGGGAGTAACCTGCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC  
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAACAGGGAACAGTGTGAAGGAACCTGTGCACATCACTG  
ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT  
GGGAGACCATAAGTGAGGGTCTTCCGCTCACCCCGAGTAGATATTTTGCATAACATTGACCCCTATACACCAAGGC  
AAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG  
GAAATTGCTTACAGGAAATCCTGGCTACAGGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACC  
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGATGGCTTTTCAACATCACAGCCGACCCATCACTG  
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAAAC  
TGCAGTGCCGCTCAGGTATCCCCCAAAGACCCAGAAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG  
GTATAAAGAGGAAACCAAGAAAAAGAACCAAGCAAAATCAGGCTGAGAAAAAGCAAAAGAAAAAGCAAAAAAA  
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA  
GGCTTGTCTTCTGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCACACTGAAACTGTCTGCTCAGTG  
CCAAGGTGCTACTCTTGAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTAGAAAAACGTG  
GTGAGTCTGAGTTCCTGCTGTGCTTCACTGCAACTGACCAAAACACTGCTTTGAATTATAGGAGGAGAAACAATA  
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGCTAGCATGATTAAACTACCTTTGATAAATTAC  
AGTCAAAGATTGTGTACCTCAAAGGCCCTGAAGAATATATTTTCTTGGTGAATTTTGTATGTCTGTATATGA  
CACTTGGGTTTTTTAATTAATTCTATTTTATATATAAATATATGTTTCTTTTCTGTGAAAAGCTGTTTTTCT  
CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCC  
ACAATGAATGTAATATTTTCTAAACACTTTACTAGAAGAACATTTCAGTATAAAAAACCTAATTTATTTTACA  
GAAAAATATTTTGTGTTTTTATAAAAAGTTATGCAATGACTTTTATTTTTATTTCTGTCATACCATTAGAAGA  
ATTTTATTTTCAATTTCTTCAAATTTCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA  
TAAAAACATCATTCAGAAAACCTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT  
ATTACTTGGAAATTCATGTTTGTGTCAGAGTTGAGACAACCTTATGTTTCTATCATAAACTATTTATGTATCTT  
AATTATTAATAATGATTTACTTTATGGCACTAGAAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAT  
GTATCATTTGGTCTTAAAAATAAAAACTTTACTAATAGGCAATTGAAGGAATGGTTTGCTAACAACCACAGTAA  
TATAATATGATTTTACAGATAGATGCTTCCCCTTGGCTATGACATGGAGAAAGATTTTCCATAATAATAACTAA  
TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAAAGT  
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCGCTGGAGTAGGTAACCTTGCTTGAAACCCC  
ACATGCAAACTCATGAGGAGAAATTAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTATCAATGAGCATA  
GATTGGTGTGGATCCTGTAGACCTGGTGTCTTTGTAAGAGTGCCCTCTCTAATGCAGAGGCCCTGAAGCTTAC

FIGURE 75B

[illegible]

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**FIGURE 76**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEEGALLAQAGEKLEPSTTSTSQ
PHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAAGVKLENYYVQPICTPSRSQFITGKYQIHTGLQHSIIRPTQP
NCLPLDNATLPQKLKEVGYSTHNVGKWHLGFNREKCMPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCGYDLYEN
DNAAWDYDNGIYSTQMYTQRVQQILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSC
DEAINNVTLALKTYGFYNNSSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGFVHSPLLKNKGTVCVELV
HITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPGQQAMGSGTLQSSQPSE
CSTGNCLQEILATATGSPLSLSATWDRGTGGTMNGSPCQLAKVYGFSTSQPTHMRGWTYLTGIQES
```

**Important Features:****Signal Peptide:**

amino acids 1-37

**Sulfatases signature 1.**

amino acids 120-132

**Sulfatases signature 2.**

amino acids 168-177

**Tyrosine kinase phosphorylation site.**

amino acids 163-169

**N-glycosylation sites.**

amino acids 157-160, 306-309 and 318-321



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**FIGURE 77**

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCCCTTTTGAAGAACAGTACTGTGGA  
GCTATTTAAGAGATAAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC  
GCCGCTGTTTACCAATCGGGGAGAGAAAAGCGGAGATCCTGCTCGCCTTGACGCGCCTGAAGCACAAAGCAGAT  
AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAAACAACGGAGGAGCTCTGACTTCCCACTGTCCATTCTAT  
GGGCGAAGGAACGTCTCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAATGAT  
TCCTGCGCGACTGCACCGGGACTACAAAGGGCTTGCTCTGCTGGGAATCCTCCTGGGGACTCTGTGGGAGACCGG  
ATGCACCCAGATACGCTATTTCAGTTCGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT  
GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACGCGAGCTTTTCGCCCT  
GAATCCGCGCAGCGGCGAGCTTGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG  
TCAATTAATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA  
CGACAATGCGCCTTACTTTCTGTAAGTGAATTAGAAATAAAAATTAGTGAAAATGCAGCCACTGAGATGCGGTT  
CCCTCTACCCACGCTGGGATCCGGATATCGGGAAGAATCTCTGTCAGAGCTACGAGCTCAGCCCGAACACTCA  
CTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCCGAATTGGTGCTGAAACGCGCCCTGGACCG  
CGAAGAAAAGGCTGCTCACCACCTGGTCTTACGGCCTCCGACGGGGGCGACCCGGTGCGCACAGGCACCGCGCG  
CATCCGCGTGATGGTTCTGGATGCGAACGACAACCGACCGCTTGGCTCAGCCCGAGTACCGCGCGAGCGTTCC  
GGAGAATCTGGCCTTGGGCACGCGAGCTGCTTGTAGTCAACGCTACCGACCCTGACGAAGGAGTCAATGCGGAAGT  
GAGGTATTCTTCCGGTATGTGGACGACAAGCGGGCCCAAGTTTCAAAGTAGATTGTAATTCAGGGACAATATC  
AACAATAGGGGAGTTGGACCACGAGGAGTCAGGATTCTACCAGATGGAAGTGCAAGCAATGGATAATGCAGGATA  
TTCTGCGCGAGCCAAAGTCTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCTCACCTCTCT  
CGCCAGCTCGGTTCCCGAAAATCTCCAGAGGGACATTAAATTGCCCTTTTAAATGTAAATGACCAAGATTCTGA  
GGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAAATTACTA  
TAGTTTAGTACAGACATAGTCTTGGATAGGGAACAGGTTTCTAGCTACAACATCACAGTGACCGCCACTGACCG  
GGGAACCCCGCCCCATCCACGGAAATCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCGCGCGTCTT  
CCCTCAGGCCTCCTATTCCGCTTATATCCAGAGAACAATCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA  
CGACCCCGACTGTGAAGAGAACGCCAGATCACTTATCCCTGGCTGAGAACACCATCCAAGGGGCAAGCCTATC  
GTCCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCCGAGA  
CTTGCAAGTGAAAGTGATGGCGCGGGACAACGGGCACCCGCCCTCAGCAGCAACGTGTGCTTGGCCTGTTTCTG  
GCTGGACCAGAACGACAATGCGCCGAGATCCTGTACCCCGCCCTCCCCACGGACGGTTCCACTGGCGTGGAGCT  
GGCTCCCCGCTCCGCGAGGCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAGAACGC  
CTGGCTGTCTACCGTCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG  
CACGGCGGAGCCCTGTGGACAGAGACGCGCTCAAGCAGAGCCCTCGTAGTGGCCGTCCAGGACCACGGCCAGCC  
CCCTCTCTCCGCCACTGTACGCTCACCGTGGCGGTGGCCGACAGCATCCCCAAGTCTGGCGGACCTCGGCAG  
CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTG  
CGTCTTCTTGGCCTTCTGTCATCTTGTGCTGGCGCTCAGGCTGCGGCGCTGGCACAGTCAACGCTGCTGCAGGC  
TTCAGGAGGCGGCTTGACAGGAGCGCCGGCTCGCACTTTGTGGGCGTGGACGGGGTGCAGGCTTTCTGTCAGAC  
CTATTTCCACGAGGTTTCCCTCACCACGGACTCGCGGAAGAGTCACTGATCTTCCCCAGCCCAACTATGCGAGA  
CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAGCGAGCCCTTTTGTGCTGTCAGGTGATTTCGGTATTTTCTAAAGA  
CAGTCATGGGTTAATTGAGGTGAGTTTATATCAAATCTTCTTTCTTTTAAATTGCTCTGTCTCCCAAGC  
TGGAGTGCAGCGTACGATCATAGCTCACTGCGGCCTCAAATCCTAGGCTCAAGCAATTATCCACCTTTGCCT  
CCGGTGTAAACAGGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTATCTATCTATCTATCTATCTATCTAT  
CTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT  
CGAGGCGGGTGGATCACCTGAGGTTGGGAGTTTGAGACGAGCTGACCAACATGGAGAAACCCCGTCTATACTAA  
AAAAATACAAAATTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAAT  
TGCTTTAACCTGGGAGGTGGAGGTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTG  
AAACTCTATCTCA

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**FIGURE 78**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306
><subunit 1 of 1, 916 aa, 1 stop
><MW: 100204, pI: 4.92, NX(S/T): 4
MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVP EELEKGSRVGDISRDLGLEPRELAERGVRIIPRGRTQLF
ALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVRDINDNAPYFRESELEIKISENAATEM
RFPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGADGSKYPELVLKRALDREEKAAHHLVLTASDGGDPVRTGT
ARIRVMVLDANDNAPAFAPQPEYRASVPENLALGTQLLVVNATDPDEGVNAEVRYSFYVDDKAAQVFKLDCNSGT
ISTIGELDH EESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLVNDQD
SEENGQVICFIQGNLFPKLEKSYGNYYSLVTDIVLDREQVPSYNITVTATDRGTPPLSTETHISLVNADTNDNPP
VFPQASYSAYIPENNPRGVSLSVSTAHPDCEENAQITYSLAENTIQQASLSSYVSINSDTGVLYALSSFDYEQF
RDLQVKVMARDNGHPPLSSNVLSLSFLVDQNDNAPEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVD RDSGQ
NAWLSYRLLKASEPGLFSVGLHTGEVVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPOVLADL
GSLESPANSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLQASGGGLTGAPASHFVGVDGVQAFL
QTYSHVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGLIEVSLYQIFFLFFFNCSVS
QAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLSIYLSIYLSIYLSIYLLLSCTDGS LTPVIPVLW
EAEAGGSPEVGSLRPA
```

**Signal sequence:**

amino acids 1-30

**Transmembrane domains:**

amino acids 693-711, 809-823, 869-888

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**FIGURE 79**

AGCCGCTGCCCCGGGCGGGCGCCCGCGGGCACC**ATG**AGTCCCCGCTCGTGCCTGCGTTGCTGCGCCTCCTC  
GTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCAAGCTGTCTCGTGGGAGCATCTCA  
GAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATCCAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTC  
ATGGACTCGGTGCGCCGCGGTGCCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCGGGAACCGGCGCTGGAAC  
TGCTCCACACTCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCCTTCGTGTAC  
GCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGCAGCAGTGGGGAGCTGGAGAAGTGCGGCTGT  
GACAGGACAGTGCAATGGGGTCAGCCACAGGGCTTCCAGTGGTCAGGATGCTCTGACAACATCGCCTACGGTGTG  
GCCTTCTCACAGTCGTTTGTGGATGTGCGGAGAGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTC  
CACAACAATGAGGCCGCGCAGGAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTCAAGC  
TCCTGTGAGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTCAAGCACTGAAGGAGAAGTTT  
GATGGTGCCACTGAGGTGGAGCCACGCCGCTGGGCTCCTCCAGGGCACTGGTACCACGCAACGCACAGTTCAG  
CCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCGACTTCTGTGAGCAGGACATGCGCAGCGGCGTG  
CTGGGCACGAGGGGCGCACATGCAACAAGACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGC  
GGCTTCCACACGGCGCAGGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCTAGTGGTGTGCTTCGTCAAGTGC  
CGGCAGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGAT**TGA**CCGCCCTGCCTAGCCCTGCGCCGCAACCACTA  
GTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCACCACCTACCCCAAGAGATACTGGTTGTATTTTTTGT  
CTGGTTTGGTTTTTGGGTCTCATGTTATTTATTGCCGAAACCAGGCAGGCAACCCCAAGGGACCAACCAGGGC  
CTCCCCAAGCCTGGGCCTTTGTGGCTGCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTG  
GCTGCCACTGACCACTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTA  
TTACCACCACATGGCTACTGACCGTGTCTATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATAGGTACCGACTTG  
ATGGAAGTCACACCCTCTGGA AAAAAGAACTCTTAACCTCTCCAGCACACATACACATGGACTCCTGGCAGCTTGA  
GCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGGGAACAAGCAGATACCAGGTCAAGGGCACCAGGTTCAATT  
TCAGCCCTTACATGGACAGCTAGAGGTTTCGATATCTGTGGGTCCCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAG  
AGACGACTGAAGTCCCACCCTAGAACCCAGCCTGCCCCAGCCTGCCCCTGGAAGAGGAACTTAACCACTCCCC  
AGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTTTGCAGTCATGCCCGA  
GTCACCTTTACAGCGCTGTTCTCCATGAAACTGAAAAACACACACACACACACACACACACACACACACAC  
ACACACACACGGACACACACACACACCTGCGAGAGAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAG  
TCACCTTTCACAGCACTGTTCTC

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**FIGURE 80**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328  
<subunit 1 of 1, 351 aa, 1 stop  
<MW: 39052, pI: 8.97, NX(S/T): 2  
MSPRSLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLAI  
EECQYQFERNRRWNCSTLDSLPLVFGKVVTQGTREAAFVYAISSAGVAFVTRACSSGELEKCGCDRTVHGVSPQGF  
QWSGCSDNIAYGVAFSQSFDVRRERSKGASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTWCWRAVP  
PFRQVGHALKEKFDGATEVEPRRVGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTC�KNTS  
KAIDGCELLCCGRGFHTAQVELAERCCKFWCCFVKCRQCQRLVELHTCR

**Important features:****Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 88-91 and 297-300

**Wnt-1 family signature.**

amino acids 206-215

**Homologous region to Wnt-1 family proteins**

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

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**FIGURE 81**

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT  
CTGATGGTGGGTCGTTAACCTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATCAAGAAT  
TGGGGTCTGGCTCAGAAATTCCTGCAGCTGGTGAAAATCTGTTTTCTAGAAGAGGTTAATTAATGCCTGCAGTCT  
GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTTCCGCAACCGCTTCT  
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT  
CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCCTGTGACGGAGCCCCCTGTGA  
CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTTCATGCCC  
CGCATCATTTTAAGCTGGTCTCAGTGCATGTGTTTCATTGCCACGGAGACAGGTACCCACTGTATGTTCATTCCCA  
AAACAAAGCGACCCAGAAATTTGACTGCACTCTGGTGGCTAACAGGAAAACCGTATCACCCAAAACCTGGAAGCTTTCA  
TTAGTCACATGTCAAAGGATCCGGAGCCTCTTTGAAAAGCCCCCTGAACTCCTTGCCCTCTTTACCCAAATCACC  
CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTCAGAAACGGTCAGTGTCTGAGGGATA  
TCTATCTAAAGAAACCAAACCTCCTGCCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCACTGGGAAAA  
GCCGGACCCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCCAGATTTTGAAGGAAAGATTTATTTCA  
GGCACCAGCCAAGTGCCTGTTCTGCTCTGGAAGCTGCTATTGGCCCGTAAGAAACAGTATCTGGAAAAGGAGC  
AGCGTCGTACGTACCTCCTACGTTTGAAGAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCGTGG  
ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTACAGCT  
TTCCCTGTACCAGAAATGGCTGTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA  
GGGAAAGACGGGAGAAGAAATTTGACTTCGGGTATTCTCTCCTGGGTGCCACCCCATCCTGAACCAAACCATCG  
GCCGATGCAGCGTGCCACCGAGGGCAGGAAGAAGAGCTCTTGGCCTCTACTCTGCTCATGATGTCACTCTGT  
CACCAGTTCTCAGTGCCTTTGGGCCTTTGAGAAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT  
GGCAAGACAGAGAAAAGCCAGTGAACATTCCGTCCGGATTCTTTACAATGGCGTCGATGTACATTCCACACCT  
CTTTCTGCCAAGACCACCAAGCGTTCTCCCAAGCCCATGTGCCCGCTTGAAGAACTTGGTCCGCTTTGTGAAAA  
GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATTATTATGATGCATGTACAGGGAAGGATTCTAAAGG  
TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTTGTCTGTAC  
TAAGGGTAGAAGATTATTTGCTTTTAAAGGCTAAATATTGTTTGTGGGAACCACAGATGGTTGGGGTTGAACAGT  
AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTCACAGAGGAATAGAAGGTACTT  
TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC  
TCTTCTGGCCTGCCCCATGTTACTATGTGATGGAACAGCACACCTCAACCAAAATTTTTTAATCTTAGACATT  
TTTACCTTGTCTTGTAAAGAAATTTCTTGAAGTGATTTATCTAAAAATAAGGTTGGCAAACCTTTTTCTGTAAAGG  
GCCAGATTGTAATATTTTCAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTCTAATACTCAACTCTGT  
TTCTGAAGCAGGAAGGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCAGGCCAGACAAAACA  
GATGGTGACCAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC  
ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCATGGTTCTCCAGTAACCTCTGCTAGAAACA  
CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA  
AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTAAAGTATGTTCTAAATATTTGT  
CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTGTATGCCATTTAGTATTTTTATAGTTTAGGAAAATATT  
TTCTAAGACCAGTTTTAGATGACTCTTATTCCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG  
GAGGCTAGAAGATGAATTCAGGCACCTTCTTCCAATAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA  
ACTGGATTCATTTTTAAACATTTTCATCAGTTTCAAATGGTAAATTTCTGATTGATTTTTAAATGCGTTTTTGG  
AGAATTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG  
TGATTTCTGAACATAATGGTGCTAATTCAGAGAATGGAAAGTGAAAGTGAGATTCTCTGTTGTCATCGGCATTCC  
AACTTTTTCTCTTTGTTTTGTCCAGTGTTCATTGAATATGTCTGTTTCTATAAATAAATTTTTTAAGAATAA

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**FIGURE 82**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329
><subunit 1 of 1, 480 aa, 1 stop
><MW: 55240, pI: 9.30, NX(S/T): 2
MLFRNRFLLLLALAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDVTEPPVTDPVYEALLYCNIPSVAE
RSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKPYPHPKLEAFISHMSKGSGASFESPLNS
LPLYPNHPLCEMGELTQTGVVQHLONGQLLRDIYLLKKHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDF
DWKKIYFRHQPSALFCSGSCYCPVRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMC
HFCHNVSPCTRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELFALY
SAHDVTLSPVLSALGLSEARFRFAARLIFELWQDREKPSEHSVRILYNGVDVTFHTSFCQDHHKRSPPKPMCPLE
NLVRFVVKRDMFVALGGSGTNYDACHREGF
```

**Signal sequence:**  
amino acids 1-18

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**FIGURE 83**

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGT  
GACGTTTGTGGAGATGGGGAGCGTCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC  
CCGTGTTTGTATGTCGATGCTGTCTAGTGGAAACAACCTCCACTGTAACCTAGATTGATCTATGCACTTTTCTTG  
CTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAACTGAATAAGATTCCTGGGATTT  
TGTGAGAATGAGAAAGGTGTTGTCCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGT  
TTGGCTATGTTCTATCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTG  
CACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATGGGGCATTCTTCATTCAGGAAGGA  
ACTTTTACAACGTGTGTGGTTTATGTAGGCATGGCAGGTGCCCTTTTGTTCATCCTCATACAACCTAGTCTTACTT  
ATTGATTTTGCACATTCATGGAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCA  
GCCTTGTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCTGTTCTTTGTCTACTACACT  
CATCCAGCCAGTTGTTTCAGAAAAACAAGGCGTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG  
TCTATACTGCCAAAAATCCAAGAATCACAACCAAGATCTGGTTTGTACAGTCTTCAGTAATTACAGTCTACACA  
ATGATTTTGACATGGTCAGCTATGACCAATGAACCAGAAACAATTTGCAACCCAGTCTACTAAGCATAAATTGGC  
TACAATACAACAAGCACTGTCCCAAAGGAAGGCGAGTCAGTCCAGTGGTGGCATGCTCAAGGAATTATAGGACTA  
ATTCTCTTTTTGTTGTGTGATTTTATCCAGCATCCGTACTTCAAACAATAGTCAGGTTAATAAACTGACTCTA  
ACAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGATGGATCAGTGGAGGATGGGGACGATGTT  
CACCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACAGTTATTCTCTTTCACTTCATGCTTTTCTGGCT  
TCACTTTATATCATGATGACCTTACCACCTGGTCCAGGTATGAACCTCTCGTGAGATGAAAAGTCAGTGGACA  
GCTGCTGGGTGAAAATCTCTTCCAGTTGGATTGGCATCGTGCTGTATGTTTGGACACTCGTGGCACCACCTTGTT  
CTTACAAATCGTGATTTTGAAGTTGTGTATGTTTTGCTTCCCATGTAACCTCTCCAGTGTCTGGCATGAATTA  
GATTTTACTGCTTGTCAATTTTGTATTTTCTTACCAAGTGCATTGATATGTGAAGTAGAATGAATTCAGAGGAA  
AGTTTTATGAATATGGTGATGAGTTAGTAAAGTGGCCATTATTGGGCTTATTCTCTGCTCTATAGTTGTGAAT  
GAAGAGTAAAAACAATTTGTTTGAATTTTAAATTTATATTAGACCTTAAGCTGTTTTAGCAAGCATTAAAGC  
AAATGTATGGCTGCCCTTTGAAAATTTTGTATGTTGCTTGGCTGGCAGGATACTGCAAAGAACATGGTTTATTTTAAA  
ATTTATAACAAGTCACCTTAAATGCCAGTTGTCTGAAAAATCTTATAAGGTTTTACCCTTGATACGGAATTTTACA  
CAGGTAGGGAGTGTTTAGTGGAACAATAGTGTAGGTTATGGATGGAGGTGTCGGTACTAAATGAATAACGAGTAA  
ATAATCTTACTTGGGTAGAGATGGCCTTTGCCAACAAAGTGAACCTGTTTTGGTTGTTTTAACTCATGAAGTATG  
GGTTCACTGGAAATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTTAGAAGGAA  
GTGTTTTGAAAGTCACCTTGAAGGTTAGTTTTGGGCCCAGCACGGTAGCTCACCTTGGTAATCCAGCACTTTG  
GGAGCTTAAGTGGGTAGATTACTTGAAGCCAGGAATTCAGACCAAGCTTGGCACATGGTGAACCTGTTCTATAAAA  
ATAATCTGGCTTTGAGCATATGCCTGTGGTCCAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCCAGAGCCAAAG  
GTTGCAGTGAGCAAGTCACGTCACCTGCACTCTAGCTGGCAGAGTAAGCCAAAAAATATATATATATTGAAAT  
CAAGGAGGCAAAATTTGACAGGGAAGGAAGTAAGTGCAAAACCACTAGGCTTTAGTAGGTAATATATAAAATC  
TAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATAGCTCAGATAGCTAATTAGGAA  
ATTTCAAGTTGGCCAATAATAGCATTCTCTGACATTTAAAAAATAATTTCTATTCAAATACATGCATATTGAT  
TTACACCTCATACTGTGATAATTAATGTGATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTGAGAAGA  
ATGATGGAATGTTTGAATAAACTCCTGCTTATAGTATACTACACAGTTCAAAGATGTTTAAATGCTTTTTGT  
ATTTACTGCCATGTAATTGAAATATATAGATTATTGTAACCTTTCAACCTGAAAATCAAGCAGTATGAGAGTTTA  
GTTATTTGTATGTGTCAGTGTCTAATGAAGCTTTTAAATCTACAATTTCTTCTTTAAAAATATTTTAAAT  
GTGAATGGAATATAACAATTCAGCTTAATCCCCAACCTTATTCTGTGTGATGACATTGTATCCACAATTTTGA  
ATGGCTGTGTTTTACCTCTAAATAAATGAATTCAGAGAAAAA

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**FIGURE 84**

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQLNKIPGFCENE  
KGVVPCNILVGYKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFIT  
VWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKMEEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPAS  
CSENKAFISVNMLLCVGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTT  
STVPKEGQSVQWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVHRAV  
DNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVVKISSWIGIVLYVWTLVAPLVLNRFDF



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**FIGURE 85**

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGAGCTGCTGGGCAGA  
GAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCCTCGTGGGATGGATCACAGGTGCTGCT  
GTGGCGGTCTGCTGCTGCTGCTGCTGGCCACCTGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGG  
AACCGTACAGCTGCAGGGGGAAACCGAGTCCGCCGGGCCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGA  
ATCTTTCACCATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCC  
CGCCACACCCCTCACACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCACGCTCGCTGAGGCTGC  
TGTCGCCGGTGCCCTGTGGACAGCAGCTGCCCCTGCCCTCCCATCTGTTCCCAGGACAAGTGGACCCCATGTTTCC  
ATGTGGAAGGATGCATCTCTGGGGTGAACGAGGGGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGC  
ATGCCCCAGTGTACTATGGCAGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAG  
AGCAAGGGTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATGACAAGC  
GTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTCATCAGGCTGCTGCAGGCCT  
CTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTTGGTTTGGAGAAGGCAGTGTGAGGCTGCACAGT  
CAATTCATCGGTGCCTTAGTCCAAGAAAATAAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 86**

MLGLLGSTALVGWITGAAVAVLLLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVVRAQPWPFRRRGHLGIFHHHRH  
PGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

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**FIGURE 87**

CCCACGCGTCCGTCCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGGTCAAGGCTGGCTTG  
GCCAGAACGGCGCGCGCGCGCACGACGACACACGCGGGGAACTTTTTTAAAAATGAAAGGCTAGAAGA  
GCTCAGCGGGCGCGCGGGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGT  
CGCCCCGGCCCCGGCTCGGCGCCCGGTGGGATGGTGCAGCGCTCGCCGCGGGCCCCGAGAGCTGCTGCACTGAAG  
GCCGCGACGATGGCAGCGCGCGCCGCTGCCCGTGTCCCCGCGCGCCCTCCTGCTCGCCCTGGCCGGTGTCT  
GCTCGCGCCCTGCGAGGCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTGAGTGCCTCTGT  
TCGGAGTGGGGACCTCTGGATCCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGTGAATATTCGACT  
ACAACGGGAAAGCAAAGAACTGATCATAAATCTGGAAAGAAATGAAGGTCTCATTGCCAGCAGTTTCACGGAAAC  
CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT  
ACGGGGATATTTCTGATTGAGCAGTCACTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGA  
AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAACTCTTCCCAGCGAAGAAGCTGAAAAGCGT  
CCGGGGATCATGTGGATCACATCACACACCAAACTCGCTGCAAGAATGTGTTTCCACCACCTCTCAGAC  
ATGGGCAAGAAGGCATAAAAGAGAGACCTCAAGGCAACTAAGTATGTGGAGCTGGTGTGCTGGCAGACAACCG  
AGAGTTTTCAGAGGCAAGGAAAAGATCTGGAAGAAAGTTAAGCAGCGATTAAATAGAGATTGCTAATCAGTTGACAA  
GTTTTACAGACCACTGAACATTCGGATCGTGTGGTAGGCGTGGAAGTGTGGAATGACATGGACAAATGCTCTGT  
AAGTCAGGACCCATTACACAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCA  
TGACAATGCGCAGCTTGTGAGTGGGGTTATTTTCCAAGGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG  
CACGGCAGACAGTCTGGGGGAATTGTGATGGACATTGACACAATCCCCTTGGTGCAGCCGTGACCCTGGCACA  
TGAGCTGGGCCACAATTTTCGGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA  
AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTT  
GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCTGTTTAACTGCCGGAAGTCAGGGAGTCTTTCGGGGGCCA  
GAAGTGTGGGAACAGATTTGTGGAAGAGGAGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG  
CTGCAATGCCACCCTGTACCCTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT  
GAAGCCTGCAGGAACAGCGTGCAGGGACTCAGCAACTCCTGTGACCTCCAGAGTTCTGCACAGGGGCCAGCCC  
TCACTGCCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT  
CTGCCAGACTCACGAGCAGCAGTGTGTACGCTCTGGGGACCAGGTGCTAAACCTGCCCCTGGGATCTGCTTTGA  
GAGAGTCAATTTGCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCTTTGCCAAATGCGAGAT  
GAGAGATGCTAAATGTGGAAAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC  
CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGGACCCACGTGTAATTTGGGCGATGA  
CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA  
AAATATTAGTGTCTTTGGGGTTACGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACAACAGGAAGAA  
CTGCCACTGCGAGGCCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCC  
CATCCGGCAAGCAGAAGCAAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG  
ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGTGACCACTG  
CTGCTGCAGAGGAGTCAAGCGTCCCCAAGGCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT  
TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCAGCTCTGCAGAAA  
CAGTGCAGGAAGGGCAGCGACTTCTGGTTGAGCTTCTGCTAAACATGGACATGCTTCACTGCTGCTCCTGAG  
AGAGTAGCAGTTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAGTCTGGCCTTTC  
ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCAGTGTCCCTTTCCCACTGACACCTCAGCCT  
TGGCAGCCCTGATGACTGGTCTCTGGCTGCACTTAATGCTCTGATATGGCTTTTAGCATTTATTATATGAAAAT  
AGCAGGGTTTTAGTTTTTAAATTTATCAGAGACCTGCCACCATTCATCTCCATCCAAGCAACTGAATGGCAA  
TGAAACAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACCTCTGGCTCTTTGCTGTGGACATGCGTGACCAAGC  
AGTACTCAGGTTTGAGGGTTTGAGAAAGCCAGGGAACCCACAGAGTACCAACCTTCATTTAAACAAGTAAGAA  
TGTTAAAAAGTGAACAAATGTAAGAGCCTAACTCCATCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT  
GAAAT

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**FIGURE 88**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624
><subunit 1 of 1, 735 aa, 1 stop
><MW: 80177, pI: 7.08, NX(S/T): 5
MAARPLPVSPARALLLAGALLAPCEARGVSLWNQGRADEVVVSASVRSGDLWIPVKSFDKSNHPEVLNIRLQRE
SKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVVRGYSDSAVSLSTCSGLRGLIVFENESYV
LEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLAAKNVFPFPSQTWARRHKRETLKATKYVELVIVADNREFQ
RQGKDLEKVKQRLIETIANHVDFYRPLNIRIVLVGVEVWVNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNA
QLVSGVYFQGTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFVGMNHDTLDRGCSCQMAVEKGGC
IMNASTGYFPFPMVFSSCSRKDLETSLKGMGVCLFNLPEVRESFVGQKCGNRVVEEGEEDCGEPEECMNRCCNA
TTCTLKPDVAHAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGASPHCPANVYLHDGHSCQDQDGYCYNGICQT
HEQQCVTLWGPAGKAPAGICFERVNSAGDPYGNCGKVSFSSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIET
NIPQQGGRILCRGTHVYLGDDMPDGLVLAGTKCADGKICLNRRCCQNI SVFGVHECAMQCHGRGVCNNRKNCHC
EAHWAPPFCDFGFGGSTDGSPIRQAEARQEAESNRERGGQEPVGSQEHASTLTI
```

**Signal peptide:**

amino acids 1-28

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**FIGURE 89**

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGG  
CGCGGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTGACCTGAAAAAATGCTCTGGATTTCTA  
GAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTA  
CTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCA  
TACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGT  
GATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTT  
GGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCTGGA  
ATTGCTGTATTTTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTA  
TGGCAGTGAACACATCTGATTTCCACAGCACAAACAGCCCTGCATGGGTTTGTTTGTTTTTTTACTGCTCACTCC  
CAACCTTTTGTAAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACTAAAATC  
ACGAGAACACCTAAACAACAACCAAAATCTATTGTGGTATGCCTTGATTAACCTATAAAATGTTAGAGGAAAC  
TTTCACATGAATAATTTTGTCAAATTTATCATGGTATAATTTGTAAAAATAAAAAGAAATTACAAAAGAAATT  
ATGGATTTGTCAATGTAAGTATTTGTCATATCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGT  
GTTTATTCAAATGTGGTCTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCC  
GTGGTCAAATTTCTTCTCACTATAAT'GGTATTTACTTTTACCAAAAATTTCTGTGAACATGTAATGTAAGTGGC  
TTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCATGGTCCAGCCACCAGGCTCCCTG  
TGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATTCCAAGGGCAGGAAGATGTGACTCAGCCATGACACG  
TGGTTCTGGTGGGATGCACAGTCACTCCACATCCACCACTG

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**FIGURE 90**

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDA AVIYPTMKDFNHSYHACGVIATIAFLMINAVSN  
GQVRGDSYSEGCLGQTGARIWLFVGFMLAFGLIASMWILFGGYVAKEKDIVYPGIAVFFQNAFIFFGGLVFKFG  
RTEDLWQ

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**FIGURE 91**

CGACGCCGGCGTGAATGGCTTCCGCTGGTGTCTCCTGGCTGTGCTGCTGCTGGCCGCTCCTCTGCAAAGTTTA  
CTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTCAAACGGCCCCCAGCGCCCTGGTAAC  
TGACAAGGAGGCCAGGAAGAAGTTCTCAAACAAGCTTTTTAGCCAACCAAGTGCCGGAGAAGCTGGATGTGGT  
GGTAATTGGCAGTGGCTTTGGGGGCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCTCTGGTGTCT  
GGAAACAACATACCAAGGCAGGGGGCTGCTGTCATACCTTTGGAAAGAATGGCCTTGAATTTGACACAGGAATCCA  
TTACATTGGGCGTATGGAAGAGGGCAGCATTGGCCGTTTTATCTTGGACCAGATCACTGAAGGGCAGCTGGACTG  
GGTCCCCCTGTCTCTCCTTTTGACATCATGGTACTGGAAGGGCCCAATGGCCGAAAGGAGTACCCCATGTACAG  
TGGAGAGAAAGCCTACATTCAAGGCCTCAAGGAGAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAA  
GCTGGTTAAGGTGGTATCCAGTGGAGCCCCCTCATGCCATCTCTGTTGAATTCCTCCCATTGCCCGTGGTTAGCT  
CCTCGACAGGTGTGGGCTGTGACTCGTTTTCTCTCCATTCTTTCAAGCATCCACCCAGAGCCTGGCTGAGGTCTCT  
GCAGCAGCTGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCACTTACGGTGTCAACCCCAA  
CCACAGTGCCTTTTCCATGCACGCCCTGCTGGTCAACCACTACATGAAAGGAGGCTTTTATCCCCGAGGGGGTTC  
CAGTGAATTTGCCCTTCCACACCATCCCTGTGATTGAGCGGGCTGGGGGCGCTGTCTCTACAAAGGCCACTGTGCA  
GAGTGTGTTGCTGGACTCAGCTGGGAAAGCCTGTGGTGTGAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTA  
TTGCCCATCGTGGTCTCCAACGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGCCGCTGCCT  
GCCAGGTGTGAAGCAGCAACTGGGGACGGTGGCGCCCGGCTTAGGCATGACCTCTGTTTTCTCTGCTGCGAGG  
CACCAAGGAAGACCTGCATCTGCCGTCCACCAACTACTATGTTTACTATGACACGGACATGGACCAGGCGATGGA  
GCGCTACGTCTCCATGCCAGGGAAGAGGCTGCGGAACACATCCCTCTTCTCTTCTGCTTTCCCATCAGCCAA  
AGATCCGACCTGGGAGGACCGATTCCAGGCCGGTCCACCATGATCATGCTCATACCCACTGCCTACGAGTGGTT  
TGAGGAGTGGCAGGCGGAGCTGAAGGGAAGCGGGGCGAGTACTATGAGACCTTCAAAAACCTCCTTTGTGGAAGC  
CTCTATGTGAGTGGTCTGAAACTGTTCCACAGCTGGAGGGGAAGGTGGAGAGTGTGACTGCAGGATCCCCACT  
CACCAACCAAGTTCTATCTGGCTGCTCCCCGAGGTGCTGCTACGGGGCTGACCATGACCTGGGCCGCTGCACCC  
TTGTGTGATGGCTCCTTTGAGGGGCCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTACCTG  
TGGACTGGTCCGGGGCCCTGCAAGGTGCCCTGCTGTGCAGCAGCGCCATCCTGAAGCGGAACCTTGTACTCAGACCT  
TAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAAATTAGTTCCATCAGGGAGGAGTCAAGGAATTTG  
CCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTGCAATTAGTTCTTGCAGTATAAAGCACT  
CTAATTTGGTTCTGATGCCGTGAAGAGAGGCTAGTTTAAATCACAATTCCGAATCTGGGGCAATGGAATCACTGC  
TTCCAGCTGGGGCAGGTGAGATCTTTACGCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATA  
GCTTGATGTCTCATGACGAGCGCGCTCTGCATCCCTCACCCATGCCTCCTAACTCAGTGATCAAAGCGAATATT  
CCATCTGTGGATAGAACCCCTGGCAGTGTGTGCTCAGCTCAACCTGGTGGGTTGAGTTCTGTCTCTGAGGCTTCTGCT  
CTCATTCAATTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGGGGAAAAGGGAGACTAATGAGGCTTAACTCAAA  
ACCTGGGCGTGGTTTTGGTTGCCATTCCATAGGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTGAGTGGCT  
CTTCAGGGGACAGGAAATGCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGT  
TAGTAGGGTGCATGTGAGATGATCATATCCAATTCATATGGAAGTCCCGGGTCTGTCTTCTTATCATCGGGGTG  
GCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCTCAATCAAGCCTTATCCACCAATACACAGG  
GAAGGGTGATGCAGGGAAGGGTGACATCAGGAGTCAGGGCATGGACTGGTAAGATGAATACTTTGCTGGGCTGAA  
GCAGGCTGCAGGGCATTTCCAGCCAAGGGCACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGGAGGGGAAGTC  
ACATCAGAAAAGGGAAAGCCACGGAATGTGTGTGAAGCCAGAAATGGCATTTGCAGTTAATTAGCATATGTGAG  
GGTTAGACAGGTAGGTGAATGCAAGCTCAAGTTTGGAAAAATGACTTTTCAGTTATGTCTTTGGTATCAGACAT  
ACGAAAGGTCTCTTTGTAGTTTCGTGTTAATGTAACATTAATAAATTTATTGATTCCATTGCTTTAAAAA

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**FIGURE 92**

MWLPLVLLLVALLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDKEARKKVLKQAFSANQVPEKLDVTVIGS  
GFGGLAAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIGRMEEGSIGRFILDQITEGQLDWAPLS  
SPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQEEAIIIDKYIKLVKVVSSGAPHAILLKFLPLPVVQLLDRC  
GLLTRFSPFLQASTQSLAEVLQQLGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIA  
FHTIPVIQRAGGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAAGLFNTYEHLLPGNARCLPGVK  
QQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYVYYDTMDQAMERYVSMPEEAAEHIPLLFFAFPSAKDPTW  
EDRFPGRSTMIMLIPTAYEWFEEWQAEKKGKRGSDYETFKNSFVEASMSVVLKLFPPQLEGKVESVTAGSPLTNQF  
YLAAPRGACYGADHDLGRLHPCVMASLRAQSPIPNLYLTGQDIFTGGLVGLQGALLCSSAILKRNLYSDLKNLD  
SRIRAQKKKN



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**FIGURE 93**

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGTGCGGCTCGGGATGG  
GTCCAGGATGTTACTCCTTCTTCTTTTGTGGGGTCTGGGCAGGGGCCACAGCAAGTCGGGGCGGGTCAAACGTT  
CGAGTACTTGAACGGGAGCACTCGCTGTGCAAGCCCTACCAGGGTGTGGGCACAGGCAGTTCTCACTGTGGAA  
TCTGATGGGCAATGCCATGGTGATGACCCAGTATATCCGCTTACCCAGATATGCAAAGTAAACAGGGTGCCTT  
GTGGAACCGGGTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAATCCATGGACAAGGAAAGAA  
GAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGCCTGTGTTGGAAACAT  
GGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAATGAGGAGAAGCAGCAAGAGCGGGTATTCCC  
CTACATCTCAGCCATGGTGAACAACGGCTCCCTCAGCTATGATCATGAGCGGGATGGCGGGCTACAGAGCTGGG  
AGGCTGCACAGCCATTGTCCGCAATCTTCATTACGACACCTTCTGGTGATTTCGCTACGTCAAGAGGCATTTGAC  
GATAATGATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGAGTCCGCTGCCCGCGG  
CTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCAATTTCTTGAAGTTGTTTGA  
ACTGACAGTGGAGAGAACCCAGAAAGAGGAAAAGCTCCATCGAGATGTGTTCTTGCCCTCAGTGGACAATATGAA  
GCTGCCTGAGATGACAGCTCCACTGCCGCCCTGAGTGGCCTGGCCCTCTTCTCATCGTCTTTTCTCCCTGGT  
GTTTTCTGTATTTGCCATAGTCATTGGTATCATATCTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTA  
CTGAGCCCTCCTGCTGCCACCACTTTTGTGACTGTCAACCATGAGGTATGGAAGGAGCAGGCCTGGCCTGAGCA  
TGCAGCCTGGAGAGTGTTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTGTCACTGGAGTTTGAATGCAGG  
GACCCCGCATTTCCCATGGTTGTGCATGGGGACATCTAACTCTGGTCTGGGAAGCCACCCACCCAGGGCAATGCT  
GCTGTGATGTGCCCTTCCCTGCAGTCCTTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGC  
CAAAATCACAGAACAGAAATTCATAGCCCAGGCTGCCGTGTTGTTTGACTCAGAAGGCCCTTCTACTTCAGTTTT  
GAATCCACAAAGAATTAAAAACTGGTAACACCACAGGCTTTCTGACCATCCATTTCGTTGGGTTTTGCATTTGACC  
CAACCCTCTGCCTACCTGAGGAGCTTTCTTTGGAACCAGGATGGAAACTTCTTCCCTGCCTTACCTTCCTTTCA  
CTCCATTCAATGTCTCTCTGTGTGCAACCTGAGCTGGGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGG  
CTGCAGAACACACCTGCGTTTTCACTGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTG  
TTCCCTAGCATGGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTGAA  
GTTTGGCTAAAGGTTGGTGTAATAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATGGATTAGCTGTGCAAC  
TGACCAGCTCCAGGTTTGATCAAACCAAAAGCAACATTTGTGATGTGGTCTGACCATGTGGAGATGTTTCTGGAC  
TTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGTTACGATTTTGGAAATCCCACTTTGAGTGCTGAAAGTGTAAG  
GAAGCTTTCTTCTTACACCTTGGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTCTTAATGGACAA  
GAGACAGTTGCTGTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTTCACTG  
TCATTGAGCAGCACAGCCTGAGTGTGGCCTCTGTCAACCCTTATTCCTGCTTATTTGACAAGGGGTTACAT  
GCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAGAGTCTCCTTGGAGGGCCTGGAACCTGAGTC  
CTCCTATGAACCTCTGTAGCCTAAATGAAATTTCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCG  
GCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

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**FIGURE 94**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1
MAATLGPLGSWQQWRRCLSA RDGSRMLLLLLLLGSGQGPPQVGAGQTFEY LKREHSLSKPYQGVGTGSSSLWNLM
GNAMVMTQYIRLTPDMQSKQ GALWNRVPCFLRDWELQVHF KIHGQGKKNLHGDGLAIWYTKDRMQPGPVFGNMDK
FVGLGVFVDTPNEEKQQER VFPYISAMVNNGSLSYDHERDGRPT ELGGCTAIVRN LH YDTFLVIRYVKRHITIM
MDIDGKHEWRDCIEVPGVRLPRGY YFGTSSITGDLSDNHDVISL KLFELTVERTPEEEKLHRD VFLPSVDNMKLP
EMTAPLPPLSGLALEFLIVFFSLVFSVFAIVIGIILYNKWQE QSRKRFY
```

**Signal sequence:**

amino acids 1-38

**Transmembrane domain:**

amino acids 310-329

**FIGURE 95**

CTGTGTTAAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACACACATCCCCAAGA  
ACCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTCGCTTGTCCATCTCCCTCCCGGGGGAG  
CCGGCGCGCGCTCCCACCTTTGCCGCACACTCCGGCGAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGA  
ACTCGGATTGCACTCTGAACCCCATGGTGGTTTTTTAAACACTTCTTTTCTTCTTCTCTCTCGTTTTGATTGC  
ACCGTTTCCATCTGGGGGCTAGAGGACAAAGCAGCAGCTTCCCAGCAGCCCTTGTGGCTTGCATCGTCCCA  
TCTGGCTTATAAAAGTTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCCTCGGCTGGCAGAAGGGGGTG  
ACGCTGGGCAGCGGCGAGGAGCGCGCGCTGCTTGGCGGGCTTTGCGCTTGAGGGGCAAGGTGAAGAGCGCA  
CGGCCGTGGGGTTTACCGAGCTGGATTGTATGTTGCACCATGCGCTTCTTGGATCGGGGCTGTGATTCTTCCCCT  
CTTGGGGCTGCTGCTCTCCCTCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTA  
CGGTGCCAAGGGATTACGCTTGGCGGACATCCCCTACCAGGAGATCGCAGGGGGAACACTTAAGAATCTGTCTCTCA  
GGAATATACATGCTGCACCACAGAAGTGAAGACAAGTTAAGCCAAACAAAGCAAACTCGAATTTGAAACCTTGT  
GGAAGAGACAAGCCATTTTGTGCGCACCACCTTTTGTGTCAGGCATAAGAAATTTGACGAATTTTCCGAGAGCT  
CCTGGAGAATGCAGAAAAGTCACTAAATGATATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGA  
AGTCTTCCAGGACCTCTTTCACAGAGCTGAAAAGGTACTACACTGGGGGTAAATGTGAATCTGGAGGAAATGCTCAA  
TGACTTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCTCAGTATCACTTCAGTGAAGACTACCT  
GGAATGCTGTGAGCAATACTACGACAGCTCAAGCCATTGTGGAGAGCTGCCCCGGAACCTGAAGATTACGGTTAC  
CCGCGGCTTCAATTGCTGCCAGGACCTTTGTCCAGGGGCTGACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAA  
GGTCAGCCCCAACCCAGGGGTGTATCCGTGCCCTCATGAAGATGCTGTACTGCCATACCTGTGCGGGGCTTCCCAC  
TGTGAGGCCCTGCAACAACACTACTGTCTCAACGTTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGA  
GTGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACATTGAGTCGGTCAT  
GGACCCGATAGATGTCAAGATTTCTGAAGCTTATGAAACATGCAAGAAAAACAGCATGCAGGTGTCTGCAAAGGT  
CTTTCAGGATGTGGTCAGCCCCAACCTGCTCCAGCCCTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATAC  
ACGTTTCAGGCCCTACAATCCTGAGGAAAGACCAACAACCTGCTCAGGCACAAGCTTGACCGGCTGGTCAAGAGA  
CATAAAAGAGAAATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGCGT  
GACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTTGCCTGAGATCATGAA  
TGATGGGCTCACCAACCAGATCAACAATCCCAGGTTGGATGTGGACATCACTCGGCCTGCACTTTTCATCAGACA  
GCAGATTATGGCTCTCCGTGTGATGACCAACAACATAAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGA  
CACAAGTGATGAATCCAGTGGCTCAGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCTCCACGAGTTTGAGTT  
TGTCAACCAAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGGTTGGACTCTTCTCAGCCCCAGCGTGGCCACTC  
CCTGCTCTCCTGGTCTCTCACCTGCATTGTCTGGCACTGCAGAGACTGTGCAGATAAATCTTGGGTTTTTGGTCA  
GATGAAACTGCATTTTAGCTATCTGAATGGCCAACCTCACTTCTTTCTTACACTCTTGGACAATGGACCATGCCA  
CAAAAACCTTACCGTTTCTATGAGAAGAGAGCAGTAATGCAATCTGCCTCCCTTTTTTGTTCCTCAAAGAGTACC  
GGTGCCAGACTGAATGCTTCTCTCTTCTTCACTATCTGTGGGGACCTTGTTTATTCTAGAGAGAATTCTTA  
CTCAAATTTTTCTGACCAGGATTTTCTTACCTTCATTGCTTTTATGCTGCAGAAGTAAAGGAATCTCACGTT  
GTGAGGGTTTTTTTTTTCTCATTTAAAT

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**FIGURE 96**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914
><subunit 1 of 1, 555 aa, 1 stop
><MW: 62736, pI: 5.36, NX(S/T): 0
MPSWIGAVILPLLGLLLSLPAGADVKA RSCGEVRQAYGAKGFSIADIPYQEIAGEHLRICPQEYTCCTTEMEDKL
SQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMFVRTYGMLYMQNSEVFQDLFTELKRY
TGGNVNLEEMLNDFWARLLERMFQLINPQYHFSE DYLECVSKYTDQLKPFGDVPRKLKIQVTRAFIAARTFVQGL
TVGREVANRVSKVSPTPGCIRALMKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAE
RLEGPFNIESVMDPIDVKISEAIMNQENSMQVSAKVFGCGQPKPAPALRSARSAPENFNTRFRPYNPEERPTT
AAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGH SKARYLPEIMNDGLTNQINNPEVD
VDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSGSGSGCMDDVCPTEFEFVTT EAPAVDPDRR
EVDSSAAQRGHSLLSWSLTCIVLALQRLCR
```

**Signal peptide:**  
amino acids 1-23

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**FIGURE 97**

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTGTTGGTGTCCCTGTCTTGCGTGATATTGACAAACTG  
AAGCTTTTCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGACAGCTTTAGTGGCCGGCCGGCCGCTC  
TCATCCCCCGTAAGGAGCAGAGTCCTTTGTACTGACCAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAA  
TGGGAAGGTTTTATTGAAAACCTACAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTG  
CAGAAATTTTATCCAACTTTGTTTGAAGCTTATATGACAATACCATTTTTCATAGAGTTGTGCCTGGTTTCAT  
AGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGCCATTCAAAGATGAATT  
TCATTACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCAAATGCTGGTTCTCATGATAATGGCAGCCA  
GTTTTTCTTCACACTGGGTTCGAGCAGATGAACCTAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATAC  
AGTATATAACATGTTGCGACTGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAA  
AAGCTGTGAGGTTTTGTTAATCCTTTTGATGACATCATTCCAAGGGAAATTAAGGCTGAAAAAGAGAAACC  
AGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTAGTTTACTTTTCAATTTGGAGAGGAAGCTGA  
GGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAGGGCAAAGCAAAAGTAGTCATGACTTGCTTAA  
GGATGATCCACATCTCAGTTCTGTTCCAGTTGTAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGG  
AGAAGATGAAAGTGCAGAGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAA  
AAAATTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATCAGTCAGCCG  
CAGTGAAGAGCTCAGAAAAAGCAAGACAATTAACCGGAACTCTTAGCAGCAAAACAAAAAAGTAGAAAAA  
TGCAGCAAAACAAGCAGAAAAAGAAGTGAAGAGGAAGAAGCCCTCCAGATGGTGCTGTTGCCGAATACAGAAG  
AGAAAAGCAAAAGTATGAAGCTTTGAGGAAGCAACAGTCAAAGAAGGGAACCTCCCGGGAAGATCAGACCCTTGC  
ACTGCTGAACCAGTTTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGA  
AGTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGTGAAGATGCAAG  
CATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGAATAAAAGAAGGAGGGAAGAAAGCAA  
AAAGCTGATGAGAGAGAAAAAGAAAGAAGATATAATGAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCT  
ACAATGGCCTTGTAACAGCCATTGTTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTGAACCTGTT  
GTCTGGTTTTGAAAAACAATTATCTTGTGTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGGTA  
CATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCTTCCACAAAAA  
AAAAAAAAAAAAAAAAAAAA

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**FIGURE 98**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFIVQGGDPTGTGSGG
ESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNQSQFFFTLGRADELNNKHTIFGKVTGDTVYNMLRLSEVDID
DDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEKPEEEVKKLKPKGTKNFSLLSFGEEAEVEVNRVSQSM
KGKSKSSHDLKDDPHLSSVPVVESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKS
GEGEVEKKS VSRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAEPPDGAVAEYRREKQKYEALRKQ
KKGTSREDQTLALLNQFKSKLTQAI AETPENDIPETEVEDDEGWMSHVLQFEDKSRKVKDASMQSDTFEIIDPR
NPVNKRREESKKLMREKKERR
```

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 109-112 and 201-204

**Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

**Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

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**FIGURE 99**

CTTTTCTGAGGAACCAACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTATCCTCCTGGTACTA  
TTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTACCGCTGAAGTCTGTGCCACACACACA  
ATTTACCAAGGACCCAAAGGAGATGATGGTGAAAAAGGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGA  
CGCATGGGGCCGAAAGGAATTAAAGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCC  
ATTGGGAAGAAGGGTGACAAAGGGGAAAAAGGTTTGTCTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACTGTC  
TGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCTCAAGACATCTATGAAG  
TTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAATTTACTACATCGTGCAGGAAGAGAAGAAC  
TACAGGGAATCCCTAACCCACTGCAGGATTCGGGGTGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACA  
CTCATCGCTGACTATGTTGCCAAGAGTGGCTTCTTTGCGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGA  
CAGTACATGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGACCCCTAT  
GGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCATCTTACCATGTACTTT  
GTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCTACGTATTTGCTATTTTCTGTGACCGTCATTA  
CAGTTATTGTTATCCATCCTTTTTTCTGATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAAATGCTAA  
ACTGAGGTATGGAGCCTCCATCATCAAAAAAAAAAAAAAAAAA

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**FIGURE 100**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980
><subunit 1 of 1, 277 aa, 1 stop
><MW: 30645, pI: 7.47, NX(S/T): 2
MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPEGEGKHGKVGRMGPKGI
KGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGGRYRKFFVGQLDISIARLKTSMKFVKNVIA
GIRETEEFYYIVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDN
TFLQNYSNWNEGEPSDPYGHEDCVEMLSGRWNDTECHLTMYFVCEFIKKKK
```

**Signal peptide:**  
amino acids 1-25



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**FIGURE 101**

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCGCGCGCGGCGCGGACCCCAACCCCGACCCAGAGCTTCTCC  
AGCGGCGGCGCAGCGAGCAGGGCTCCCCGCTTAACTTCCTCCGCGGGGCCAGCCACCTTCGGGAGTCCGGGTT  
GCCACCTGCAAACCTCTCCGCTTCTGCACCTGCCACCCCTGAGCCAGCGCGGGCCCCGAGCGAGT**CATG**GCCA  
ACGCGGGGCTGCAGCTGTTGGGCTTCATTCTCGCTTCTCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGC  
CCCAGTGGAGGATTTACTCCTATGCCGGCGACAACATCGTGACCGCCAGGCCATGTACAGGGGCTGTGGATGT  
CCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGC  
AAGCAACCCGTGCCCTGATGGTGGTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA  
AGTGATGAAGTGCTTGGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGTGCGATATTTCTTC  
TTGAGGTCTGGCTATTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATCTATGACCCTATGA  
CCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGG  
GAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCAAGGCCCTATCCAAAACCTG  
CACCTTCCAGCGGGGAAAGACTACGTG**TGAC**CACAGAGGCAAAAGGAGAAAATCATGTTGAAACAAACCGAAAATGG  
ACATTGAGATACTATCATTAACATTAGGACCTTAGAATTTGGGTATTGTAATCTGAAGTATGGTATTACAAAAC  
AAACAAACAAACAAAAAACCCTATGTGTTAAATACTCAGTGCTAAACATGGCTTAATCTTATTTATCTTCTTTC  
CTCAATATAGGAGGGAAGATTTTCCATTTGTATTACTGCTTCCCATTTAGTAATCATACTCAAATGGGGGAAGG  
GGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTCTATTAAAAATAGACAGTAAAATACTATTCT  
CATTATGTTGATACTAGCATACTTAAATATCTCTAAATAGGTAAATGTATTTAATCCATATTGATGAAGATG  
TTTATTGGTATATTTCTTTTCGTCTTATATACATATGAACAGTCAAATATCATTACTCTTCTTCTATTAGC  
TTTGGGTGCCCTTTGCCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTTCAATCTTCATGCGTGCCCTTT  
TCATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTATTTGTTTTGTGTT  
TCATTGGTCTCTATCTCCTGAATCTAACACATTTCATAGCCTACATTTTAGTTTCTAAAGCCAAGAAGAATTTAT  
TACAAATCAGAACTTTGGAGGCAAATCTTCTGCATGACCAAAGTGATAAATTCCTGTTGACCTTCCACACAAT  
CCCTGTACTCTGACCCATAGCACTCTTGTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCC  
CCAGGTGTTGTAACACAACCTTTATTGATTGAATTTTAAAGCTACTTATTCATAGTTTATATCCCCCTAAACTAC  
CTTTTTGTTCCCATTCCTTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTATATCTTCTTAATAAG  
GTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATAATCTGGTGACAAATATTTCTCTGTAGC  
TGTAAGCAAGTCACTTAATCTTTCTACCTCTTTTTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAG  
AAGAGGTAGTGTGAATATTAATTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTT  
TATTTGCTCAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATTCACTG  
CCTTCCTCTCTCTACCACTTATTTCCACTGAACAAAACCTACACACATACTTCATGTGGTTTCACTGCTTCCCT  
CTCTCTACCACTTATTTCCACTGAACAAAACCTACGCACATACTTCATGTGGCTCAGTGCTTCTCTCTCTA  
CCAGTCTATTTCCATTCTTTAGCTGTGTCTGACATGTTTGTGCTCTGTTCCATTTTAAACACTGCTCTTACTTT  
TCCAGTCTGTACAGAATGCTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAG  
ACCTGGATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTGAGCAAGGCATTTGGCTGCTGTAAGCTTATTG  
CTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCACCTCACAGTGATGTTGTGGGGATCCAGTGAGATA  
GAATACATGTAAGTGTGGTTTTGTAAATTTAAAAAGTGCTATACTAAGGGGAAAGAATTGAGGAATTAAGTGCATAC  
GTTTTGGTGTGCTTTTCAAATGTTTGAAAATAAAAAAATGTTAAG

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**FIGURE 102**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185
><subunit 1 of 1, 211 aa, 1 stop
><MW: 22744, pI: 8.51, NX(S/T): 1
MANAGLQLLGFI LAGWIGAI VSTALPQWRIYSYAGDNIVTAQAMYEG LWMSCVSQSTGQIQCKVFDSLNLSS
TLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDEDEVQKMRMAVIGGAIFLLAGLAILVATAWYGNRIVQEFYD
PMPVFNARYEFGQALFTGWAAASLCLLGALLCCSCPRKTTSYPTPRPYPKPAPSSGKD YV
```

**Important features:****Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

**N-glycosylation site.**

amino acids 72-75

**PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

**ABC-2 type transport system integral membrane protein**

amino acids 119-133

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**FIGURE 103**

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTCTGGAGCGAATTCAGCCTGCAGGGCTGATAAGCGAGG  
CATTAGTGAGATTGAGAGAGACTTTACCCCGCGTGGTGGTTGGAGGGCGCGCAGTAGAGCAGCAGCAGGCGC  
GGGTCCCGGGAGGCCGGCTCTGCTCGCGCCGAGATGTGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACC  
GCGCGCCGCCGCGCTGGCTGTGCGCTGGGCGCTGGTGTGCGGGTGGCTCTTTCTCCTCGGCTTCCTCTTC  
GGGTGGTTTATAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGATGAA  
TTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGCAGGAACAGAACAAAAC  
TTTCAGCTTGCAAAGCAAATTCATCCCAGTGGAAGAATTTGGCCTGGATTCTGTTGAGCTAGCTCATTATGAT  
GTCCTGTTGTCTACCCAAATAAGACTCATCCCACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTC  
AACACATCATTATTTGAACCACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTTC  
TCTCCTCAAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAAATTGGAA  
CGGGACATGAAAATCAATTGCTCTGGGAAAATTTGTAATTGCCAGATATGGGAAAGTTTTTCAGAGGAAATAAGGTT  
AAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCCGACCCTGCTGACTACTTTTGTCTGGGGTG  
AAGTCCATCCAGACGGTTGGAATCTTCTGGAGGTGGTGTCCAGCGTGGAATATCCTAAATCTGAATGGTGCA  
GGAGACCCTCTCACACCAGGTACCCAGCAAATGAATATGCTTATAGGCGTGGAAATTGCAGAGGCTGTTGGTCTT  
CCAAGTATTCCTGTTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAGCACC  
CCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTACTGGAACTTTTCTACA  
CAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGACGAGAATTTACAATGTGATAGGTACTCTCAGAGGA  
GCAGTGGAACCAGACAGATATGTCATTCTGGGAGGTACCCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAG  
AGTGGAGCAGCTGTTGTTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGA  
ACAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTGGTCTACTGAGTGGGCAGAGGAGAATTCA  
AGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTATAGAAGGAACTACACTCTGAGAGTT  
GATTGTACACCGCTGATGTACAGCTTGGTACACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAA  
GGCAAATCTCTTTATGAAAGTTGGACTAAAAAAGTCCTTCCCCAGAGTTTCAAGTGGCATGCCAGGATAAGCAAA  
TTGGGATCTGGAAATGATTTTGGGTGTTCTTCCAACGACTTGGAAATGCTTCAGGCAGAGCACGGTATACTAAA  
AATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATATGAGTTGGTGGAAAAG  
TTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTTCAGGAGGGATGGTGTGTTGAGCTAGCCAAT  
TCCATAGTGCTCCCTTTTGATTGTGAGATTATGCTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATT  
TCTATGAAACATCCACAGGAAATGAAGACATACAGTGTATCATTGATTCACTTTTTTCTGCGAGTAAAGAATTTT  
ACAGAAATTGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCAATAGTATTAAGAATGATG  
AATGATCAACTCATGTTTCTGGAAAGAGCATTTTATGATCCATTAGGGTTACCAGACAGGCCTTTTTATAGGCAT  
GTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTCATTCCCAGGAATTTATGATGCTCTGTTTGAT  
ATTGAAAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTG  
CAGGCAGCTGCAGAGACTTTGAGTGAAGTAGCCTAAGAGGATTTTTTAGAGAATCCGTATTGAATTTGTGTGGTA  
TGTCACCTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAATTTGGTATATTTGAAATAAAGTTGAATATT  
ATATATAA

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**FIGURE 104**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756
><subunit 1 of 1, 750 aa, 1 stop
><MW: 84305, pI: 6.93, NX(S/T): 10
MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEATNITPKHNMKAFLDELKAENIKKFLH
NFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTHPNYISIINEDGNEIFNTSLFEPPPPG
YENVSDIVPPPSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKIVARYGKVFRGNKVNAQLAGAKGV
ILYSDPADYFAPGVKSYPDGWNLPGGGVQQRGNILNLNGAGDPLTPGYPANNEYAYRRGIAEAVGLPSIPVHPIGYY
DAQKLEKMGGSAPPDSSWRGSLKVPYNVGPFTGNFSTQKVKMHIHSTNEVTIRYINVIGTLRGAVEPDRYVILG
GHRDSWVFGGIDPQSGAAVVHEIVRSFGLTKKEGWRPRRTILFASWDAEEFGLLGSTEWAEENSRLLOERGVAYI
NADSSIEGNYTLRVDCTPLMYSLVHNLTKEKSPDEGFEGKSLYESWTKKSPSPFSGMPRISKLGSGNDFEVFF
QRLGIASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY
AVVLRKYADKIYSISMKHPQEMKTYSVSFDLSFSAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAF
IDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA
```

**Signal sequence:**

amino acids 1-40

**N-glycosylation sites.**amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340, 459-463,  
476-480, 638-642**Tyrosine kinase phosphorylation sites.**

amino acids 363-372, 605-613, 606-613, 617-626

**N-myristoylation sites.**amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341, 360-366,  
427-433, 529-535, 707-713

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**FIGURE 105**

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAAGTGTATTTACTGCTGCGTTTTTATGTTGGGAATT  
CCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGAAAGTCAAGCAGCCAGTGGCATCTCAT  
TTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTTTTTTGTACCAGAGGAAATGAATACGACTAGTCATCACATC  
GGCCAGCTAAGATCTGATTTAGACAATGGAAACAATTCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGT  
ACTTTTATCATTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTCTAC  
ATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGAGTTTGTCTATCAAAGTT  
TCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATGAGGCCATTGTACCAGAGATGTCCTCCAGAA  
GGAACATTAGTTATCCAGGTGACAGCAAGTGATGCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTAC  
AGCTTACTTCAAGGCCAGCCATATTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGAT  
AGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTGTCTGGA  
ACAACAAGTGTATTAATTAACCTTTTCAGATGTTAATGACAATAAGCCTATATTTAAAGAAAGTTTATACCGCTTG  
ACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAAT  
GCAGAAATGGATTACAGCATTGAAGAGGATGATTGCGAAACATTTGACATTATTACTAATCATGAACTCAAGAA  
GGAATAGTTATATTAAGAAAGAAAGTGGATTTTGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAAC  
CATCATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAGATCCAGGTGGAAGAT  
GTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTTTGAAGAAACCCACAGGGATCATT  
GTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAATCTCCTATCAGGTATTCTATTACTAGGAGCAAAAGTG  
TTCAATATCAATGATAATGGTACAATCACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTA  
AGTATTACAGCCACAGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATC  
AATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCTGGTCAGGTAATT  
CAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTTTACTTTAATCTATCTGTAGAAGAC  
ACTAACAATTCAGTTTTTACAATCATAGATAATCAAGATAACACAGCTGTCATTTTGACTAATAGAACTGGTTTT  
AACCTTCAAGAAGAACCTGTCTTCTACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACA  
AACACCCCTTACCATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTGTG  
CTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTTCATTATGATCATATTTGGGTTTATTTTT  
TTGACTTTGGGTTTTAAACAACGGAGAAAAACAGATTCTATTTCTGAGAAAAGTGAAGATTTTCAAGAGAAATATA  
TTCCAATATGATGATGAAGGGGTGGAGAAGAAGATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACC  
ATAATGCGGGAACGCAAGACTCGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTT  
GGCCCCGACAGTGCCATATTTCAGGAAATTCATTCTGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTGCCCT  
CCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCCCTGAGCTCCTTAGAATCA  
GCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTTGGGACCTCGCTTTAAAGATTAGCATGCATG  
TTTGGTTCTGCAGTGCAGTCAAATAATTAGGGCTTTTTTACCATCAAATTTTTTAAAGTGCTAATGTGTATTCTGA  
ACCCATGGTAGTCTTAAAGAGTTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGA  
TTTCCCTGGAGTAAATACTCCATGGTTATTTTAAAGTACCTACATGCTGTTCATTGAACAGAGATGTGGGGAGAAA  
TGTAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAATAATGTAGGAAGATATTAAGAGTAGA  
TGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATATCATTATTTACTTAGGAAAGAGTAAAAATACCAAA  
CGAGAAAATTTAAAGGAGCAAAAATTTGCAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTAT  
CATATTGACATGAAAATGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTCCTTT  
ATTTAAA

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**FIGURE 106**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNN
SFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSNDINDNEPKFLD
EPYEAIVPMSPEGTLVIQVTASDADDPSSGNNARLLYSLQGPYFSVEPTTGIVIRISSKMDRELQDEYWVIIQ
AKDMIGQPGALSGTTSVLIKLSVDNDNKPIFKESLYRLTVSESAPTGTSGITIMAYDNDIGENAEMDYSIEEDDS
QTFDIITNHETQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPYY
VFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVENINDNGTITTSNSLDREISAWYNLSITATEKYNIEQ
ISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEEHFYNLSVEDTNNSSFTIIDNQ
DNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIA
ILICIMIIFGFIFLTLGLKQRRKQILFPEKSEDFRENI FQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTS
AEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDLSLQTYAFEGTGSLSLSSLESASVSDQDESVDYL
NELGPRFKRLACMFGSAVQSNN
```

**Important features:****Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 597-617

**N-glycosylation sites.**

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518, 516-519 and 534-537

**Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

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**FIGURE 107**

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAACTCCGGTAAGTACCTAGCCCACATGATTTGACTCAGAGATT  
CTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCCCAAATGCTATATCTATTTCAGGGGCTC  
TCAAGAACAATGGAATATCATCCTGATTTAGAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCT  
CAAAGCAATACCAGGATAGCTGTTGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCT  
GTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGTTCTTTCCAGC  
CCTTGTCTCCTAATTTGGATTATATATGAGAAGAGCTGTTATCTATTTCAGCATGTCACTAAATTCCTGGGATGGA  
AGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCTAAAGATAGACAGCTCAAATGAATTGGGATTTATAGTA  
AAACAAGTGTCTTCCCAACCTGATAATTCATTTTGGATAGGCCTTTCTCGGCCCAGACTGAGGTACCATGGCTC  
TGGGAGGATGGATCAACATTCTCTTCTAACTTATTTTCAGATCAGAACACAGCTACCCAGAAAACCCATCTCCA  
AATTGTGTATGGATTACGTGTGCTCAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGTGAGAAG  
AAGTTTTCAATGTAAGAGGAAGGCTGGAGAAGGAGAGAGAAAATATGTGAGGTAGTAAGGAGGACAGAAAACAGAA  
CAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATGTTTAGAGAGCTTGGCCAACTGTAATCTTAACC  
AAGAAATGAAGGGAGAGGCTGTGATTTCTGTATTTGTGACCTACAGGTAGGCTAGTATTATTTTCTAGTTAG  
TAGATCCCTAGACATGGAATCAGGGCAGCCAAGCTTGAGTTTTTATTTTATTTTATTTTATTTTATTTTATTTT  
GTCTCACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGCCTCAGCCCC  
TCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTGTTTTTTGTAGAGACTGGGTTTT  
GCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAGTGATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGA  
TTACAGATGTGAGCCACCACACCTGGCCCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGG  
TAAGCCATAAGCGAATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGG  
TGTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAAGTGAAGGTGAAATATATTTCTGAAT  
AGCTAAATGAAGAAATGGGAAAAATCTTCACCACAGTCAGAGCAATTTTATTTATTTTCATCAGTATGATCATAA  
TTATGATTATCATCTTAGTAAAAAGCAGGAACCTCTACTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATC  
TGCCATATCTCTAATAGAATCTTTTTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTCGCTCTTGTGTTGCCAGGCTG  
GAGTGCAACGGCACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCCTGCCTCAGCCTCC  
CAAGTAGCTGGGATTACAGTCAGGCACCAACACACCCGGCTAATTTTGTATTTTTTTAGTAGAGACAGGGTTCT  
CCATGTCGGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGCCTGCCTCGGCCCTCCCAAGTGCTGGGATT  
ACAGGCGTGAGCCACTGCACCCAGCCTAGAATCTTGATAATATGTAATTGTAGGGAACTGCTCTCATAGGAAA  
GTTTTCTGCTTTTTAAATACAAAAATACATAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACC  
TCATTGGAACAAGTATTAAACATTTTGAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTTACCAT  
TTTTTTCAGTAATTACTGTAAATGGTATTATTGGAATGAACTATATTTCTCATGTGCTGATTTGTCTTATTT  
TTTTCATACTTTCCCACTGGTGCTATTTTTATTTCCAATGGATATTTCTGTATTACTAGGGAGGCATTTACAGTC  
CTCTAATGTTGATTAATATGTGAAAAGAAATTGTACCAATTTTACTAAATTATGCAGTTTAAATGGATGATTTT  
ATGTTATGTGGATTTCAATTTCAATAAAAAAACTCTTATCAAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTT

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**FIGURE 108**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912  
<subunit 1 of 1, 201 aa, 1 stop  
<MW: 22563, pI: 4.87, NX(S/T): 1  
MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAVVLGTMGVLSSPCP  
PNWIIYEKSCYLFMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQVSSQPDNSFWIGLSRPQTEVPWLWED  
GSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQLCSVPSYSICEKKFSM

**Important features:****Type II transmembrane domain:**

amino acids 45-65

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

**N-myristoylation sites.**

amino acids 35-40 and 151-156

**Homologous region to LDL receptor**

amino acids 34-67 and 70-200.



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**FIGURE 109**

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCACA  
ATATCTTAACCTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAGAC  
CTACCTACCCGTACGCATACATACATATGTGTATATATATGTAACTAGACAAAGATCGCAGATCATAAAGCAAG  
CTCTGCTTTAGTTTCCAAGAAGATTACAAAGAATTTAGAGATGTTATTTGTCAAGATCCCTGTCGATTTCATGCCCT  
TTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCCTTTGGTTTGGGGACATTATGATTTGTGTAAGACTCAGAT  
TTACACGGAAGAAGGGAAAGTTTGGGATTACATGGCCTGCCAGCCGAATCCACGGACATGACAAAATATCTGAA  
AGTGAAACTCGATCCTCCGGATATTACCTGTGGAGACCCTCCTGAGACGTTCTGTGCAATGGGCAATCCCTACAT  
GTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTGAGCTGATGTTTGATTTGAAGGAAG  
ACATCCCTCCACATTTTGGCAGTCTGCCACTTGGAAAGGAGTATCCCAAGCCTCTCCAGGTTAACATCACTCTGTG  
TTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACCAAATGATCCT  
GGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTAGATGCTTTTCA  
CATGGATCCTAAATCCGTGAAGGATTTATCAGCATAACGGTCTTAGAAATCATTTGCACAGAAGAGTACTCAAC  
AGGGTATACAACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTCCGCGCTTTTTGCTGGACCTCGCCT  
ACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAAACTCAGAGATTTCTTTACAGTACACAGACCT  
GAGGATAAGGCTGTTAAGACCAGCCGTTGGGGAAATATTTGTAGATGAGCTACACTTGGCAGCTACTTTTACGC  
GATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCCATGCCACTGTATGTGTGTATGACAACAGCAA  
ATTGACATGCGAATGTGAGCACAACACTACAGGTCCAGACTGTGGGAAATGCAAGAAGAATATCAGGGCCGACC  
TTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAAGGCACTGCAAAATACCTGTATCCCCAGTATTTCCAGTATTGG  
TACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGACGTGCCACAACAACGTGCGCTGCCTGTG  
CCGGCCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGCAGCTGCGGCTCCGACTCTGG  
CCAGGGCGCGCCCCCGCACGGCACCCCGAGCGCTGCTGCTGCTGACCACGCTGCTGGGAACCGCCAGCCCCCTGGT  
GTTCTAGGTGTACCTCCAGCCACACCGGACGGGCCTGTGCCGTGGGGAAGCAGACACAACCCAAACATTTGCTA  
CTAACATAGGAAACACACACATACAGACACCCCACTCAGACAGTGTACAACTAAGAAGGCCCTAACTGAACTAA  
GCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTCTGACTCCAGAGGAGTTGGCAGCTG  
TTGATATTATCACTGCAAAATCACATTGCCAGCTGCAGAGCATATTGTGGATTGGAAAGGCTGCGACAGCCCCCA  
AACAGGAAAGACAAAAACAAACAAATCAACCGACCTAAAAACATTGGCTACTCTAGCGTGGTGCGCCCTAGTAC  
GACTCCGCCCAGTGTGTGGACCAACCAATAGCATTCTTTGCTGTGAGGTGCATTGTGGGCATAAGGAAATCTGT  
TACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAACCTGTGCTTTAGTGAACGTTGCTCTGTAA  
CCCTCGTTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGATGCACATGTGTAACAGCCCCCTCTAAAAGCGCAAG  
CCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGAGCACACCCCACTATACAAGAGTGGCTATA  
GGAAAAAGAAAGTGTATCTATCCTTTGTATTCAAATGAAGTTATTTTCTTGAACACTGTAAATATGTAGATT  
TTTTGTATTATTGCCAATTTGTGTACCAGACAATCTGTTAATGTATCTAATTCGAATCAGCAAAGACTGACATT  
TTATTTTGTCTCTTTCTGTTCTGTTTGTCTTCACTGTGCAGAGATTTCTCTGTAAGGGCAACGAACGTGCTGGCA  
TCAAAGAATATCAGTTTACATATATAACAAGTGAATAAGATTCCACCAAAGGACATTCTAAATGTTTTCTTGT  
GCTTTAACACTGGAAGATTTAAGAATAAAAACTCCTGCATAAACGATTTTCAAGGATTTGTATTGCAATTTCTTA  
AGATGAAAGGAACAGCCACCAAGCAGTTTCACACTCACTTTACTGATTTCTGTGTGGACTGAGTACATTGAGCTG  
ACGAATTTAGTTCCAGGAAGATGGATTGATGTTCACTAGCTTGGACAACCTCTGCAAAATATGAGACTATTTCC  
ACTTGGGAAAAATTACAACAGCAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 110**

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLKVKLDPDPDITCGDP  
PETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI  
TFESGRPDQMILEKSLDYGRWQPYQYYATDCLDAFHMDPKSVKDLSQHTVLEICTEEYSTGYTTNSKIIHFEI  
KDRFALFAGPRLRNMASLYGQLDTTKKLRDFFTVDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN  
LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPKPGTANTCIPSISSIGTNVCDNELLHCQN  
GGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLTGASPLVF

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**FIGURE 111**

GCGTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCTGCGCCTGCACCGCGTAGACCGAC  
CCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCGTGCCCCGACCGGTCCCCGCGCTTTTGTAAAACT  
TAAAGCGGGCGCAGCATTAACGCTTCCCGCCCCGGTGACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCGGC  
TAAGGAACATGGCGAAGGTGGAGCAGGTCTGAGCTCGAGCCGCGAGCAGAGCTCAAATTCGAGGTCCCTTCA  
CCGATGTTGTACACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTACAG  
CACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATTAATGTATCTGTGATGT  
TACAGCCTTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTTTATGGTTTCAGTCTATGTTGCTCCAAGT  
ACACTTCAGATATGGAAGCAGTATGGAAGGAGGCAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGT  
TTGAATTGCCAGCAGAGAATGATAAACACATGATGTAGAAATAAATAAATTATATCCACAAGTGCATCAAAGA  
CAGAAACACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGGAAGAAT  
GTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAACAAGCAGTTCAGGAAGAAGATGGACTGCGGA  
TGAGGAAGACAGTGCAGAGCAACAGCCCCATTTAGCATTAGCCCCAACTGGGAAGGAAGAAGGCCCTTAGCAGCC  
GGCTCTTGGCTCTGGTGGTTTTGTCTTTATCGTTGGTGTAAATTATTTGGGAAGATTGCCTTGTAAGGTTAGCATG  
CACAGGATGGTAAATTGGATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGA  
AATTAATGTATGATGACATCTCACAGGTCTTGCCTTTAAATTACCCCTCCCTGCACACACATACACAGATACACA  
CACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAAGTATTGAGGGGGAAAAAGAATGAT  
CTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAATGGCATAATGTAAATGTCATTTTAAACATTGGTAGG  
CCTTGGTACATGATGCTGGATTACCTCTCTTAAATGACACCCCTTCCTCGCCTGTTGGTGTGCGCCCTTGGGGAG  
CTGGAGCCCAGCATGCTGGGGAGTGCGGTGAGTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCAGGCT  
GCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGTCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAA  
TTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGA  
AATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTTCATGTAGTGAAGTCAAAGT  
TTATTCAGAGATGTTTAAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTATTGTCACAAGAGT  
ACAGTTAATGCTGCGTGCTGCTGAACCTCTGTTGGGTGAACCTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCTGT  
CTCTGGAGAGTCTGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCAGGAAGTGTTTTTTCT  
GGGTGAGTAAATAACAACCTGTCATAGGGAGGGAAATTTCTCAGTAGTGACAGTCAACTCTAGGTTACCTTTTTTAA  
TGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATACCACCTCTCAACCATTACTCACACTTCCAGCGCCCAGGTCC  
AAGTCTGAGCCTGACCTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAA  
GCGAGGGCACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTACTAGTT  
GAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTCTGTTTGACTATGTAGCATCTTGAAA  
AGAAAAATTATAATAAAGCCCCAAAATTAAGAAAA

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**FIGURE 112**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

&lt;subunit 1 of 1, 243 aa, 1 stop

&lt;MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFTDVVTTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIIDAGASINVSVMLQP  
FDYDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRCVFELPAENDKPHDVEINKIISTTASKTET  
PIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREENKQFKEEDGLRMRKTVQSNSPISALAPTGKEEGLSTRLL  
ALVVLFFIVGVIIGKIAL**Important features:****Transmembrane domain:**

amino acids 224-239

**N-glycosylation site.**

amino acids 68-71

**N-myristoylation site.**

amino acids 59-64, 64-69 and 235-240

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**FIGURE 113**

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTGCGCTAAGATTGCTGAGGAGGCGGCGGGTAGCTGGCA  
GGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCTCATGACTTCTCTTGTGGACCATGTCGGTGATCTT  
TTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCCCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTT  
TTTGGAATGGAGGAGACGGCTCAAGAGTTTAGCCTTGCGACTGGCCCAGTATCCAGGTCGAGGTTCTGCAGAAGG  
TTGTGACTTTAGTATACATTTTTCTTCTTTTCGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCCAGC  
AGCCATGGCCTTCTGCTTCTTGAGACCCCTGTGGTGGGAATTCACAGCTTCTATGACACTACCTGCATTGGCCT  
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATTTTAACTATGTAAG  
TTCCTCTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCT  
GGAGGACACAGATGTGGCAAATGGGGTGATGAATGGTCACACACCGATGCACTTGGAGCCTGCTCCTAATTTCCG  
AATGGAACCACTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCTCATTCTG  
AGGAGTTCACCTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTCTGCTGGTTGGACCAAACCTCGTGAGC  
CAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCATCCGGGAGCAGTGATGTCAAACCTCTGCTGCTG  
GGGAAATCTCATCAGCAGGGAGCCTGTGGAAAAGGGCATGTCAAGTGAATCTGGGAATGGCTGGATTCCGAAACA  
TCTGCCCATGTGTATTGATGGCAGAGCTGTTGCCACAAAGCGCCTTTTATTTAGGGTAAATTAACAAATCCATT  
CTATTCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTTACATTTATATGATTCTGGGGTTGCTTCAGAA  
GTGTTATTTTCATGAATCATTATATGATTGATCCCCCAGGATTCTATTTGTTTAATGGGCTTTTCTACTAAAA  
GCATAAAATACTGAGGCTGATTTAGTCAGGGCAAACCATTTACTTTACATATTCGTTTTCAATACTTGCTGTTT  
ATGTTACACAAGCTTCTTACGGTTTTCTTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAACAAAC  
TCAGTAGTACAACCTAACTTGTATAAAAGTGTGTAATAATGTATAGCCATTTATATCCTATGTATAAATTAAT  
GAGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTATTATTAATAAAAAAAAAAAAAAAAAAAAAAG

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**FIGURE 114**

MSVIFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHFSSFGDVACMAICS  
CQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVWHFNYVSSSQMECSLEKIQEELKLQPP  
AVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPV TALGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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**FIGURE 115**

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTGCATTGAAACGTGAGCGCGACCCGACCTTAAAG  
AGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGTTGCCTGCCCTTTAAGGGCGGGGCGTCC  
GGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTC  
TGGGTGCTTGGCGGCGGGCGGCTTCCTCCCCGCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCT  
GAGCAGAGTATGGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAG  
TGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTCAAGAAGCCT  
GCTGAGTTTACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGCGCTCGAGCTGTGCACCTTTACCCCTG  
GCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCCTCGG  
AACTACTACATCCAGTGGCTCAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTTCTCTTCCCCAACCTG  
TCCTCATCTTCTCATGCCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAGGGTGTC  
CTGGGCGGGCTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCTAGGTATGGTGTTGGGTGGCA  
TCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCTATGACTTTTGGGAGTACTATCTCCCCTACCTC  
TACTCATGCATCTCCTTCTGGGGTTCTGCTGCTCCTGGTGCTACTCCACTGGGTCTCGCCCCGATGTTCTCC  
GTCACCTGGGAAGCTGCTAGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAG  
GAGGCAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGTGCTTTAGACATGGAGCTGCTACACAGA  
CAGGTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGCTTCAGCCTGGCAACGGAACCTG  
GGCTACCCCTGGCTATGCTGTGCTTGGTGCTGACGGGCTGTCTGTGCTCATTGTGGCCATCCACATCCTG  
GAGCTGCTCATCGATGAGGCTGCCATGCCCCGAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAG  
CTGGGCTCCTTTGGTGCCGTCATTGAGTTGTACTCATCTTTTACCTAATGGTGCTCCTCAGTTGTGGGCTTCTAT  
AGCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCACGACACTGCCATGACGCAGATAATTGGGAAGTGTGTC  
TGTCTCCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTGGGGCTCACTCGCTTTGACCTGCTGGGT  
GACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACATTGTGTTCTCTACAACGCAGCCTTTGCAGGCCTCACC  
ACACTCTGTCTGGTGAAGACCTTCACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCTTTGGGCTGGACAGACTG  
CCGCTGCCCGTCTCCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCAGTCACTCCAGCTGGGGGTGGGAAG  
GAAAAAACTGGACACTGCCATCTGCTGCCTAGGCTGGAGGGAAGCCCAAGGCTACTTGGACCTCAGGACCTGGA  
ATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACTATTGCATAATCTGAGCCAGAGTTTGGGACCA  
GGACCTCCTGCTTTTCCATACTTAAGTGTGGCCTCAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCCTGAT  
CCCAAATCTGTTTACACATCAATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTGA  
TGTGCAATAGGGTGGGGTAGGGGCAGGGAAAGGACTGGGGCAGGGCAGGCTCGGGAGATAGATTGTCTCCCTTGC  
CTCTGGCCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACCTGAAAGACCAAGGGGATAGG  
GAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGAAAAAA

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**FIGURE 116**

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNKIALELCTFTLAIA  
LGAVLLLPFSIISNEVLLSLPRNYIIQWLNGSLIHGLWNLVFLFPNLSLIFLMPFAYFFTESEGFAGSRKGV LGR  
VYETVVMMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLPYLYSCISFLGVLLLLLVCTPLGLARMF SVTG  
KLLVKPRILLEDLEEQLYCSAFEEAALTRRICNPTSCWLP LDMELLHRQVLALQTQRV LLEKRRKASAWQRNLGYP  
LAMLCLLVLTGLSVLIVAIHILELLIDEAAMP RGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVG FYSSP  
LFRSLRPRWHD TMTQIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDFGRENWLGNFYIVFLYNAAFAGLT TLC  
LVKTFTA AVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ



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**FIGURE 117**

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCTGCTGTCTCGCTG  
CTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTG  
TGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCGACAAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG  
TTCAAAGCAGTGACTGAGACAACCAAGGGTGTCTCTGTGGCCACAAACCACCAGAGTCGAGAGGTGGAAATGAGC  
ACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAGTCTCTCTGGTGATCAGAGACGCGCAGATG  
CAGGATGAGTCACAGTACTTCTTTTCGGGTGGAGAGAGGAAGCTATGTGACATATAATTTTCATGAACGATGGGTTC  
TTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCAGGACCACAACACCGACCTCACCTGCCATGTGGAC  
TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCAGAGACCTTGTTATC  
AGCATTTACGTGACAACACGCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCAAAA  
GGCCAGTTCTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGCAGAACAGA  
GTCTCTCTCTCGTCCCATCCCTGGGGCCCTAGACCCTGGGGCTGGAGCTGCCCCGGGTGAAGGTGGGGATTCA  
GGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTGCAGTATCCT  
CCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTCTTGAAACCTTGGGAACGGCAGCTCTCTC  
CCAGTACTGGAGGGCCAAAGCCTGTGCCTGGTCTGTGTACACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACC  
CAGAGGGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCGGGGTCTTGAGCTGCCTCGGTTCAAGTGGAG  
CACGAAGGAGAGTTTACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCAGCTCTCTCTCAGCTCTCGGTGCAC  
TATAAGAAGGGACTCATCTCAACCGGATTCTCCAACGGAGCGTTTCTGGGAATCGGCATCACGCTCTTCTTTTC  
CTCTGCTGGCCCTGATCATCATGAAGATTCTACGAAGAGACGGACTCAGACAGAAACCCCGAGGCCAGGTTTC  
TCCCGGCACAGCACGATCCTGGATTACATCAATGTGGTCCCGACGCTGGCCCCCTGGCTCAGAAGCGGAATCAG  
AAAGCCACACCAAACAGTCTCGGACCCCTCCTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACCAGAAA  
AAGCAGTATCAGTTGCCAGTTTCCCAGAACCCAAATCATCCACTCAAGCCCCAGAATCCCAGGAGAGCCAAGAG  
GAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCTGAGGCCCGGATGCCCAAGGGCACCAG  
GCGGATTATGCAGAAGTCAAGTTCCAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGG  
TAGAGTAAGAGGTTGAAGATAACAGAGTGCAAAGTTTCTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT  
CTCTTTCTCTCTCTTTTAAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATCCAGCACTTTGGGAG  
GTTGAGGTGGGCAGATCGCCTGAGGTGCGGAGTTCGAGACCAGCCTGGCCAACTTGGTGAAACCCCGTCTCTACT  
AAAAATACAAAATTAGCTGGGCATGGTGGCAGCGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAA  
TCACTTGAACCTGGGAGACGGAGGTTGCAGTGAGCCAAGATCACACCATTCACAGCCAGCCTGGGCAACAAAGCG  
AGACTCCATCTCAAAAAAAATCCTCCAAATGGGTGGGTGTCTGTAATCCAGCACTTTGGGAGGCTAAGGTG  
GGTGGATTGCTTGAGCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAACCCCATCTCTACAAAAAATACA  
AAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAGTCCAGCTGTGACACATTTAAACCAGAGCAACTCCATCTGG  
AATAGGAGCTGAATAAAATGAGGCTGAGACCTACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAG  
GATGAGACAGGAGGTCCGTACAAGATACAGGTCAATAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCA  
ACCAAATCCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCTGCTCACTGCTACACTCCTGACAGCAC  
CATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCAAAAGGGGGAGGAATGAATAAT  
CCACCCCTTGTTTTAGCAAATAAGCAAGAAATAACCATAAAAGTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGT  
CTATGGAGTAGCCATTCTTTTGTTCCTTTACTTTCTTAATAAACTTGCTTTCACCTTAAAAAA

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**FIGURE 118**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002
><subunit 1 of 1, 544 aa, 1. stop
><MW: 60268, pI: 9.53, NX(S/T): 3
MLLPLLLSSLLGGSQAMDGREWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYWFKAVTETTTKGAPVAT
NHQSREVEVMSTRGRFQLTGDPFAKGNC SLVIRDAQM QDESQYFFRVERGSYVTYNFMNDGFFLKVTVLSFTPRPQD
HNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLCAADSQPP
ATLSWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDSVQYPPENLRVMVSQANRTV
LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSQSPDQPGVLELPRVQVEHEGEFTCHARHPLGS
QHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPT
AGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPR
PEARMPKGTQADYAEVKFQ
```

**Important features:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins signature.**

amino acids 365-371

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**FIGURE 119**

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCCTTGGGGGGCCTCCGGGATTGCTACCTTTT  
TGGCTCCCTGCTCGTCAACTGCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCCTTGCGCAA  
GGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG  
GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGAGCAGGCGAATCGCACTGGAGGCCCTCTTCGCTTG  
CCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAGGAAAGCAA  
GGAGAACCAGTGGTTGGGAGTCACTGTTTCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACACCGATA  
TGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTCGCTGCTTTGTGCTCAGCCAGGA  
CCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATT  
TGGGTTCTGCCAGCAGGGCACAGCTGCCGCTTCTCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC  
CTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGACGACGG  
TCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCTCATCCCGGTCCCTGCCAACAGCTACTTTGGCTT  
CTCTATTGACTCGGGGAAAGGTCTGGTGCGTGCAGAAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCACCA  
CAAGGGTGCTGTGGTCTCCTGCGCAAGGACAGCGCAGTCCGCTGGTGCCCGAGGTTATGCTGTCTGGGGAGCG  
CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTATGGCTGGCCAGACCTGATAGTGGG  
TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGTGCTGTGTATGTGTACTTGAACCAGGGGGGTCACTG  
GGCTGGGATCTCCCCTCTCCGGCTCTGCGGCTCCCCTGACTCCATGTTTCGGGATCAGCCTGGCTGTCTGGGGGA  
CCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCCCTTTGATGGTGATGGGAAAGTCTTCATCTACCA  
TGGGAGCAGCCTGGGGGTTGTGCGCAAACTTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG  
CTACTCCCTGTGAGGCAGCTTGATATGGATGGGAACCAATACCTGACCTGCTGGTGGGCTCCCTGGCTGACAC  
CGCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCT  
GGAGCAGCCCACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCC  
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGT  
TCCCGTGTGACGTTCCCTGAGCCGTAACCTGGAAGAACCAAGCACCAGGCCTCGGGCACCGTGTGGCTGAAGCA  
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAATGTCAAAGACAAGCTTCGGGGCCATTGT  
AGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCGGCGACAGGCTCCTGGCCAGGGGCTGCCCTCAGTGCG  
CCCCATCCTCAATGCCCCACCAGCCAGCACCCAGCGGGCAGAGATCCACTTCCCTGAAGCAAGGCTGTGGTGAAGA  
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCACACC  
TCTGCCCATGGATGTGGATGGAACAACAGCCCTGTTTGCAGTGAAGTGGGCAGCCAGTCAATTGGCCTGGAGCTGAT  
GGTCACCAACCTGCCATCGGACCCAGCCAGCCAGGCTGATGGGGATGATGCCCATGAAGCCCAGCTCCTGGT  
CATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCTCGGAGAGAAGCACTGCTGCTGTCCAA  
TGAGAAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCAGGTCACTTCTACCTCAT  
CCTTAGACCTCCGGGATCAGCATTGAGACCACGGAACCTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAACA  
GGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTCAATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCC  
CCAGCAACTCTTCTCTCTGGTGTGGTGGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGT  
CAAGTATGAGGTACGGTTTCCAACCAAGGCCAGTGCCTCAGAACCCTGGGCTCTGCCTTCTCAACATCATGTG  
GCCTCATGAGATTGCCAATGGGAAGTGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCTGG  
GCAGAAAGGGCTTTGCTCTCCAGGCCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGCGGCGGGGA  
GCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGGAGCGGAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGC  
TGAGAAGAAGAAAAACATCACCTGGACTGCGCCCGGGGCACGGCCAACTGTGTGGTGTTCAGCTGCCACTCTA  
CAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCGCTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC  
TGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCACAGTGAAGTCTCCATAAAGAAGTTGATGCTCCGAGA  
TGCTCCACAGTGATCCCAGTGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCTGGTGGGT  
CATCTCCTGGCTGTACTGGCTGGGCTGCTGGTGCTAGCACTGCTGGTGCTGCTCCTGTGGAAGATGGGATTCTT  
CAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCGAGTACCATGCGGTGAAGATTCTCGGGAAGACCGACAGCA  
GTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAGCCCCCGGGGAGGGGCCCGGATGCACA  
CCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCCCTAGGTTCC  
CATGTCCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT  
GGGCTGCTGGTGTGCGATCAAGATTTGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCCACCCACAAGAAC  
TCTTCCCACCAACTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGG  
TGAGAAGGGCAGGGGTGCTGATGCAAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCATTACCCCTGT  
GTAACAGGACCCCAAGGACCTGCCTCCCCGGAAGTGCTTAACCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGA  
CTCAGGCTGCTCCTTCTTAGTTTCCCTCTCATTTGACCTTAGTTTGTGCTGCCATCAGTCTAGTGGTTTCGTGGT  
TTCGTCTATTTATTAATAAATATTTGAGAACAAAAA

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**FIGURE 120**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737
><subunit 1 of 1, 1141 aa, 1 stop
><MW: 124671, pI: 5.82, NX(S/T): 5
MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQLQPRPQSWLLVGAP
QALALPGQQANRTGGFLFACPLSLEETDCYRVDIDQGADMQKESKENQWLGVSVRSQPGGKIVTCAHRYEARQRV
DQILETRDMIGRCFVLSQDLAIRDELDGGEWKFCGRPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGT
ARVELCAQGSADLAHLDDGPYEAGGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVI
LRKDSASRLVPEVMLSGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVYVYLNQGGHWAGISPL
RLCGSPDSMFGISLAVLGD LNQDGFDPDIAVGAPFDGDGKVFIYHGSSLGVVAKPSQVLEGEAVGIKSFYSLSGS
LDMDGNQYPDLLVGS LADTAVLFRARPILHVSHEVSIAPRSIDLEQPN CAGGHSVCVDLRVCF SYIAVPSSYSPT
VALDYVL DADTD RRLRGQVPRVTFLSRNLEEPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTL SYS
LQTPRLRRQAPGQGLPPVAPILNAHQ PSTQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVD
GTTALFALS GQPVIGLELMVTNLPSDPAQFPQADGDDAHEAQLLVMLPDSLHYS GVRALDPAEKPLCLSNENASHV
ECELG NPMKRGAQVT FYLILSTSGIS IETTELEV ELLLATISEQELHPVSARARVFIELPLSIAGMAIPQQLFFS
GVVRGERAMQSERDVGSKVKYEVT VSNQGQSLRTLGS AFLNIMWPHEIANGKWLLYPMQVELEGGQGPQGKGLCS
PRPNILHLDVDSRDRRRRELEPPEQQEPGERQE PSMWWPVSSAEKKKNITLDCARGTANC VVFSCPLYSFDRAA
VLHVWGRLWNSTFLEEYS AVKSLEIVIRANITVKSSIKNLMLRDASTVIPVMVYLDPM AVVAEGVPWWVILLAVL
AGLLVLALLVLLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKKEKTGTILRNNWGS PRREGPD AHPILAAD
GHPELGPDGHPGPETA
```

**Important features:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 1040-1062

**N-glycosylation sites.**

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

**Integrins alpha chain proteins.**

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

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**FIGURE 121**

GGCAGGAGGCGGGGCGGGGAGTGC GCGGGATGCGCCCCGGGAGCCACAGCCTGAGGCCCTCAGGTCTCTGCAGGTGTC  
GTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCAGCAGCTTTAGCCCATGAGGAGGATGT  
GACCGGGAGTGAAGTCAGGAGCCCTCTGGAAGCATGGAGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCA  
TCTTTCTGGCTTCGTTTGCAGCCTTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGC  
GCTATGATTCTAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAACTGG  
ACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATCGAAGATGCCTCGGGTC  
TCATGTCCCCTGCATTGCCATCTTGAAGATTTGTCACACTCTGACAGAGAAGCTTGTTGCCATGACAATGGGCT  
CTGGGGCCAAGATGAAGACTTCAGCCAGTGTGACGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGG  
ATGATGTTGTGAAGTCGATGTACCCCTCCGTTGGACCCCCAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGT  
CTGTCACTCACCTGGTGCTGGTGACAAGGAATGCCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACCAGTCTC  
TGTCGGCTGCTGAGGAGCATTTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAGCCAGATAAAGGCCTCCCAG  
GCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTTTAGTGCCTACAGGCCAGCAGCTAGCCATGAAGGCCCTGC  
CGCCATCCCTGGATGGCTCAGCTTAGCCTTCTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTT  
CAGCTGTGTGTGCATAGTAAAGCAGGAGATCCCCGTCACTTTATGCCTCTTTGCAAGTGCAGGAGTGTGGCTGGT  
GAGTGGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAACCTGGTGGAC  
TGTCAGCTTTATTTAGCTCACCTAGTGTTCAGAAAATTGAGCCACCGTCTAAGAAATCAAGAGGTTTCACAT  
TAAAATTAGAAATTTCTGGCCTCTCTCGATCGGTGAGAATGTGTGGCAATTCTGATCTGCATTTTCAGAAGAGGAC  
AATCAATTGAACTAAGTAGGGGTTTCTTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTTATT  
TGTATTATCTGCCTGGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAAGTTTGGGTTTGAAGCTGAGGAAC  
TACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTGGATAGTAAATTT  
ATACTTATGTTTCCCTCAAAAAAAAAAAAAA

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**FIGURE 122**

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSELELDDVVITNPHIE  
AILENEDWIEDASGLMSHCIALKICHTLTEKLVAMTMGSGAKMKTSASVSDIIVVAKRISPRVDDVVKSMYPPL  
DPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWIDQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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**FIGURE 123**

CCCTTACATCCTCCTAGGACCCGGTCGGTAGTCGTCGCCCCAGCCCCGCCGGGGGCGCAGCGCCCGAGCCGCGGCC  
CTCGAGACGGGACCGAGAGCATC**ATG**GGCAGCACTGTCCCGCGCTCCGCCTCCGTGCTGCTTCTGCTGCTGCTCC  
TGCGCCGGGCGGAGCAGCCCTGCGGGGCGGAGCTCACCTTCGAGCTGCCGGACAACGCCAAGCAGTGCTTCCACG  
AGGAGGTGGAGCAGGGCGTGAAGTTCTCCCTGGATTACCAGGTCATCACTGGAGGCCACTACGATGTTGACTGCT  
ATGTAGAGGACCCCCAGGGGAACACCATCTACAGAGAAACGAAGAAGCAGTACGACAGCTTCACGTACCGGGCTG  
AAGTCAAGGGCGTTTATCAGTTTGGCTTCAGTAATGAGTTTTCCACCTTCTCTCACAAGACCGTCTACTTTGACT  
TTCAAGTGGGCGATGAGCCTCCCATTTCTCCAGACATGGGGAACAGGGTCACAGCTCTCAGGATGGAGTCCG  
CCTGCGTGACCATCCATGAGGCTCTGAAAACGCTGATTGACTCCCAGACGCATTACCGGCTGCGGGAGGCCCAGG  
ACCGGGCCCGAGCGGAAGACCTTAATAGCCGAGTCTCTTACTGGTCTGTTGGCGAGACGATTGCCCTGTTCTGTTG  
TCAGCTTCAGTCAGGTGCTACTGTTGAAAAGCTTCTTCACAGAAAAACGACCCATCAGCAGGGCAGTCCACTCCT  
**AG**CCCCGGCATCCTGCTCTAGGGCCCCCTCATGCCCCAGGCTGGAGCAGCTCTCCTAGGTCACAGCCTGCTGGGCT  
GGGTGCGGTAGCCCAGGGTGGAGGCAGAACGATGCTGCTGTGGTAGCCCTTTGCCTTTTCATGCCCATGCTTGATT  
CTTGCACCTCAGCAGCTGAAGGTCTCAGAGACCAGTAATCAGAAGGCATCCGACTGCATTAAGTGTGCAGCGCTG  
AAAAGACATTTACAAC TAGGCCAGGGATTAGCCACTGTGGGAGGGTGGACAGGCAATGGTTTCAAGTGGCCTGGCTG  
TTGGCAGGAACCTCAAGTGCCAGGCCTCTTGGGCAGCTTAGGGCCCTGCCTCTGTTTCATGATGCATGGGTCAT  
TTGTCTTGGGTGTCCTATCCCATATGGAGAAGAAAGGGGCTCTAAGTTCTGGCTCTTCTTTCTTTGGGGTTCTCT  
GTACCTGAGGAAACAGGCCCTGGGTGACTTTGCAGATCTGCTCACCCCTCGGTGAGCAACAGTGTGAGCCATGCA  
AGCAGGACAGAATGGTGACTGGGTGCCCTTGGTGAGCTGTGTATTTCTAGGAGGTAGAAAACCTGTGGGAAACTG  
TGGCTAATAAAAACTAAGTGTGAGCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 124**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56052
<subunit 1 of 1, 217 aa, 1 stop
<MW: 24777, pI: 5.55, NX(S/T): 0
MGSTVPRSASVLLLLLLLLRRAEQPCGAELTFELPDNAKQCFHEEVEQGVKFSLDYQVITG
GHYDVDCYVEDPQGNTIYRETKKQYDSFTYRAEVKGVYQFCFSNEFSTFSHKTVYFDFQV
GDEPPILPDMGNRVLTALTQMESACVTIHEALKTVIDSQTHYRLREAQDRARAEDLNSRVS
YWSVGETIALFVVSFSQVLLKSFTEKRPISRAVHS
```

**Important features:****Signal peptide:**

amino acids: 1-23

**Transmembrane domain:**

amino acids: 187-201

**N-myristoylation sites:**

amino acids: 26-32, 48-54, 131-137

**Tyrosine kinase phosphorylation site:**

amino acids: 82-91

**Glycosyl hydrolases family 25 proteins:**

amino acids: 53-61



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**FIGURE 125**

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTAGCCCATTTGGCCCCGACGCCTCTGT  
TCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCCTAACGGACTGCAAGATGGAGGAAGGCGGGAACCTAG  
GAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGTCAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCT  
CAGGCTTCCTGCTTTTCCGAAGCCTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTCTTCCCCTTCTACT  
TCCACATCTCCATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCACAT  
TCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTGAGCCTTACGCTGGCCACTGTCAACGCCCGCTGGCTGGAAC  
CCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGAGCGAGGCCTGGGTGGGGAGGTACCAGGCA  
GCCACCAGGGTCCCGATCCCTACCGCCAGCTGCGAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCT  
TCCGCTACCATGGGCTGTCCTCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTG  
CCCTGAAATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAAAAAAAA  
AAAAAA

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**FIGURE 126**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

&lt;subunit 1 of 1, 231 aa, 1 stop

&lt;NX(S/T): 0

MEEGGNLGGLIKMHVLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISMGCAFINLCILASQ  
HAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKERGLGGEVPGSHQGPDPYRQLREKDPKY  
SALRQNFERYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85

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**FIGURE 127**

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCGGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGC  
**CATG**ATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGATTTGGAGTGTTTTCCTGTTCTTTGG  
AATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAAT  
TGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGT  
ATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTGTTCAGGGG  
CTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAATTTACCTGGAATTAG  
ATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTAT**TAA**CAACAAGTGAATTTGAAGACTCATTTAAATA  
TTGTGTTATTTATAAAGTCATTTGAAGAATATTCAGCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTT  
TACAGGAGTTTTAAACGTATAGCCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAACACAGGCTTCTA  
CTCAAGTGAACAAAGAAGAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAACTC  
TTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAACTGTGGTGCCTGTTTCT  
TTTCTTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCTTTTAGAAGTGTCCACTGCAATGGCAAAAA  
TATTTCCAGTTGCACTGTATCTCTGGAAGTGATGCATGAATTCGATTGGATTGTGTCAATTTAAAGTATTAAAC  
CAAGGAAACCCCAATTTTGATGTATGGATTACTTTTTTTTTGNGCNCAGGGCC

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## **FIGURE 128**

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQKHKMKATGFFLGGV  
FVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGIRSFVDKVGESNNMV

**Important features:**

**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

**N-myristoylation sites.**

amino acids 11-16, 51-56 and 116-121

**Aminoacyl-transfer RNA synthetases class-II protein.**

amino acids 49-59

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**FIGURE 129**

AATTCAGATTTTAAAGCCCATTTCTGCAGTGGAAATTTTCATGAAGTAGCAAGAGGACACCATCTTCTTGATTATACA  
AGAAAGGAGTGTAACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGGCCTCCTAATCCTCTGTGGTT  
TTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTGATAAGTACATTTTATCACTGGATGTGACT  
CGGGCTTTGGAACTTGGCAGCCAGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAAT  
CAGGATCAACAGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGA  
ATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTG  
GTGTTCCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAACCTGT  
TTGGAATCATCAGTGTGACACTAAATATGCTTCCCTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCA  
GTGTTGGAGGTCGCCCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAAGGTTTCAATGACA  
GCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAAACTTGG  
CAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCAGACATCAACAACAATATG  
GAGAAGGTTACATTGAAAAAGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGG  
TGGTAGAGTGCATGGACCACGCTCTAACAAGTCTCTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA  
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGG  
CTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGATTTCAAGAAC  
ACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGATCGTGTCTATTTGGATTGCAAA  
AGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGT  
ACATCACATAGGCAAGTCCCTGCCCTGTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTT  
GCCCATTCAAAATGATCTTTACCGTGGCCTGCCCATGCTTATGGTCCCAGCATTACAGTAACTTGGAATGT  
TAAGTATCATCTCTTATCTAAATATTTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAA

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**FIGURE 130**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESGSTALKAETSE
RLRTVLLDVTDPENVKRTAQWVKNOVGKGLWGLINNAGVPGVLAPTDWLTLEDYREPIEVNLFGLISVTLNMLP
LVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDLSRRDMKAFGVHVSCEPGLFKTNLADPVKVIKKLA
IWEQLSPDIKQQYGEGYIEKSLDKLKGKNSYVNMDLSPVVECMDHALTSLEFPKTHYAAGKDAKIFWIPLSHMPAA
LQDFLLLKQKAE LANPKAV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

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**FIGURE 131**

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAAGCCATGAACATCA  
TCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCTTGGAGTCGTTGGTGAAGTTTTTCATTCCTC  
AGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCATTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTT  
ATGAATTTGCAAAACGACAGAGCATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTG  
AGTGCCGAAAAC TAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCTCTC  
TAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACAGTATATCCAGCCGATC  
TTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAACATCCTAGGACATTTTTGGATCACAAAAG  
CACTTCCTCCATCGATGATGGAGAGAAATCATGGCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGA  
TTCTTACCTCATCCCATATTGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTC  
AGGCCTTGGGAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTACACAAAAATC  
CAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATAGATGGAATACTTACCAATA  
AGAAAATGATTTTTGTTCCATCGTATATCAATATCTTTCTGAGACTACAGAAGTTTCTTCTGAACGCGCCTCAG  
CGATTTTAAATCGTATGCAGAATATTCAATTTGAAGCAGTGGTTGGCCACAAAATCAAATGAAATGAATGAATA  
AGCTCCAGCCAGAGATGTATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTACAT  
TTTTTCAGTCCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTAATTACCTGT  
CTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGTCTGTTTTTCTTTCATGCCTCTTAAAACTTCTG  
TGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATATTTTATTTTTCCATTTAAAGGTGGACAAAAGCTACC  
TCCCTAAAAGTAAATACAAAGAGAACTTATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTG  
TAGCCATGCCACAGAATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTT  
TATCTCAACCTGGACATATTTTAAGATTGAGCATTTGAAAGATTTCCCTAGCCTCTTCCTTTTTTCATTAGCCCAA  
AACGGTGAACCTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTATAACTCTGAAGTCCACCAAAGTGGA  
CCCTCTATATTTCTCCCTTTTATAGTCTTATAAGATACATTATGAAAGGTGACCGACTCTATTTTAAATCTCA  
GAATTTTAAGTTCTAGCCCCATGATAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGAT  
GTTTAGACAATTTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAAACA  
ATGGACCCAAGAGAAGAA

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**FIGURE 132**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

&lt;subunit 1 of 1, 300 aa, 1 stop

&lt;MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIISYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSILVLWDINKRGVEE  
TAAECRKLGVTAHAYVVDSCNREEIYRSLNQVKKEVGDTVIVVNNAGTVYPADLLSTKDEEITKTFEVNIGHFW  
ITKALLPSMMERNHGHIVTVASVCGHEGIPYLI PYCSSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGF  
TKNPSTRLWPVLETDEVVRSIDGILTNKKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

**Important features:****Signal peptide:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-33 and 58-61

**Short-chain alcohol dehydrogenase family protein**

amino acids 165-202, 37-49, 112-122 and 210-219



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**FIGURE 133**

CTGAGGCGGCGGTAGCATCGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCGCACTCGCTTT  
CCAGCACCTCAACACGGACTCGGACACGGAAGTTTTCTTCTTGGGGAAGTAAAAGGTGAAGCCAAGAACAGCAT  
TACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGACATTCAGAAATATATTCCATGCTATCAGCT  
TTTGTAGCTTTTATAATTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAA  
TGTGGTAGGTTGGTACAAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAAA  
CTTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTC  
TACTCATCGACTGGAACATTCTTATATAAACTCAAAAAGGACTTTTTTACAGGGTACCTTTAGTGGTTGCCAA  
TCTGGGCATGTCTGAACAACTGGGTTATAAACTGTATCAGGTTCCGTGTATGTCCACTGGTTTTAGCCGAGCAGT  
ACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGC  
TTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACTAGTAAA  
GGATGTAAACAGATTAAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAGGCAGCAAGAGAGAAGAACAT  
CCAAAAAGACCCTCAGGAGAACATTTTTCTTTGTCAGGCATTACGGACCTTTTTTCCAAATCTGAATTTCTTCA  
TTCATGTGTTATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACACCACCATCTCGATGTAGT  
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAA  
GCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGACAAACGATC  
TAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCCCAGAAACAGATGAAGAAATTGA  
AAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACATTTGATCCTTTTAACTTACAAGGAGATTTTTTT  
ATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAAGTTCATTTGTT  
TTTACTATGTTACCTGTTTGCAGTAATACACAGATAACTCTTAGTGCAATTTACTTCACAAAGTACTTTTTTCAA  
CATCAGATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCTTACACAGACACA  
TTCTTTAGAATTGGAAGTAGGACAGGACAGTGGCTCACACCTGTAATCCCAGCACTTAGGGAAGACAAGTC  
AGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATTGAGACCATGCTATTAAAAAATAAA  
ATGGAAAAGCAAGAATAGCCTTATTTTCAAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAATA  
TTCTCCTTAAGTGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAAT  
AAATTTGCAAAACATCATCTAAATTTAAAAAATAAAAAAAAAAAAAA

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**FIGURE 134**

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLGGEVKGEAKNSITDSQMDDVEVVYTTIDIQKYIPCYQLFSFYN  
SSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQLVFLLLTPSIITESCSTHRL  
HSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEE  
LKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS  
LKNRHVSKSSCNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDLDQDKRSKANTG  
SSNQDKASKMSSPETDEEIEKMKGFGEYSRSTF

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**FIGURE 135**

GGCACAGCCGCGCGGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCC  
CAAGCAGCGCGCAGCGAACGCCCGCCGCCGCCACACCCCTCTGCGGTCCCCGCGGCGCCTGCCACCCTTCCCTCC  
TTCCCCGCGTCCCCGCCTCGCCGGCCAGTCAGCTTGCCGGGTTCGCTGCCCGCGGAAACCCCGAGGTACCAGCC  
CGCGCCTCTGCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCTGGCCCGCGCCTGGCACCGGGG  
ACCGTTGCTGACGCGAGGCCAGCTCTACTTTTCGCCCGCGCTCCTCCGCTGCTCGCTCTTCCACCAACT  
CCAACCTCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCCGCTGCCGTAGCGCCGC  
TTCCCGTCCGGTCCCAAGGTGGGAACGCGTCCGCCCGGCCCGCACCATGGCACGGTTTCGGCTTGCCCGCGCTT  
CTCTGCACCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCGA  
CGTCTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATC  
TGTCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTTCAA  
AGTGTGGTCAGCGAACAGTGCAATCATTTGCAAGCTGCTTTGCTTCACGTTACAAGAAGTTTGATGAATTCTTC  
AAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAA  
AATTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAA  
ATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTGGTGAACCTCCAGTACCACCTTACAGAT  
GAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCTCGCAAATGAAGCTC  
CAGGTTACTCGTGCTTTTGTAGCAGCCCGTACTTTTCGTCAAGGCTTAGCGGTTGCGGGAGATGTCTGTGAGCAAG  
GTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAGATGATCTACTGCTCCACTGCCGGGGT  
CTCGTGACTGTGAAGCCATGTTACAATACTGCTCAAACATCATGAGAGGCTGTTTGGCCAACCAAGGGGATCTC  
GATTTTGAATGGAACAATTTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGAGGGTCTTTCAACATTGAA  
TCGGTCATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGATAATAGTGTTCAAGTGCTC  
CAGAAGGTTTTCCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTTCTGTTCCATCTCTGAAAGT  
GCCTTCAGTGCTCGCTTCAGACCACATACCCCCGAGGAACGCCCAACCACAGCAGCTGGCACTAGTTTGGACCGA  
CTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTCTGGTCTTCCCTTCGGAGCAACGTTTGCAAC  
GATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTACCTGTTT  
GCAGTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAAACCAGACATA  
CTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG  
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCA  
GAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGTCTCT  
GGGGCACAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGGTTATGCAGAGAGAGTGAGATTATTCTCA  
AACTCTGAGAAAAAGTGTTTATCAAAAAAGTTAAAGGCCACAGTTATCACTTTTCTACCATCCTAGTGACTTTGC  
TTTTTAAATGAATGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGCTGACTTTGTTTTT  
TCATTCACTTTTGGGAGGAAAAGGGACTGTGCATTGAGTTGGTTCTGCTCCCCAAACCATGTTAAACGTGGCT  
AACAGTGATAGGTACAGAACTATAGTTAGTTGTGCATTTGTGATTTTATCACTCTATTATTTGTTTGTATGTTTT  
TTCTCATTTTCGTTTGTGGGTTTTTTTTTCCAACGTGATCTCGCCTTGTTCCTTACAAGCAAACCAGGGTCCCTT  
CTTGGCACGTAACATGTACGTATTTCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTATCATGTTATC  
TTATTAAAGAAAAAGCCCAAAAGC

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**FIGURE 136**

MARFGLPALLCTLAVLSAALLAELKSKSCSEVRRRLYVSKGFNKNDAPLHEINGDHLKICPQGSTCCSQEMEKEY  
SLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGHLYMQNSSELFKDLFVELKRY  
VVGNNVLEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGL  
AVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAE  
RLEGPFNIESVMDPIDVKISDAIMNMQDNSVQVSQKVFQCGPPKPLPAGRISRSISESAFSARFRPHHPEERPT  
TAAGTSLDRLVTDVKEKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNEV  
QVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAGKSANE  
KADSAGVRPGAQAYLLTVFCILFLVMQREWR

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**FIGURE 137**

GCGGGCTGTTGACGGCGCTGCGATGGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTTCCCTCTCAGTCGGA  
CTTCCTGACGCCGCCAGTGGGCGGGGCCCCCTTGGGCGCTCGCCACCACTGTAGTCATGTACCCACCGCCGCCGCC  
GCCGCCTCATCGGGACTTCATCTCGGTGACGCTGAGCTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGGC  
GCGCTCGTGCTGGAGGAAATGGAAGCAACTGTGCGAGATTGCAGCGGAATATGATTCTCTTCCTCCTTGCCCTTTCT  
GCTTTTCTGTGGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTTCAGGCTAGAGGAAGA  
GCAGAAGATGAGGCCAGAAATTGCTGGGTAAAACCAGCAATCCACCCGTCTTACCAGCTCCTCAGAAGGCGGA  
CACCGACCCTGAGAACTTACCTGAGATTTGTCACAGAAGACACAAAGACACATCCAGCGGGGACCACCTCACCT  
GCAGATTAGACCCCCAAGCCAAGACCTGAAGGATGGGAGGAGGAGGCCACAAAAGGCAAGAAGCCCCCTGT  
GGATCCCCGCCCCGAAGGAGATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGG  
CACCGAGCTCCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGGCACACC  
AGTGCATCTGAACATATCGCCAGAAGGGCTGATTGACGTCTTCTGCATGCATGGAAAGGATACCGCAAGTTTGC  
ATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTCAGTGAGTGGTTTGGCCTCGGTCTCACACTGATCGA  
CGCGCTGGACACCATGTGGATCTTGGGTCTGAGGAAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGGAAGAAGTT  
ACACTTTGAAAAGGACCTGGACGTCAACCTGTTTGAGAGCACGATCCGCATCCTGGGGGGCTCCTGAGTGCCCTA  
CCACCTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGCCTTCAGAAC  
ACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACCCGCCACGGTGGACCTCCGACAG  
CACTGTGGCCGAGGTGACCAGCATTAGCTGGAGTTCCGGGAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCA  
GGAGGCAGTGGAGAAGGTGACACAGCACATCCACGGCCTGTCTGGGAAGAAGGATGGGTGGTGGCCATGTTTAT  
CAATACCCACAGTGGCCTCTTCACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTA  
CCTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGAAGCCATCGAGGG  
TGTCAGAACGCACCTGCTGCGGCACTCCGAGCCAGTAAGCTCACCTTTGTGGGGGAGCTTGCCACGGCCGCTT  
CAGTGCCAAGATGGACCACCTGGTGTGCTTCCTGCCAGGGAGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGC  
CAGCCACATGGAGCTGGCCCAGGAGCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGGCTGAG  
TCCCGAGATCGTGCACTTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGGCA  
CAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCTCACAGGGGACCACAAATACAGGA  
CTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACGGGTCCCCTCGGGTGGCTATTCTTCCATCAACAA  
TGTCCAGGATCCTCAGAAGCCCAGCCTAGGGACAAGATGGAGAGCTTCTTCTCGGGGAGACGCTCAAGTATCT  
GTTCTTGCTCTTCTCCGATGACCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCACCCCTCT  
GCCTATCTGGACCCCTGCCAGGGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTGCTGGG  
TCTGTGGCATTTTCCAAGGGCCACGTAGCACCGGCAACCGCCAAGTGGCCCAGGCTCTGAACTGGCTCTGGGCT  
CCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGAGGCCGTGAGTCTTGGTGTGATGCGGGGTGGG  
CTGGGCCGCTGGAGCCTCCGCCTGCTTCTCAGAAGACAGCAATCATGACTCACGATTGCTGAAGCCTGAGCAG  
GTCTCTGTGGGCCGACCAGAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCAGGGT  
GCAGCTCTGCCCCGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGACTCCAGAG  
GCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTCCTGGCCGCCCGCAGGGGGCT  
TGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCTCCAGTGAATGGGTCTTTTCGGTGGAGATAAAAG  
TTGATTGCTCTAACCGCAA

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**FIGURE 138**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTTPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSEGESYDNSKSWRRRSCWRKW
KQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPEIAGLKPANPPVLPAPQKADTDPENLP
EISSQKTQRHIQRGPPHLQIRPPSQDLKDGTEATKRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRR
AEVPTKPPPLPPARTQGTPVHLNRYRQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSEWFGGLGLTLIDALDTMWI
LGLRKEFEERKWWVSKKLHFEKDVDVNLFEFIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKIPYS
DVNIGTGVAHPPRWTS DSTVAEVT SIQLEFRELSRLTGDKKFQEAVEKVTQHINGLSGKKDGLVPMFINTHSGLF
THLGVFTLGARADSYEYLLKQWIOGGKQETQLLEDYVEAIEGVRTLLRHSEPSKLT FVGELAHGRFSAKMDHL
VCFILPGTTLALGVYHGLPASHMELAQELMETCYQMNRMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPET
VESLFYLYRVTGDRKYQDWGWEILQSFSRFRTRVPSSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDD
PNLLSLDAYVFNTEAHPLPIWTPA
```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

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**FIGURE 139**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGACCTGAGTCATC  
CCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACTTACAGCTGCACCGACAGTTG  
CGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGA  
ATCCAGGGGTCCGAGAGGCCACAGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAAT  
GTGAGTGCAAAGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGT  
GCCCCGTGTGATCATTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATT  
CCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTGAGCGC  
CCTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTCTTCTTCTCCCACCTC  
ACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTGTTTGT  
TGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTAC  
CTGAAAGATTCCAGGAACTGTAGCTTCCTAGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAAC  
AGAAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

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**FIGURE 140**

MKVLISL L L L L L P L M L M S M V S S L N P G V A R G H R D R G Q A S R R W L Q E G G Q E C E C K D W F L R A P R R K E M T V S G L P K K Q C  
P C D H F K G N V K K T R H Q R H H R K P N K H S R A C Q Q F L K Q C Q L R S F A L P L



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**FIGURE 141**

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCTGCTATGCAGACGA  
CAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCAAAGCCAGACTTCCCCAAATTCCTAAG  
CCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGAGTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTAT  
GGAATTTGATGATAATGAAGGAAAACATTCATCAAAGTGAATCCTCAGGACACACCCATGTGGCTCCTGGACAA  
TCCAAGAGCAGCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAACTCC  
CAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACCCTGACTGCATTTTGC  
TTTGTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTGATGGAGAGGAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 142**

MAVLVLRLTVVVLGGLLVLFILTCYADDKPKDPDDKPDDSGKDPKPDFPKFLSLLGTEIIENAVEFILRSMRSTGFM  
EFDDNEGKHSSK

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**FIGURE 143**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAGAGCTGGTCTG  
CC**ATG**GACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTACCCTGCCCCTGCACCTCATGGCTCTGC  
TGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCCCCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCA  
AGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTAC  
TGGAGCTGGGCTGCGGAACCGGAGCCAACCTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAA  
ATCCCCACTTTGAGAAGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGG  
CTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGCTGTGCTCTG  
TGCAGAGCCCAAGGAAGGTCTTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGC  
ATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCCACCTGGAAACACATTGGGG  
ATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCCAGTTCTCCGAAATCCAAATGGAACGAC  
AGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCT  
CCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGA  
GAGGGACC**TAG**CAGAATGAGAGAAGACATTCATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC  
AATCTCTAACTTCAATCCC GCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGG  
ACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTCCCTTTCTT  
CGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGTCTCTAGGAACCTGGTCACAAAAG  
TCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGGCA  
CCAGGGAGAATCAGAGATGCTGGGGATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTCTCAAATATTTTT  
TAATAAATAGACGAAACCACG

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**FIGURE 144**

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSSQIKGLTGASGKVALL  
ELGCGTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDMRQLADGSMDVVVCTLVLCV  
QSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFMWQQVFEPWKHIGDGCCLTRETWKDLENAQFSEIQMERQ  
PPPLKWLPVGPIMGKAVKQSFSSKALICSFPSLQLEQATHQPIYPLRGT

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**FIGURE 145**

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGGAAGTTGCCTCATCGCAGGCAGATGTTGGGGC  
TTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAACTAATATTTATATGACAGAAGAAAA  
**AGATGT**CATTCCGTAAAGTAAACATCATCATCTTGGTCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGACCCATA  
ACTTCTCAGCTTGAGCAGTTTGTAAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACT  
TTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTGAAG  
ACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTACAGCACAACACTCGCTCCAATGTGATTTTCTACATTG  
TTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAA  
TTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTT  
TAACTTTTGAAGGTTCTACTTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAA  
TTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATT  
GTGATTCAGCCTCTACTAAAGTTGTTCATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATA  
AAAAGGAAAGAATTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAACC  
TGACGGAATGGAACGACAGAATATAACTAACCAACTGGA AAAATGGATGAACTCAATGTAGAAGAGGGACTGT  
ATAGCAGAACCCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCG  
ATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGA AAAACGATATTCACCTCAGTTGTAAAGGCTGCCA  
AGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGT  
ATATTCCAGACCCAACAGGCAAATTC AACCTAATCCGAAGATATACCGAGATCTCAAACATAAAG**TGA**AACAGAA  
TTTGAAGTGAAGCAAGCATTCTCAGGAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTC  
AATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGT  
CAGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTACTACAATGCTG  
AATGACTGGAAGAAGAACTGATATGGCTAGTTACAGTAGCTGGTACAGATAATTCAAACCTGCTGTTGGTTTTA  
ATTTTGTAACTGTGGCCTGATCTGTAAATAAACTTACATTTTTT

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**FIGURE 146**

MSFRKVNIIILVLAVALFLLVLHNFSLSSLLRNEVTD SGIVGPQPIDFVPNALRHAVDGRQEEIPV VIAASED  
RLGGAIAAINSIQHNTSRNVIFYIVTLNNTADHLRSWLNSDSLKSIRYKIVNFDPKLLEGKV KEDPDQGESMKPL  
TFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNTALKPGHAAAFSEDCDSASTKV VIRGAGNQYNYIGYLDYK  
KERIRKLSMKASTCSFNPGVFVANLTEWKRONITNQLEKMMKLNVEEGLYSRTL AGSITTPPLLIVFYQQHSTID  
PMWNVRLGSSAGKRYSPQFVKAALLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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**FIGURE 147**

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTTCCTCCAAGCA  
AGTCATTTCCCTTATTTAACCAGATGTGTCCCTCAAACACCTGAGTGCTACTCCCTATTTGCATCTGTTTTGATAA  
ATGATGTTGACACCCTCCACCGAATTCTAAGTGGAAATCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCC  
TCGCATTAGCCTTGTCTTTGGCCATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTT  
CATTGGTTATTTTGGGATGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCA  
GCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGG  
CAGTGCTGCTCGTCTTGATTTTGTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCACAAATA  
AAGCCATCAGCAGTGCTCCCTTCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCC  
TCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGAAATATA  
AGCCCCCTTCGGGCATTCGGTACATGTGGTTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCATCCTTG  
CGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGTAAAAATGATCCTCCTGATC  
ATCCCATCCTTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTAAATCT  
CTGTGGTGAGGATTCGAGAATCATTGTCTGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT  
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATG  
CATATACTACAACCTGCTATTAAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCTTGTCCAAGA  
ACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTTCTAGGAAAGGTGTTAGTGGTGTGTT  
TCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGG  
TAGCTTTTTTGGCTACTTAGTAGCCCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGT  
GTTTTGCTGTTGATCTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTT  
TCGTAAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGAGGGAA  
CAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATTTCTTCTAAGAGCCA  
TTTACAGAATAGAAGATGAGACCCTAGAGAAAAGTTAGTGAATTTTTTTTTTAAAGACCTAATAAACCTATTCT  
TCCTCAAAA

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**FIGURE 148**

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTDNLSIELDTERENMKC  
VLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLFQPLWTFAILIFFWVLWVAVLLSLGTAG  
AAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFY  
HQGTVVKGSFLISVVRIPIIIVMYMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFC  
TSAKDAFKILSKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAHSFL  
SVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR



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**FIGURE 149**

GTTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTCCTTAGAATAATTTGTA  
TGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCATTCTGTGTGGTGAAAAATTTTTGAAAAAAA  
ATTGCCTTCTTCAAACAAGGGTGTCTATTCTGATATTTATGAGGACTGTTGTTCTCACTATGAAGGCATCTGTTAT  
TGAAATGTTCCCTTGTGCTGGTGACTGGAGTACATTCAAACAAGAAACGGCAAAGAAGATTAAAAGGCCCAA  
GTTCACTGTGCCTCAGATCAACTGCGATGTCAAAGCCGAAAGATCATCGATCCTGAGTTCATTGTGAAATGTCC  
AGCAGGATGCCAAGACCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTACTCCAGTGTGTGTGGCGC  
TGCCGTACACAGTGGTGTGCTTGATAATTCAGGAGGCAAAATACTTGTTCGGAAGGTTGCTGGACAGTCTGGTTA  
CAAAGGGAGTTATTTCAAACGGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAATCCTTTATCGTCTTAGAAAG  
TAAACCCAAAAAGGGTGTAACTACCCATCAGCTCTTACATACATCATCGAAAAGTCCAGCTGCCCAAGCAGG  
TGAGACCACAAAAGCCTATCAGAGGCCACCTATTCCAGGGACAACCTGCACAGCCGGTCACTCTGATGCAGCTTCT  
GGCTGTCACTGTAGCTGTGGCCACCCCAACCCTTGCCAAGGCCATCCCCTTCTGCTGCTTCTACCACAGCAT  
CCCCAGACCACAATCAGTGGGCCACAGGAGCCAGGAGATGGATCTCTGGTCCACTGCCACCTACACAAGCAGCCA  
AAACAGGCCCCAGAGCTGATCCAGGTATCCAAAGGCAAGATCCTTCAGGAGCTGCCTTCCAGAAACCTGTTGGAGC  
GGATGTCACTGCTGAGCTGTGGCCACCCCAACCCTTGCCAAGGCCATCCCCTTCTGCTGCTTCTACCACAGCAT  
AACTGCAAAATTTGACTTGTGCTTTTTAATTGATGGGAGCACCAGCATTGGCAAACGGCGATTCCGAATCCAGAA  
GCAGCTCCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGCCGGTCCACTGATGGGTGTTGTCCAGTATGG  
AGACAACCTGCTACTCACTTTAACCCTCAAGACACACAGAAATCTCGAGATCTGAAGACAGCCATAGAGAAAAT  
TACTCAGAGAGGAGGACTTTCTAATGTAGGTGGGGCCATCTCCTTTGTGACCAAGAACTTCTTTTCAAAGCCAA  
TGGAACAGAAAGCGGGCTCCCAATGTGGTGGTGGTGTGATGGTGGATGGCTGGCCACGGACAAGTGGAGGAGGC  
TTCAAGACTTGGCAGAGAGTCAAGAAATCAACATTTTCTTCATCACCATTGAAGGTGCTGCTGAAAATGAGAAGCA  
GTATGTGGTGGAGCCCACTTTGCAACAAGGCCGTGTGCAGAACAAACGGCTTCTACTCGCTCCACGTGCAGAG  
CTGGTTTGGCCTCCACAAGACCCTGCAGCCTCTGGTGAAGCGGGTCTGCGACACTGACCGCTGGCCTGCAGCAA  
GACCTGCTTGAACCTCGGCTGACATTGGCTTCGTTCATCGACGGCTCCAGCAGTGTGGGGACGGGCAACTTCCGCAC  
CGTCTCCAGTTTGTGACCAACCTCACCAAAGAGTTTGTAGATTTCCGACACGGACACGGCGATCGGGGCCGTGCA  
GTACACCTACGAACAGCGGCTGGAGTTTGGGTTCGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAA  
GAGGGTGGGCTACTGGAGTGGTGGCACCAGCACGGGGCTGCCATCAACTTCGCCCTGGAGCAGCTCTTCAAGAA  
GTCCAAGCCCAACAAGAGGAAGTTAATGATCCTCATCACCGACGGAGGTCTACGACGACGTCCGGATCCCAGC  
CATGGCTGCCATCTGAAGGGAGTGATCACCTATGCGATAGGCGTTGCTGGGCTGCCAAGAGGAGCTAGAAGT  
CATTGCCACTCACCCCGCAGAGACCACTCCTTCTTGTGGACGAGTTTGACAACCTCCATCAGTATGTCCCCAG  
GATCATCCAGAACATTTGTACAGAGTTCAACTCAGCCCTCGGAACCTGAATTACAGCAGGCAGAGCACCAGCAA  
GTGCTGCTTTACTAACTGACGTGTTGGACCACCCACCGCTTAATGGGGCACGCACGGTGATCAAGTCTTGGGC  
AGGGCATGGAGAAACAAATGTCTTGTTATTATCTTTGCCATCATGCTTTTTTCATATTTCAAACCTTGGAGTTAC  
AAAGATGATCACAAACCTATAGAATGAGCCAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACATTTTGA  
CAATTGTTTTCAAATAAATGTTTCGGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTTGTGAGATT  
TTAAGTTGTTATTTCTGATTTGAACCTCTGTAACCTCAGCAAGTTTCATTTTGTGATGACAATGTAGGAATTG  
CTGAATTAATGTTTGAAGGATGAAAAATAAAAAAGGATGAAAAAAGGATGAAAAAAGGATGAAAAAAGGATG  
AAAAAAGGATGAAAAAAGGATGAAAAAAGGATGAAAAAAGGATGAAAAAAGGATGAAAAAAGGATGAAAAAAGGATG  
AAAAAAGGATGAAAAAAGGATGAAAAAAGGATGAAAAAAGGATGAAAAAAGGATGAAAAAAGGATGAAAAAAGGATG

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**FIGURE 150**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAGCQDPKYHVYG  
TDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSLSLPRWRESFIVLESKPKKGVITYPSAL  
TYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQE  
MDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDG  
STSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNVGRA  
ISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENKQYVVEPNFANKAV  
CRTNGFYSLHVQSWFGLHKTLOPLVKRVCDTDLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKF  
EISDTRIGAVQTYEQRLFEGFDKYSSKPDILNAIKRVGYWSSGTSTGAAINFALEQLFKKSKPNKRKLMILI  
TDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARHSHFFVDEFDNLHGYVPRIIQNICTEFNSQPRN

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**FIGURE 151**

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCT**ATG**CCTTTCCGGCT  
GCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCCTCAGCACCATGGTGCGCCAGGTCCCAGCGGCTCCGCGCC  
AGATCCCGCCCACTACAGTTTTTCTCTGACTCTAATTGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTC  
AGAATTCCAAAGAGTGGTTGAAGTGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTGA  
AACAAACATTGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGAGGC  
TGGATGGCCCTGTTCCGGGCCCTCTCCTGAGAATGGCTGAGGAGGCGGCCCGAAAACCTCCTCCCAGCCTTTCAGAC  
CCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTGAACCCAGGAGAGACCCCTGTACCTGTAC  
GGCAGGGATTGGGACCTTCATTGTTGAATTTGCCACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGT  
GGCCAGAGTGGCTTTGATGCGCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCT  
CACTGGCAAGTGGGTGGCCAGGACGCAGGCATCGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGTGAAAGG  
AGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAGCCATCCGGAACACACCCG  
CTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACTGTGTCCATGCCAGTCTTCCAGTCTTGGAGGC  
CTACTGGCCTGGTCTTCAGAGCCTCATTTGGAGACATTGACAATGCCATGAGGACCTTCTCAACTACTACACTGT  
ATGGAAGCAGTTTGGGGGGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTA  
CCCCTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCTCCTAGAACT  
CGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGGGATTGCAACAATCAAAGATCTGCG  
AGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTGGCCGAGACTGTGAAATACCTCTACCTCCTGTTGA  
CCCAACCAACTTCATCCACAACAATGGGTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGG  
GGCTGGGGGGTACATCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAA  
GGAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTGAAATTCAGAA  
AAACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACACTCTTCTACCAGAAAACCATGACCA  
GGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCCTTCTCAGCTGCCCGAGTCAGCCCTTCACCTCCAAGTT  
GGCATTACTGGGACAGGTTTTCTTAGACTCCTCA**TAA**CCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCT  
AAACTATAATAAATTGCTTTTGGCTATCATAAAA

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**FIGURE 152**

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVEVLQDSVDFDIDVN  
ASVFETNIRVVGGLLSAHLSSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPAFQTPTGMPYGTVNLLHGVNPGET  
PVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFE  
YLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDWYLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFL  
NYYTVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMYLIRATGDPTLLELGRDAVESIEKISKVECGFAT  
IKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYIFNTEAHPIDLAALHC  
CQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPSQP  
FTSKLALLGQVFLDSS

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**FIGURE 153**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTGGGAGGGGGCAGGATGGGAGGGAAAGTGAAGAAAACA  
GAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAACCGATCAGGCATGGGAACCTCCCCTTCGT  
CACTCACCTGTTCTTGCCCCCTGGTGTTCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACG  
CCTATTCCCAGGGCCACCAGAAGCTGAATTTGGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGAT  
GCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGGGGC  
CCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTATCTCATCCTGCTGTGAATAT  
GCACCTGGGGATGTCTCTGTAGAGACAGATGGTGATGGGGGATTTCATGGTGAGCTAAGGAGAGGGGTGGTGGCAG  
TGTCTCTGAAGGTCCATAAAAAGAAAAAGAGAAGTGTGGTAAGGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGT  
TAAAAACCCTAGAAAGCAAAAGGTAGGTAATGTCAGGGAGTAGTCTTTCATGCCTCCTTCAACTGGGAGCATGTTT  
TGAGGGGTGCCCTCCCAAGCCTGGGAGTAACATTTCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCTCGTGCT  
TGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCCTGTGGATGCTTCATTCCAGCCTCAGGGAAGCCTGGCA  
CCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTTCACAGAAGGAGATACTGGGTGGGAAAAAGATG  
GGGCAAAGCGGTATGATGCCTGGCAAAGGGCCTGCATGGCTATCCTCATTTGCTACCTAATGTGCTTGCAAAGCT  
CCATGTTTCCTAACAGATTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGC  
CAAGGTGGGCAGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACTCCATCTCTACTAA  
AAAAAAAAAAATACAAAATAGCTGGGTGCGCTAGTGCATGCCCTGTAATCTCATCTACTCGGAGGCTAAGACA  
GGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTGAGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTG  
ACAGAGTAAGCGAGACTCCATCTCAAAAATAATAATAATAATTGAGTCTCTATCAGGAGTCCATGATCTG  
GCCTGGCACAGTAACATCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGA  
GGTTTGAGACCAGCCTGGGCAACATAGAAAGACCCATCTCTAAATAAATGTTTAAAAAAT

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**FIGURE 154**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13352, pI: 5.99, NX(S/T): 1
MELPFVTHLFLPLVFLTGLCSPFNLDHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPWDGPGSGDRRGDVYR
CPVGGAHNAPCAKGLGDYQLGNSSHPAVNMHLGMSLLETGDGGGMVS
```

**Important features:****Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 70-73

**N-glycosylation site.**

amino acids 98-101

**Integrins alpha chain proteins**

amino acids 67-81

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**FIGURE 155**

GCGAGCTCCGGGTGCTGTGGCCCGGCTTGGCGGGGCGGCTCCGGCTCAGGCTGGCTGAGAGGCTCCCAGCTGC  
AGCGTCCCCGCCCGCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCCCTCGGGGACCAAACAAGCCTGGCAGG  
GTCTCACTTTGTTGCCAGGCTGGAGTTCAGTGCCATGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAA  
GCGATCCTGCTGAGTAGCTGGGACTACAGGACAAAATTAGAAGATCAAAATGGAATAATGCTGCTTTGGTTGAT  
ATTTTTACCCCTGGGTGGACCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAAGGT  
ACCCCGGATTGTGAGTGAAGGACTTTCATCTCACCAGCCCCGATTTGAGGCAGATGCTAAGATGATGGTAAA  
TACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCACTCCCAGCCTTTCTGAATTGGAGGATTATCTTCCCTA  
TGAGACTGTCTTTGAGAATGGCACC CGAACCTTAACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCA  
AAATATCACCACAAAGGGAGTATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCAGACAGCAGTTTCAGCATCTT  
GGACAAAAGGTTCTTAACCAATTTCCCTTTCAGCACAGCTGTGAAGCTTTCACGGGCTGTAGTGGCATTCTCAT  
TTCCCTCAGCATGTTCTAAGTGTGCTGCCCCTGTGTTTATGATGGAAAGGACTATGTCAAAGGGAGTAAAAAGCT  
AAGGGTAGGTTGTTGAAGATGAGGAATAAAGTGGAGGCAAGAAACGTCGAGGTTCTAAGAGGAGCAGGAGAGA  
AGCTAGTGGTGGTGACCAAAGAGAGGGTACCAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAA  
AAAATCTGGCCGGGTGAGAGGATTGCCGAAGGGAGGCTTCTTTTTCAGTGGACCCGGTCAAGAATACCCACAT  
TCCGAAGGGTGGGCACGAGGAGCATGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGAGCTGAAGCG  
TGCTCACAAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAATGCCTGGTGGAAATGATCCACTT  
CTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTATCGGTTTTGCAGTGTGTCCGACGAATCCAATGATCT  
CCTTTACCAATACTGCGATGCTGAGTCGGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAA  
AAAGAATTGGAAGCGCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTCAGAAGGA  
CTACAACGTTGCTGTTGCGATCACTCCCTAAAATACGCCAGATTGCTCTGGATTACAGGGAACGATGCCAA  
TTGTGCTTACGGCTTACAGAGACCTGAAACAGGGCGGTGTATCATCTAAATCACAGAGAAAACAGCTCTGCTTA  
CCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTTGAACCTCTGTCAATAGCATTTCAACATTTTCAAATCA  
GGAGATTTTCGTCCATTTAAAAATGTATAGGTGCAGATATTGAAACTAGGTGGGCACTTCAATGCCAAGTATAT  
ACTCTTCTTTACATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTTAA  
ACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCTACTCTAAGAAGAA  
CTAATAGGATGCTGGTTGTGTATTAATGTGAAATGCATAGATAAAGGTAGATGGTAAAGCAATTAGTATCAGA  
ATAGAGACAGAAAGTTACAACACAGTTTGTACTACTCTGAGATGGATCCATTAGCTCATGCCCTCAATGTTTAT  
ATTGTGTTATCTGTTGGGTCTGGGACATTTAGTTTAGTTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGC  
ATTATAAACAAAACATAAATACTGTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAATGGGA  
GAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTTTAAGATCTCAAGTTTTTA  
TTTAACATAACTCAAAATATGGAATTTTCATGTATGCATAGGGAAGACACTTCACAAATTATGAATGATCATGT  
GTTGAAAGCCACATTATTTTATGCTATACATTCTATGTATGAGGTGCTACATTTTTAGGACAAAGAATTCTGTAA  
TCTTTTTCAAGAAAGAGTCTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCCTG  
ATTAGTAATTTTAGATATGTCCTTTCTAAAATGAATAAAATTTATGAATATGA

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**FIGURE 156**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

&lt;subunit 1 of 1, 413 aa, 1 stop

&lt;MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVCGIECQKELPTPSL  
SELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQVYGTDSRFSILDKRFLTNFPFSTAVKL  
STGCSGILISPOHVLTAACHVHDGKDYVKGSKKLRVGLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQE  
RAKGRRRRKKSGRGQRIAEGRPSFQWTRVKNTHIPKGWARGGMDATLDYDYALLELKRAHKKKYMELGISPTIK  
KMPGGMIFHSGFDNDRADQLVYRFCSVDESNDLLYQYCDAESGSTGSGVYLRKDPDKKNWKRKIIAVYSGHQW  
VDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

**Important features:****Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 90-93, 110-113 and 193-196

**Glycosaminoglycan attachment site.**

amino acids 236-239

**Serine proteases, trypsin family, histidine active site.**

amino acids 165-170



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**FIGURE 157**

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCCCAGCGCAGCCGCGAGCGGACAAAGGAGCATGTCCGCG  
CCGGGGAAGGCCCGCTCCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGGGCCCCGCGCCGCGCTCCTGCCCGCCCC  
GGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCGCTCGCCCCGAGGCCCGGCCCGCAGCATGAGGCCACCC  
GGACGCCGCGGGGGCGCGCGCAGCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGA  
GGCGGCGCGGGCGGCCGCCGCGCGCTGCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGCAGG  
GCGGCGGGCGGCCGCCGAGGGCAAGTGTTGTGCAGCAGCCTGGAAGTGCAGGCTCCTGCCCGCAGATCTCTG  
CCCAACCGCACGGTCACCTGATCTGAGTAACAATAAGATATCCGAGCTGAAGAATGGCTCATTTTCTGGGTTA  
AGTCTCCTTGAAAGATTGGACCTCCGAAACAATCTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCA  
TCTCTAAAAAGATTGGATCTGACAAACAATCGAATAGGATGTCTGAATGCAGACATATTCGAGGACTACCAAT  
CTGGTTCGGCTAAACCTTTCCGGGAATTTGTTTTCTTCATTATCTCAAGGAACCTTTGATTATCTTGGCTCATTA  
CGGTCTTTGGAATTCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGATGCATCGCTGGGTAAAGGAG  
AAGAACATCACGGTACGGGATACAGGTGTGTTTATCCTAAGTCACTGCAGGCCCAACAGTCACAGGCGTGAAG  
CAGGAGCTGTTGACATGCGACCCCTCCGCTTGAATTGCCGCTCTTCTACATGACTCCATCTCATCGCCAAGTTGTG  
TTTGAAGGAGACAGCCTTCCCTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAG  
GATGGGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTTGTTGAAAAGAACATGATTCACAACCTGCTCCTTG  
ATTGCAAGTGCCTTAACCATTTCTAATATTAGGCTGGATCTACTGGAAATGGGGCTGTCTGTCCAGACCAAA  
CGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAGAGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTG  
GTAAACAACAAAGGTGACTTCAGATGGCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACCGGGAAC  
ACCCATGGCAGTGGGATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGC  
TTTTGGGCAGATGATGATTATTTCTCGCTGTGAGTATGCAAAATGATGTCACTAGAGTTCTTTATATGTTTAAATCAG  
ATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGCTTACACTGTGGAAGCAGCCAACTTT  
TCTGACAAATGGATGTTATATTGTGGCAGAAATGATTGAAAATTTGGAAGATTTACCAAGGAGGAAAAATCA  
AAAGAGCTAGGTGACGTGATGTTGACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCG  
CAGAGGGAAGCTAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTGGGA  
GCTCACGTTTATTCAACATATTCACCCAATATTGCTCTGGAAGCTTATGTATCAAGTCTACTGGCTTCACGGGG  
ATGACCTGTACCGTGTTCAGAAAGTGGCAGCCTCTGATCGTACAGGACTTTCGGATTATGGGAGGCGGGATCCA  
GAGGGAACCTGGATAAGCAGCTGAGCTTTAAGTGAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTA  
TGTTACATTCTGCAATCATTTAAGACTATTTACAGTTAAATAGAAATGCTCCAAATGTTCTGCTTCGCAAAATAA  
CCTTATTAAGATTTTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAACTAACCAG  
GAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTGCCTTTGATTCCCTTCTTCACATAAAAAATATCA  
GAAATTACATTTTATACTGCAGTGGTATAAATGCAATATACTATTGTTACATGTGAAAAAATTTTATTGACT  
TAAAGTTTATTTATTTGTTTTTTGCTCCTGATTTAAGACAATAAGATGTTTTCATGGGCCCCATAAAGTATC  
ATGAGCCTTTGGCACTGCGCCTGCCAAGCCTAGTGGAGAAGTCAACCCTGAGACCAGGTGTTTAAATCAAGCAAGC  
TGTATATCAAAATTTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTAAAAAAGTATTTTCATTGAAGCA  
AGCAAAATGAAAGCATTTTTTACTGATTTTTAAATTTGGTGCTTTAGATATATTTGACTACACTGTATTGAAGCAA  
ATAGAGGAGGCACAACCTCCAGCACCCCTAATGGAACCACATTTTTTTCACTTAGCTTTCTGTGGGCATGTGTAATT  
GTATTCTCTGCGTTTTTAAATCTCACAGTACTTTATTTCTGTCTTGTCCCTCAATAATATCACAAACAATATTCC  
AGTCATTTTAAATGGCTGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAA  
TATTGAATGAATGAACGAAAAAAAAAAAAAAAAA

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**FIGURE 158**

MEPPGRRRRGRAQPPLLLPLSLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGKVVCSSLELAQVLP  
PDTLPNRTVTLLLSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGAFWGLSSLKRLDLTNNRIGCLNADIFR  
GLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLFQTEYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPV  
TGVKQELLTCDPPLLELPsfymTPSHRQVVFEgDSLpfQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIH  
NCSLIASALTISNIQAGSTGNWgCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLAGITAYLQ  
CTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNLNLNAVATARQLLAYTVE  
AANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDVMVDIASNIMLADERVLWLAQREAKACSRIVQCLQRIATYR  
LAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCTVFQKVAASDRtGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSL  
ALKVCYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336, 433-437,  
453-457, 592-596**N-myristoylation site.**amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57, 57-63, 99-105,  
123-129, 142-148, 162-168, 317-323, 320-326, 384-390, 403-409, 554-560

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**FIGURE 159**

GGGGAATCTGCAGTAGGTCTGCCGGCGATCGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTGGCTGCTGTTGTTT  
CTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGAAAGTATTTATTGACCAAATTAACAGG  
TCTTTGGAGAATTACGAACCATGTTCAAGTCAAACCTGCAGCTGCTACCATGGTGTATAGAAGAGGATCTAACT  
CCTTTCCGAGGAGGCATCTCCAGGAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATC  
ACTAAGAACAGACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATTTTG  
GAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCAGGTTCTTAAATGGATG  
GAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACCATGATATCATGTATCCTGCTTGGACATTT  
TGGGAAGGGGGACCTGCTGTTTGGCCAATTTATCCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTG  
GTAAGGTGAGCAGCACAGTGGCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCA  
GAACGAGATCCTCTCATTCTTCTGTCTCGAAAAACCCAAAACCTTGTGATGCAGAATACACCAAAAACAGGCC  
TGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGTGGATCACTGCAAATACAAG  
TATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTAAACACCTCTTCCCTGTGTGGCTCACTTGTTTTT  
CATGTTGGTGATGAGTGGCTAGAAATTTCTCTATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACA  
GATCTCTCCAATGTCCAAGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGG  
GGAAGCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTGAGTGAATAC  
TCTAAATTCCTGTCTTATAATGTAAAGGAAAGGTTATGATCAAATTATTCCCAAAATGTTGAAAACCTGAA  
CTATAGTAGTCATCATAGGACCATAGTCCTCTTGTGGCAACAGATCTCAGATATCCTACGGTGAGAAGCTTACC  
ATAAGCTTGGCTCCTATACCTTGAATATCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAG  
AGCAACTCTTGAGAAAAGATTTAAATGTGTCTAATACTGATATGAAGCAGTTCAACTTTTGGATGAATAAGG  
ACCAGAAATCGTGAGATGTGGATTTTGAACCCAACTCTACCTTTTCAATTTCTTAAGACCAATCACAGCTTGTGCC  
TCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCATGTGATGATGCCCTTGTCCCATT  
TTTGGAGCAGAAAATTCGTCAATTGGAAGTAGTACAACCTATTGCTGGAATTGTGAAATTATTCAAGGCGTGATC  
TCTGTCACTTTATTTAATGTAGGAAACCCTATGGGGTTTATGAAAAATACCTGGGGATCATTCTCTGAATGGTC  
TAAGGAAGCGGTAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAAAACCATAACTCTGTTACTCAGGA  
GGTTTCTATAATGCCACATAGAAAGAGGCCAATGTCATGAGTAATTATGCAATTGGATTTTCAGGTTCCCTTTTT  
GTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

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**FIGURE 160**

MEWWASSPLRLWLLLFLPSAQGRQKESGSKWKVFIDQINRSLENYEPCCSSQNCSCYHGVIIEEDLTPFRGGISRK  
MMAEVVRRKLGTHYQITKNRLYREND CMFPSRCSGVEHFILEVIGRLPDMEMVINVRDYPQVPKWMEPAIPVFSF  
SKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDLFREDLVRSAQWPWKKNSTAYFRGSRTSPERDPLILLS  
RKNPKLVDAEYTKNQAWKSMKDTLGKPAAKDVHLVDHCKYKYLNFNRGVAASF RFKHLFLCGSLVFHVGDEWLEF  
FYPQLKPWWHYIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDITCYWENLLSEYSKFLSYNVT  
RRKGYDQIIPKMLKTEL

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**FIGURE 161**

CCGAGCACAGGAGATTGCCTGCGTTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGCCAAA  
CCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCAACACAGATCTGAGTGTTTTAATTAAGCATGGAATACAGAAAA  
CAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTT  
GGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGTCTCCGACTACTCACCCCGAGTGTAAGAACCCTTCGGCTCG  
CGTGCTTCTGAGCTGCTGTGGATCGCCTCGGCTCTCTGGACTGTCCTCCGAGTAGGATGTCACTGAGATCCCTC  
AAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCTTCCCCACTACAATGTG  
ATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTACAGACAAGACTTTCACCTTCACACTTCGA  
GAGCATTCAAACCTGCTCTCATCAAAATCCATTTCTGGTCATTCTGGTGACCTCCCACCCCTTCAGATGTGAAAGCC  
AGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTA  
GGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTATGGTGACATA  
ATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGCATTACAGGTGGGTAACTGAG  
TTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTAT  
CTTTTAAACCTAAACCACTCAGAGAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTT  
TACCAAAAAACCATATTTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTAT  
ATAATGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTCACGTAAAACCCATCAAGTTTGAAGATGTT  
TATGTCGGGATCTGTTTGAATTTATTAAGTGAACATTATATCCAGAAGACACAAATCTTTCTTTCTATAT  
AGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACT  
TTTTGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAAGTTTACACTTCACATTCTACAAAAAGCCTAGAAGGACAGG  
ATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGGAATAATTCATGGGGAGGTCAGTGTGCTGGCTTACACT  
GAAGTGAAGTCAATGAAAAACCCAGACTGGAGACTGGAGGTTTACACTTGTGATTTATTAGTCAGGCCCTTCAAA  
GATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGGACCAACAATTTG  
GACATGTCATTCTGTAGACTAGAATTTCTTAAAAGGGTGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAA  
AACATGTAGAGTTTTATTTATTGAACAATGTAGTCACCTGAAGGTTTTGTGTATATCTTATGTGGATTACCAAT  
TAAAAATATATGTAGTTCTGTGTCAAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTTTG  
GTCATTTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTAATTTCAACTTTGTGTT  
TTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAATCATTTCTTACATGCAACATTTTCCAGT  
TACTTAACTGATCAGTTTATTATTGATACATCACTCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTA  
ATCTCTTGGACTTTGTTAAATATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAA

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**FIGURE 162**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPiYRQDFHFTLREHSNCSSH  
QNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EKEDKMLALSLEDEHLLYGDIIRQDFLD  
TYNNLTlKTI MAFRWVTEFCPNAKYVMKTD TDVFINTGNLVKYLNLNHSEKFFTGYPLIDNYSYRGFYQKTHIS  
YQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVC  
QLRRVIAAHGFSSKEIITFWQVMLRNTTCHY

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**FIGURE 163**

CATTTCTGAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATATTAACTTTTTAGG  
AGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCGCTCATATATAGGAAAATCGCATATGG  
TCCTAGTATTAAATTCCTATTGCTTACTGATTTTTTTGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTG  
AATATAAATAAGAGAAGAAAAAGAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGTGGTT  
TGTTTACATGCAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTTG  
TTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTTCAGATTCGGTTGCCAA  
CTCGTCCCCATTGGTTTCTCTTTTTGGTACTACAGAAGAGGAAATCCAGGAAATCTGCATAGAAACACTTAGGC  
TTTATACCAGAAAAAGCCAACTATGAATTACTGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAG  
CCAAATTAAGCAAAGGGATTGAATCCGGATGGAATCCAGCCCTTCAACCCTGGGTGGATTTTCTCCAGCCT  
CCAAGCCATCATCACCAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAGTCAAAA  
AAGAACCCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAAGAAAAGACAGCAAGAGAAGTAGAA  
ATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACGTTCTAGATCACATACTCCAAGAAGACACTATA  
ATAATAGGCGGAGTCGATCTGGAACATACAGTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTC  
GAAGACATCATAATCATGGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGAC  
ATGGTCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAGCCAAGAAAC  
ACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTTGAGAGGTCCCATAAAAGCAAGC  
ACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCGCTGACTTTCTCTTCTTCTGAGCCTGCATCAGTTCT  
TGGTTTTGCCTATCTACAGTGTGATGTATGGACTCAATCAAAAACATTAAACGCAAACTGATTAGGATTTGATTT  
CTTGAAACCCTCTAGGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAGAAGAACTATGTTAATTTTTTTGCACAT  
TAAATGCCCTAGCAGTATCTAATTAATAAACCATGGTCAGGTTCAATTGTACTTTATTATAGTTGTGTATTGTTT  
ATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTTATACAGATAAAATGCAGACACTGT  
TCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAATACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATT  
TTTACAAGGAAATAAAATACAAATCTTGTTTTTCTAAAAAAGT

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**FIGURE 164**

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRLYTRKKPNYELLEKE  
VEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEKSPISINVKTVKKEPEDRQQASKSPYN  
GVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYNNRRSRSGTYSSRSRSRSRSHSESPRRHHNHGSPHLKAKH  
TRDDLKSSNRHGHKRKKSRSRSQSKSRDHSDAAKKHRHERGHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHRR



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**FIGURE 165**

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAACGTGGCTTA  
ATCTGAAGGTTCTCAGTCAAATTCCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTT  
GGCTGGTTTGGGCCCTTGTAAGTGCAGAGAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGC  
TTCTGTTGCTGGTCTTGCCTTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCTGTATT  
CAGAACTCTGTAAAGGTGCCTCCCCTACGGCTGACCAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAG  
ACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAG  
ACGAGCCTGGCCTAGACAACCTGCTTACGTGCTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACT  
CTGGCCGGAGCAACCGAACTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAA  
ATCGAGCTTTGAGTGTCTTGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGGGCAGGGAAA  
ATTCTGAAAACACCACTGCCCCGAAGTCTTTCAAGGTTGTACCACCTGATTCAGATGGTGAAATTACCAGCA  
TCAAGATCAATCGAGTAGATCCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCC  
ATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTC  
TAAAGGTCAACGGGATGGACATCAGCAATGTCCTCACAACTACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGG  
TGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCGAGCAGGAACATGGACAGGCCCCGGATGCCTACAGAC  
CCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAATAAACTGGTGCAGCA  
AGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGACATGGTCAGCTTGAGG  
AGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCAGAAAGTGGCGCTCATCTGATTC  
AGGCCAGTGAAAGACGTGTTACCTCGTCGTGTCGCCGACGGTTCGGCAGCGGAGCCCTGACATCTTTCAGGAAG  
CCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACTCCCAAGCCCTCCATCCTA  
CAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCTCGGCATGACCGTCGAGGGG  
GAGCATCACATAGAGAATGGGATTTGCCTATCTATGTGATCAGTGTGAGCCCGGAGGAGTCATAAGCAGAGATG  
GAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACTGACAGAGGTGAGCCGAGTGAGGCAG  
TGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGCCCCAGGAAG  
ACTGCAGCAGCCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCTGGGTCA  
TGTGGCTGGAATTACCACGGTGCTTGTATACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTCTGG  
GCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAACAAACCTTTTTTCATCAAATCCATTGTTGAAGGAA  
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTGCTGTCAATGGTAGAAGTACATCAGGAA  
TGATACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAATCTATTGTTTCTTGGCCTG  
GCACTTTTTTATAGAAATCAATGATGGGTGAGAGGAAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACT  
ATATTTATCTTGTGAGTCTTTTATATTTAAAGAAAGATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAA  
TGAAAGCCAGTTACACCTCAGAAAATATGATTCCAAAAAAATTAATACTACTAGTTTTTTTTTTCAGTGTGGAGGAT  
TTCTCATTACTCTACAACATTGTTTATATTTTTCTATTCAATAAAAAGCCCTAAAACAACATAAATGATTGATT  
TGTATACCCCACTGAATTCAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTAT  
GGCCATTTTTAATTTACAGCTAAAATATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTCATCAAACAAGAAT  
AAATATTTTTTCAAGGTTAAA

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**FIGURE 166**

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDGCASLTATAPSPEVSAAATIS  
LMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINRALSVLRRTKSGSAVANHADQ  
GRESENTTAPFVFPRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIIQHIYRDGVIARDGRLLPG  
DIILKVNMGDISNVPHNYAVRLLRQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIK  
LVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRQSPDI  
FQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPYVISVEPGGVI  
SRDGRIKTGDILLNVGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPPSDWSP  
SWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFIFKSIVEGTPAYNDGRIRCGDILLAVNGRS  
TSGMIHACLARLLKELKGRITLTIVSWPGTFL

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**FIGURE 167**

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTGCCTTGGGCCTCAC  
AATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAAATGGAGTTGATCCCAACCATAACATCGTGGAG  
GGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTGGTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCA  
TGAACCTCTGGCTGTTGATCAAAAGAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCT  
AGCAGAAGACTCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAATGGATTCTACATCAA  
CGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTGGGAGGCCAACCCACAGAACAGCATTT  
CTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGCATTGCTTTTTTCCCCAAAATTAACACATT  
GTGGAGAAGTGATGATACTCTCCCTTACCTTTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATT  
AAACCTTGCAGCAAGGGACCTTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTT  
CCTGTATCATCCTTTTCAATAAACTGTATTCATTTGAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 168**

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHLEWLLIKREFGFYSKSQYRTWQKKLAEDSTWPPINRTDY  
SGDGKNGFYINGGYESHEQIPKRKLKLGGOPTQHFWARL

**FIGURE 169**

[illegible]

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**FIGURE 170**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYTIPCCRNEENE  
CDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGDCMRCGQVLRAPKGQILLESYPLNAHC  
EWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGOIKRVCGNERPAPIQSIGSSLHVLHSDGSKN  
FDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI  
NGRHAKIGTVVSFFCNSYVLSGNEKRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLHQLY  
SAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIE  
NITAPKTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADLKVVLG  
KFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAG  
WNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPG  
RASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPEFKDWIERNMK

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**FIGURE 171**

CTGTCGTCTTTGCTTCAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCCAAGTGTGGCTTA  
ATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACCGCTGCCATGCCAGTGACGGTAACCCG  
CACCACCATCACAACCACCACGACGTATCTTCGGGCCTGGGGTCCCCCATGATCGTGGGGTCCCCCTCGGGCCCT  
GACACAGCCCCCTGGGTCTCCTTCGCCTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGT  
GGGCGCCTGGACGGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTCTGCTTCTCCGTGACCCTGATCAT  
CCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCCATCACCTTCGCCTG  
CTATGCGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCACCTATGTCCAGTTCTGTCCCACGGCCG  
TTCGCGGGACCACGCCATCGCCGCCACCTTCTTCTCCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTG  
GACCCGGGCCCGGCCCGGCGAGATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTT  
CGTTGCCTGCATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGTGCCT  
GGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGGGAGTGCACCAACGTGCT  
ACCCATCCCCTTCCCCAGCTTCTGTGCGGGCTGGCCTTGTCTGTCTGCTCCTCTATGCCACCGCCCTTGTCT  
CTGGCCCCCTCTACCAGTTCGATGAGAAGTATGGCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAG  
CCATGCCTACTACGTGTGTGCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTA  
TGTGGCTGACCTGGTGCATCTGCCCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCCCGTTCCC  
TCTCCAACCTCTTTGTTCTTCTTGCCGAGTTTTCTTTATGGAGTACTTCTTTCCTCCGCCCTTTCCTCTGTTTT  
CTCTTCTGTCTCCCCCTCCCTCCACCTTTTTCTTTCCTTCCCAATTCCTTGCACTCTAACCAGTTCTTGGATGC  
ATCTTCTTCTTCCCTTTCCTCTTGTCTGTTTCCCTTCTGTGTTGTTTTGTTGCCACATCCTGTTTTACCCCTG  
AGCTGTTTTCTTTTTCTTTCTTTCTTTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCAGGCTG  
GAGTGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTTCAAGCGATTCTCCTCCCCAGCCTCC  
CAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTTTTTTCCACTCTTCTTTTTTCTCATC  
TCTTTTCTGGGTGCTGTGCGGCTTCTTATCTGCCTGTTTTGCAAGCACCTTCTCCTGTGTCTTGGGAGCCCT  
GAGACTTCTTCTCTCCTTGCTCCACCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGACGCCGTCC  
ATGCCACAGCCCCCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC  
GTGTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCTCCAGTGGAGGAA  
GGTGTGCAGTGTACTTCCCCTTTAAATTAAAAAACATATATATATATATATTTGGAGGTCAGTAATTTCCAATGG  
GCGGGAGGCATTAAGCACCGACCCTGGGTCCCTAGGCCCGCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAG  
AATTTTTGCCAGGCTTACAGAACACCCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCAT  
CCCAACTATTCTCTGTGGTATGAAAAAG

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**FIGURE 172**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTGSMGNWSMFTWCFC
FSVTLLIILIVELCGLQARFPLSWRNFPI TFACYAALFCL SASIIYPTTYVQFLSHGRSRDHAI AATFFSCIACVA
YATEVAWTRARPGEITGYMATVPGLLKVLETFVACII FAFISDPNLYQHQP ALEWCVAVYAICFILAAIAILLNL
GECTNVLPIPFPSFLSGLALLSVLLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILT
AINLLAYVADLVHSAHLVFVKV
```

**Important features:****Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

**N-glycosylation site.**

amino acids 66-69

**Glycosaminoglycan attachment site.**

amino acids 18-21



**FIGURE 173**

[illegible]

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**FIGURE 174**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKPVHMDPNYCHPSTSLHLCSLAWSFTRLLHPPL  
SPGISQVVVDHVTKPTAMAGQGRVAHLIEWKGWSKPSDSPAALSAFSSYSDLSEGEQEARFAAGVAEQFAIAEAK  
LRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLGPHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSS  
LCSLEDGLLGSPARLASQLLGDELLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPL  
CPPLTGSWERQRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232, 285-289,  
324-328**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

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**FIGURE 175**

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTGGCACCCCTCCTGC  
TCAGTGCACATTGTGACACTTAACCCATCTGTTTTCTCTAATGCACGACAGATTCCCTTCAGACAGGACAACCTG  
TGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAGCCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTT  
CTTCATCTGCAAAATGGGCATAATAACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACC  
AATACCAAAGAAGCCTACAATGTTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCTATC  
GGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTTTTAAAAACAATGGAAA  
TAAACCTATTTCTTTGGAAAGTGAAGCAAACCTAAACTCAGATAAAGAAAATATAACCACCTCAAATCTCAAGGC  
GAGTCATTCCCCCTCTTTGAATCTACCCAACAACAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGA  
GCATTCTTTGGGCAGTCTAAAACCCACATCTACCATTTCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAA  
AGTGCCTTGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACCTGCTCT  
GTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCTGATAACAGTTCCATTACAGTTAG  
CATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTGATAGTGGAACCAAGTGGATGGCTTACCACAAA  
CAGTGATAGCTTCACTGGGTTTACCCCTTATCAAGAAAAACAACCTCTACAGCCTACCTTAAATTCACCAATAA  
TTCAAAACTCTTTCCAAATACGTGAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTT  
AGGTGCTATTCTGGGTGTCTCATTGCTTACTCTGTGGGCTACTTGTGTGTGGAAAAGGAAAACGGATTCAAT  
TTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACAATGCACCGGAACCTTATGATGT  
GAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAATGATTCAGCCATGCCAGAAAGTGAAGAAAATGCACG  
TGATGGCATTCCATATGGATGACATACCTCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACA  
GCAAGTGTCACTACATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGA  
TTTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCATCAAAGGTTTTT  
TTTCTTACAATTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATTTGTATTTTAGTAGTATTTTCTTAGT  
AGAAAATATTTGTGGAATCAGATAAACTAAAAGATTTACCATTACAGCCCTGCCTCATAACTAAATAATAAAA  
ATTATTCCACCAAAAAATTCTAAAACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATT  
CAAGATTGCATTTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAGGA  
CATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTCTAGTACGTTATAATT  
TTCTAGATCAGCACACATGATCAGCCCACTGAGTTATGAAGCTGACAATGACTGCATTCAACGGGGCCATGGC  
AGGAAAGCTGACCTACCCAGGAAAGTAATAGCTTCTTTAAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGTC  
TTAATATATCTTAGGCTTCAATTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

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**FIGURE 176**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732  
><subunit 1 of 1, 334 aa, 1 stop  
><MW: 36294, pI: 4.98, NX(S/T): 13  
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENITTSNLKASHSPPL  
NLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNAPIADEDLLPISAHPNATPALSSSENF  
WSLVNDTVKTPDNSSITVSISSSEPTSPSVTPLIVEPSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLF  
TSDPQKENRNTGIVFGAILGAILGVSLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSS  
YYNPTLNSAMPESEENARDGIPMDDIPPLRTSV

**Signal peptide:**  
amino acids 1-23

**Transmembrane domain:**  
amino acids 235-262

**N-glycosylation site.**  
amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159, 163-167, 218-222,  
225-229, 298-302, 307-311

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**FIGURE 177**

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAAGCTCAACTTGAAGCTTTCTTGCCCT  
GCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACTTTCCACCTTTCTTA  
CAAAATCCGATTACTGTTGCTGTTGACTTTGTGCCGTGACAGTGGTTGGGTGGGCCACCAGTAACACTTCGTGGG  
TGCCATTCAAGAGATTCCATAAGCAAAGGAGTTTCATGGCTAATTTCCATAAGACCCCTATTTTGGGGAAGGGAAA  
AACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTTGACAACCTGTCCTTCTGTGTCTCCTTACCTCAGAGG  
CCAGAGCAAGCTCATTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGG  
CCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTTCGCCATCCTCGTTCCCCACCGGAACAGAGAGAAAACA  
CCTGATGTACCTGCTGGAACATCTGCATCCCTTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCA  
CCAGGCTGAAGGTAAAAAGTTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAA  
TTGGGACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAGCA  
TCCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGGGGGTGTTAC  
TGCCCTAAGCAGAGAGCAGTTTTCAGGTGAATGGATTCTCTAACAACTACTGGGGATGGGGAGGCGAAGACGA  
TGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAAT  
GGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACAGAGT  
CTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAATTAGTATCTGTGGAACACAATCCTTTATATATCAACAT  
CACAGTGGATTTCTGGTTTGGTGCATGACCCCTGGATCTTTTGGTGAATGTTTGAAGAAGTGAATCTTTGTTTGCA  
ATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTAAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTT  
TCCTTTTGTATTTTCTTAGCAGAGCTCCTGGTGAATGATAGAGTATAAACAGTTGTAACAAGACAGCTTTCTTAG  
TCATTTTGTATCATGAGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGSATGACTCAAAGGA  
TAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGATAAAA  
GGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAAAGGTACGAAGA  
TACAATACTGTTATTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAA  
GAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTCCGGC  
TGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCCAGGTATGCCTTC  
CAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAATGATTTTGTACAAGTAGG  
ATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAAATATGTCTATCAAATACCTCTGTAGTAAAAAT  
GTGAAAAAGCAAAA

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**FIGURE 178**

MGFNLTFLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLLGKGKTLTNEASTKKVELD  
NCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPHRNREKHLMYLLEHLHPFLQR  
QQLDYGIYVIHQAEKGKFNRAKLLNVGYLEALKEENWDCFIHVDVLPENDFNLYKCEEHPKHLVVGRNSTGYR  
LRYSGYFGGVLTALSREQFFKVNGFSNNYWGWWGEGEDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAE  
RMKLLHQVSRVWRDGLSSCSYKLVSVEHNPLYINITVDFWFGA

**Important features:****Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

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**FIGURE 179**

CGTGGGCCGGGGTCGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGCGAGTTCTCGAGCTCCAGCTGC  
ATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGCCCCGCAATGGCCCCAGGCAGTGTGGTTCGCGCCTCGG  
CCGCATCCTCTGGCTTGCCTGCCTCCTGCCCTGGGCCCCGGCAGGGGTGGCCGAGGCCTGTATGAACCTCAATCT  
CACCACCGATAGCCCTGCCACCACGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAG  
CCTGGCCCTGCCCGCTGACGCCCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGTCTACTGGCAAGAT  
GGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTTCGGCCACGTGCCCGGGGAATTCCTGGTCTCTGTCTGGGTAC  
TGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTGTGGTCTCCCATCACAGAGTTCCCTCGTGGG  
GGACCTTGTTGTACCCAGAACACTTCCCTACCTGGCCAGCTCCTATCTCACTAAGACCGTCTGAAAGTCTC  
CTTCTCTCCACGACCCGAGCAACTTCTCAAGACCGCCTTGTCTCTACAGCTGGGACTTCGGGGACGGGAC  
CCAGATGGTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCACCGTGAAGCTCAAAGT  
GGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGACCGGGGACTTCTCCGCTC  
GCTGAAGCTGCAGGAAACCTTCGAGGCATCAAAGTGTGGGGCCCCACCCTAATTCAGACCTTCCAAAAGATGAC  
CGTGACCTTGAACCTTCCCTGGGGAGCCCTCCTCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCTCCCGCTGGA  
GGAAGGGGAGTGCCACCCCTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCTGGGGA  
CTACTGCTTCAGCATCCGGGCCCCAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGTGTGGCCCTC  
CAGAATCCAGCCGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGATGTTGGCCTTCATCATGTACAT  
GACCTTCCGGAATGCCACTCAGCAAAAGGACATGGTGGAGAACC CGGAGCCACCTCTGGGGTCAGGTGCTGCTG  
CCAGATGTGCTGTGGGCCTTCTTGCTGGAGACTCCATCTGAGTACCTGGAAATTGTTCTGTGAGAACCACGGGCT  
GCTCCCGCCCCCTCTATAAGTCTGTCAAACTTACACCGTGTGAGCACTCCCCCTCCCCACCCCATCTCAGTGTTA  
ACTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCAATTTGCGTGGGGCTG  
TTGGCCTGGATCATCCATCCATCTGTACAGTTTCCAGCCACTGCCACAAGCCCCCTCCCTCTCTGTACCCCTGACCC  
CAGCCATTACCCCATCTGTACAGTCCAGCCACTGACATAAGCCCCACTCGGTTACCACCCCTTGACCCCTACC  
TTTGAAGAGGCTTCGTGCAGGACTTTGATGCTTGGGGTGTTCGCTGTTGACTCCTAGGTGGGCCTGGCTGCCAC  
TGCCCATTCCTCTCATATTGGCACATCTGCTGTCCATTGGGGGTTCTCAGTTTCTCCCCAGACAGCCCTACCT  
GTGCCAGAGAGCTAGAAAGAAGGTCATAAAGGGTTAAAAATCCATAACTAAAGGTTGTACACATAGATGGGCACA  
CTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACACACACAGAAATATAAACACATG  
CGTCACATGGGCATTTTCAGATGATCAGCTCTGTATCTGGTTAAGTCGGTTGCTGGGATGCACCTGCACTAGAGC  
TGAAAGGAAATTTGACCTCCAAGCAGCCCTGACAGGTTCTGGGCCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCA  
GTTCTTGCGCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACTAATAC  
TGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTGAAACTTTCAGTGAGGAAA  
AGGCCTTGACGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGG  
AGGCCGAGGCGGGTGGATCACGAGATCAGGAGATCGAGACCACCTGGCTAACACGGTGAAACCCCGTCTCTACT  
AAAAAATACAAAAAGTTAGCCGGGCGTGGTGGTGGTGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGA  
GAATGGTGCGAACC CGGAGGCGGAGCTTGCAGTGAGCCAGATGGCGCCACTGCACTCCAGCCTGAGTGACAGA  
CGGAGACTCTGTCTCCA

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**FIGURE 180**

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLALPADAHLYRFHWI  
HTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGFVVLPITEFLVGDLVVTQNTSLPWSS  
YLTFTVLKVSFLLHDPNFKTALFLYSWDFGDTQMVTEDSVVYYNYSIIIGTFTVKLKVVAEWEEVEPDATRAV  
KQKTGDFSASLKLQETLRGIQVLGPTLIQTFQKMTVTNLFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYN  
LTHTRDPGDYCFSSIRAENIISKTHQYHKIQVWPSRIQPAVFAPPCATLITVMLAFIMYMTLRNATQQKDMVENP  
EPPSGVRCCCMCCGPFLLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 339-362

**N-glycosylation sites.**

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367



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**FIGURE 181**

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCCGGTGGGCCCTCGGGCCTGACAGATGGCAGTGGC  
CACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCGGCCCCCGGGTTCGTGGGGCCAGGGT  
CCAGCGGCTGCCGAGAGGCGGGGACCCCGGCCTCATGCACGGGAAGACTGTGCTGATCACCGGGCGAACAGCGG  
CCTGGGCGCGGCCACGGCCGCCGAGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGG  
CGCCGAGGAGGCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGAGTGCGGCCCAGAGCCTGGCGTCAG  
CGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCGCCTTCTGCCAGGAAAT  
GCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGGATCTTCCAGTGCCCTTACATGAAGACTGA  
AGATGGGTTTTGAGATGCAGTTCGGAGTGAACCATCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCT  
CAAAAGTTCAGCTCCCAGCAGGATTGTGGTAGTTTCTTCCAAACTTTATAAATACGGAGACATCAATTTTGATGA  
CTTGAACAGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAACCTGGCTAACATTTCTTTTACCAG  
GGAAGTAGCCCGCCGCTTAGAAGGCACAAATGTCAACGTCATGTGTTGCATCCTGGTATTGTACGGACAAATCT  
GGGGAGGCACATACACATTCACCTGTTGGTCAAACCACTCTTCAATTTGGTGTGATGGGCTTTTTTCAAAACTCC  
AGTAGAAGGTGCCAGACTTCCATTTATTTGGCCTCTTCACTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGG  
GGATTGTAAAGAGGAAGAACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAACTCTGGGATATCAGTGA  
AGTGATGGTTGGCCTGCTAAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAAACTGCATATCAGTTATATCTG  
TGATCAGGAATGGTGTGGATTGAGAACTTGTACTTGAAGAAAAAGAATTTTGATATTGGAATAGCCTGCTAAGA  
GGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTTGGGATAAGAGAATTTTCAGCAAAGATGTTTTAAAT  
ATATATAGTAAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAATAATTATACTGGGCAAGCA  
TGGATGACATATTAATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGT  
TTCATGGCCAAAGTGTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGGAATATCTGCCTGGTGTGTGCA  
CACAAGTCTTACTTGAATAAATTTACTGGTAC

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**FIGURE 182**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

&lt;subunit 1 of 1, 336 aa, 1 stop

&lt;MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAELLRLGARVIMGCR  
DRARAEAAAGQLRRELROAAECGPEPGVSGVGELIVRELDLASLRVRAFCQEMLQEEPRLDVLINNAGIFQCPY  
MKTEDGFEMQFGVNHFGHLLTNLLLGLLKSSAPSRIVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANI  
LFTRELARRLEGTVNTVNVLHPGIVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSG  
RYFGDCKEEELLPKAMDESVARKLWDISEVMVGLLK

**Important features:****Signal peptide:**

amino acids 1-21

**Short-chain alcohol dehydrogenase family protein**

amino acids 134-144, 44-56 and 239-248

**N-glycosylation site.**

amino acids 212-215 and 239-242

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**FIGURE 183**

AACAGGATCTCCTCTTGCGAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGCAGCCCGAAGATTCACTATGGTGAAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGGAGGCGCGGCAAGACGTGGAGGCCCTCTGAGCCGCGACGGTCAGAACTCAGATACTGACCGGCAAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCTCTTAGGCCCTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACTTCATGCCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCAAATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTTCGTGAGGATGACAACATTGCAATCATTGATGTGCCGTGTCCCGAGTTTCTCTGATAGTGACCCTGCAGCAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTTGCTGGGGAACCTGCTATCTGATGCCCCCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTTGGCAAACCTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTGTGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGAAAGTCCTTCCGCCTTCGTGCGCAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAAATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGTAAAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAACATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTTAAAAAAAAGGAAAAAAAACCTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAATTGGCATTGCTTGTTTTTTGAACTGAAATTACATGAGTTTCATTTTTTCTTTGCATTTATAGGGTTTAGATTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCCGTTGTTTTTTTGTGTTGTTGTGTTTTCTTTTCTTTTAAAGTAAGCTCTTTATTCATCTTATGGTGGAGCAATTTTAAATTTGAAATATTTTAAATGTTTTTGAACCTTTTGTGTAATAATATATCAGATCTCAACATTGTTGGTTCTTTTGTGTTTTTCATTTTGTACAACCTTTCTTGAATTTAGAAATTACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATTTTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGGAATGCACAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTAGGTTGTATGAATCTACAACCCTATAATAAATTTTACTCTATACAAAAA

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**FIGURE 184**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828  
<subunit 1 of 1, 263 aa, 1 stop  
<MW: 29741, pI: 5.74, NX(S/T): 1  
MVKIAFNTPTAVQKEEARQDVEALLSRTVTRTQILTGKELRVATQKEGSSGRCMLTLLGLSFILAGLIVGGACIY  
KYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIAIIDVPVPSFSDSDPAIIHDFEKGMT  
AYLDLLLGNCYLMLPLNTSIVMPPKNLVELFGKLASGRYLPQTYVVREDLVAVEEIRDVSNLGIIFIYQLCNNRKSF  
RLRRRDLLLGFNKRAIDKCWKIRHFPNEFIVETKICQE

**Type II transmembrane domain:**  
amino acids 53-75

**N-glycosylation site.**  
amino acids 166-170

**Casein kinase II phosphorylation site.**  
amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**  
amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**  
amino acids 63-74



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**FIGURE 186**

MALSSQIWAACLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPICIFCCGCCHR  
SKCGMCCKT

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**FIGURE 187**

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGCCTGGATCTTCCAC  
**CATGTT**CCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGCATCTCCCTGACTGTCTCTTCAACCCT  
CCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGGAGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCT  
GTTAAAAATCTTTGCGTGGGCTACCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCC  
CTACACCAACGGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCTGCGAAGTGGTAG  
TAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCCGAAAGGAATGGAGAC  
CATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTGGAGTCTTGGAACTGCTGAGCAGAACC  
TTATAACTTCCAGTACATCAGCCTTCGGCTCACGGTCTGTGGGGTTAGGAGTGTGATTCTGGTACTGCTTTCT  
GCTGCCGCTCAGGATAGCACTGGCTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTT  
GCCAAATGGGAGGTTTAAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGGCAGCGCT  
GACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCTGTGTGGCCAATCATACCTC  
ACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCCATGGTGGGTCAAGTGCACGGGGGACTCATGGG  
TGTGATTTCAGAGAGCCATGGTGAAGGCTGCCACACGCTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCT  
GGTGGCTAAGAGACTGACTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAAGGAACCTG  
CATCAATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGGAGCCACAGTTTACCCTGTTGCTAT  
CAAGTATGACCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGATGGTGACGTACCTGCTGCGAAT  
GATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTGCCTCCCATGACTAGAGAGGCAGATGAAGATGCTGT  
CCAGTTTGCGAATAGGGTGAAATCTGCCATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCT  
GAAGAGGGAGAAGGTGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGGAACCA  
CAAGGACAGGAGCCGCTCCT**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAACGGGCTCAGAGC  
TGGAGTTGCCGCCGCCGCCCTGCTGTGTCTTTCCAGACTCCAGGGCTCCCCGGGCTGCTCTGGATCCCAG  
GACTCCGGCTTTGCGCCGAGCCGCGAGCGGGATCCCTGTGCAACCGGCGCAGCCTACCTTGGTGGTCTAAACGGAT  
GCTGCTGGGTGTTGCGACCCAGGACGAGATGCCTTGTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAG  
TGAATCCCCACCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGATGG  
CGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGCGGCCACCCGCTCTCCAGGAAAGGC  
ACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCAGCCTTGGAGCTCTGCAGACATGATAGGAAG  
GAAACTGTCTATGCAAGGGGCTTTACGCAAAATGAAGGTTAGATTTTTATGCTGCTGCTGATGGGGTTACTAAA  
GGGAGGGGAAGAGGCCAGGTGGGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTTCGTACTCCAGGCTAACCCCTG  
AACTCCCCATGTGATGCGCGCTTTGTTGAATGTGTGTCTCGGTTTCCCCATCTGTAATATGAGTCGGGGGAATG  
GTGGTGATTCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGTGCGGGTGAGTGAAGGACACATCACGTTTCAG  
TGTTTCAAGTACAGGCCACAAAACGGGGCACGGCAGGCCTGAGCTCAGAGCTGCTGCACTGGGCTTTGGATTTG  
TTCTTGTGAGTAAATAAACTGGCTGGTGAATGA

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**FIGURE 188**

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSEFGIRKLYMKSLLKIFAWATLRMERGAKEKNHQLYKP  
YTNGIIAKDPTSLEEEIKEIRRSKSSKALDNTPEFELSDIFYFCRKGMEITIMDEVTKRFSAAELESWNLLSRTN  
YNFYISLRLTVLWGLGVLIRYCFLPLRIALAFTGISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRAL  
TAITYHDRENRPNGGICVANHTSPIDVILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHL  
VAKRLTEHVQDKSKLPILIFPEGTCINNTSVMFCKGSFEIGATVYPVAIKYDPOFGDAFWNSSKYGMVTYLLRM  
MTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGGLVDLLWDGGLKREKVKDTFKEEQQKLYSKMIVGNH  
KDRSRS



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**FIGURE 189**

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCACGTCTCCTCCAGG  
**GATGG**CGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCACACCTGGCAGGCCAGGCTGTTCCAC  
CATCCTGCCCCCTGGGCCTGGCTCCAGACACCTTTGACGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAA  
GGCAGCCCCCTGCTAAAGGAGGAAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGAC  
CTGGGAGGACAAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCAGAATGGAATAGCCATTATGGTCTA  
CACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAGGCTCCCGGGAGCTCTA  
CATGAGGCACTTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGGGCCCTGCAGCTGCTGCGAGGCAGTGGGG  
CTGCAGCAGGGGACCTGGGGAGGTGGTGTTCCGAGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGA  
CTCTGTCCGCTTGGGCCAGTTTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGGCG  
GGGCTGTGTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTGGAAGAC  
TCTGCTCTTGGCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGCCCT**TGA**AAGTCCAACATCTGCCACTTAGGAGC  
CCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAGCAGCCTTGAGAAGCAAGAATGGTTCCGGAC  
CCAGCCCTAGCAGCCTTCTCCCCAACAGGATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAATCTGCTA  
TGTGATGGGACTTCCTGGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGA  
GACATGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

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**FIGURE 190**

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHHALLRESWEAAQET  
WEDKRRGLTLPPGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSRELYMRHFPPKALHFYLIRALQLLRGSGG  
CSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSSLDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKT  
LLLAPGEFQLSGVGP

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**FIGURE 191**

GTGGCTTCATTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCCTCATCTATAT  
CCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTTCGGTTCGGTTGGTGGGGCCGTGAC  
TTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCAT  
ACAGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTA  
CTCCCTGAAGCTCAGCAAACTGAAGAAGTACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCA  
GCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCA  
GAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATAC  
CTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGA  
AAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAA  
GCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCCCTCCTGTGTCTCCTGTTGGTGGCCCTCCTGCT  
CAGTCTCTTTGTAAGTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAA  
GAGAGTGGACATTTGTGCGGAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCC  
TCACACTAATAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT  
GGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGC  
AGTGCACTCCCCTAAGTCTCTGCTCA

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**FIGURE 192**

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEGGTIIIVTON  
RNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLT  
CCMEHGEEDEVITYWKALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSS  
MVLLCILLVPLLLSLFVLGLFLWFLKRERQEEYIEKKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPA  
NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI



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**FIGURE 194**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPALSPTSMGPQPTTLG
GPSPTNFLDGI VDFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKASAYYPSSFPPKKKYVDQSDRAGGPRAF
SEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSPTRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVP
VETPEAQEEPCSGVLEGAVVAGEGQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV
```

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199, 211-217, 238-244,  
242-248

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**FIGURE 195**

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCTGCTGTGTTTGGGA  
CTGACCCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGAACTTTAATGTAGAAAAGATTAATGGG  
GAATGGCATACTATTATCCTGGCCTCTGACAAAAGAGAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTG  
GAGCAAATCCATGTCTTGGAGAATTCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTA  
TCTATGGTTGCTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACTATA  
CCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGAAACCTTCCAGCTGATG  
GGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAAGGTTTGACAACTATGTGAGGAGCATGGA  
ATCCTTAGAGAAAATATCATTTGACCTATCCAATGCCAATCGCTGCCTCCAGGCCCGAGAATGAAGATGGCCTGA  
GCCTCCAGTGTTGAGTGGACACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTA  
TAAATTCTGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACCTAGGAT  
ACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTGATACACCCTTGACAATTTTTCATGAAATTATTCCT  
CTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

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**FIGURE 196**

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHG NFR LFLEQIHVLENSLV LKVH  
TVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLINEKDGETFQLMGLYGREPDLSSDIKE  
RFAQLCEEHGILRENIIDLSNANRCLQARE



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**FIGURE 197**

GGCTCGAGCGTTTCTGAGCCAGGGGTGACC**ATG**ACCTGCTGCGAAGGATGGACATCCTGCAATGGATTTCAGCCTG  
CTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCTTAGTTGAGGAAGACCAATTT  
TCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCA  
ACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTC  
AGTGTGATCACAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATG  
TGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTTCATCCAGAATCC  
TTCAACTTGCACTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTTCAATAAACCACCCAGTAACGACACC  
ATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCA  
GTATTTTTAGGTCTATTGCTTGTTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTT  
GGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTG**TAG**TTTAATGGGAATAAAATGTAAGTATCAGTA  
GTTTGAAAAAAAAA

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**FIGURE 198**

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPATTMSLTARKR  
ACCNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDS  
CAPPTGFNKPTSNDTMASGWRASSFHFDSSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRR  
SQIV

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**FIGURE 199**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGAAGGAGCAGTG  
AGGAACTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAGATCCGTGGGCTGCAGACCCC  
CGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCT  
ACTGGCAGGCCTGACTGCCTTGGGAAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAA  
AAACCTGCAGCTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAA  
ATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCCTCATCACTCCAGGCTC  
TGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCAGCACCTCCTC  
CCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGC  
TTCTTTATGAATTAACTCGCCCCACCACCCCTCA

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**FIGURE 200**

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSSQKQHSPVPE  
KAIPLITPGSATTC

FIGURE 201

[illegible]

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**FIGURE 202**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGFLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVSEALGQGT
REAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDEVIRHGADAVRGSWQGVPGHSGAWETSGGHGI
FGSQGGGLGGQGGQNPGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQ
NEGCTNPPPSGSGGGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGS
RGDSGSESSWGSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLLGGS
GDNYRGQGSSWGSGGDAVGGVNTVNSETPGMFNFDTFWKNFKSKLGFINWDAINKDQRSSRIP
```

**Signal peptide:**  
amino acids 1-21

**N-glycosylation site.**  
amino acids 265-269

**Glycosaminoglycan attachment site.**  
amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**  
amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**  
amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96,  
96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169,  
178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245,  
240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276,  
271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297,  
292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,  
387-393, 389-395, 395-401

**Cell attachment sequence.**  
amino acids 301-304

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**FIGURE 203**

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGGCTGGGCCTCA  
GACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCTACTCGCCCGCATCCTGGCTT  
GGACCTATGCCCTTCTATAACAACCTGCCGCCGGCTCCAGTGTTTCCCACAGCCCCAAAACGGAACCTGGTTTTGGG  
GTCACCTGGGCTGATCACTCCTACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTTCCAGG  
GCTTTACGGTATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCA  
ATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATAC  
TGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCCGCTTCCATTTCAACATCCTGAAGT  
CCTATATAACGATCTTCAACAAGAGTGCAAAACATCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCA  
GTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACA  
GCCATTGTCAGGAGAGGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAAGAGCC  
AGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCC  
TGGTGCATGACTTCACAGACGCTGTCTATCCGGGAGCGGCGTCGCACCCCTCCCCACTCAGGGTATTGATGATTTTT  
TCAAAGACAAAGCCAAGTCCAAGACTTTGGATTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG  
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCC  
TCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGCAAGAGCTTC  
TGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCCCTTCTGACCATGTGCGTGAAGG  
AGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATCTCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCC  
GAGTCATCCCCAAAGGCATTACCTGCCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATC  
CTGAGGTCTACGACCCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCCTTTCT  
CCGAGGGCCAGGAACCTGCATCGGGCAGGCGTTGCGCATGGCGGAGATGAAAGTGGTCCTGGCGTTGATGCTGC  
TGCATTCCGGTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGCGCGCCGAGGGCGGGC  
TTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCAGTGACTTCTTGACCATCCACCTGTTTTTTTGCAGATT  
GTCATGAATAAAACGGTGCTGTCAA

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**FIGURE 204**

MSLLSLPWLGLRPVAMSPWLLLLLVGWSLLARILAWTYAFYNNCRRLQCFPPPKRNWFWGHLGLITPTEGLK  
DSTQMSATYSQGFTVWLGPIIPFIVLCHPDITRSITNASAAIAPKDNLFIRFLKPWLGEIGILLSGGDKWSRHRM  
LTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATI  
LELSALVEKRSQHILQHMDFLYYLSHDGRRFHRACRLVHDFTDAVIRERRRTLPTQGIDDFKDKAKSKTLDFID  
VLLLSKDEDGKALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCRQEVQELLKDRDPKEIEWDDL  
AQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENS  
KGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFREFLPDHTTEPRRKLELIMRAEGGLWLRVEPLNVGLQ



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**FIGURE 205**

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTGAAGACTCTCTGCT  
TTTGCCACAGCAGTTCTTGCAGCTTCCTTGAGGTGTGAACCCACATCCCTGCCCCCAGGGCCACCTGCAGGACGC  
CGACACCTACCCCTCAGCAGACGCCGGAGAGAAAATGAGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCGTGATC  
CTCTTTGCCCTCATCACCATCCTCATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTG  
CGGGGCCGTAGCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGCAAC  
AAGACACTGCCCTCTCGGTGCCACCAGTGTGTGATTGTGAGCAGCTCCAGCCACCTGCTGGGCACCAAGCTGGGC  
CCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGACCCACCACTGGCTACTCAGCTGATGTGGGC  
AACAAGACCACCTACCGCGTCGTGGCCCCATTCCAGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAAC  
CGGACCCCTGAAACCGTGTTTCATCTTCTGGGGGCCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGT  
GTGATCCAGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCCGGCCGATGCGGCAATTT  
GACGACCTCTTCCGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTTCGTGGTTGAGCACAGGCTGGTTTACC  
ATGGTGATCGCGGTGGAGTGTGTGACCACGTGCATGTCTATGGCATGGTCCCCCCCCACTACTGCAGCCAGCGG  
CCCCGCTCCAGCGCATGCCCTACCACTACTACGAGCCCAAGGGGCCGGACGAATGTGTACCTACATCCAGAAT  
GAGCACAGTCGCAAGGGCAACCACACCGCTTCATACCCGAGAAAAGGGTCTTCTCATCGTGGGCCCCAGCTGTAT  
GGCATCACCTTCTCCACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAGAGGAGAAGC  
AGCCTCCGCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTGCTGGAGTGTCTCCAGCCAATC  
AGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCCTGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGT  
CTATGTGGTTAATCAGGGGTGTCTTTCTTGTGCAGTCAGGGTCTGCCACAGTCAATCAGGGTAGAGGGGTATT  
TCTGAGTCAATCTGAGGCTAAGGACATGTCTTTCCCATGAGGCCTTGTTTCAGAGCCCCAGGAATGGACCCCC  
AATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACCTGGTGTGGCCCCCTCAATTT  
CCAGCACCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCCCGGCCAGAGAATTTGTGGGGTGTGG  
AGGTTGTGGGGGCGGTGGGGAGGTCCCAGAGGTGGGAGGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTG  
GACAAACCTTCCCCCTCTCTGGGCACCCCTTCTGCCACACCAAGTTCCAGTGCGGAGTCTGAGACCCCTTCCAC  
CTCCCCCTACAAGTGCCTCGGGTCTGTCTTCCCGTCTGGACCTCCCAGCCACTATCCCTTGCTGGAAGGCTCA  
GCTCTTTGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTAGGGTATTTTTGCGCAAACCTCCTTCAGG  
GTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCTTAGCCCCCTCAGCCAGCTGCCATTAGCTT  
GGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCTCTAGCAGGGAGGTTTTCCAACGTGTGGAGGCGCCTTTGGGG  
CTGCCCCCTTGTCTGGAGTCACTGGGGGCTTCCGAGGGTCTCCCTCGACCCCTCTGTCGTCTCTGGGATGGCTGTCTG  
GGAGCTGTATCACCTGGGTCTGTCTCCCTGGCTCTGTATCAGGCACCTTATTAAAGCTGGGCCTCAGTGGGGTGT  
GTTTGTCTCCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGAGGCTGGAGGGACAGATG  
GAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGGGGGCGGTGACTGCCCCAGACTTGGTTTTGTA  
ATGATTTGTACAGGAATAAACACACCTACGCTCCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 206**

MSSNKEQRSVAVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPILGNKTLPSRCHQCV  
IVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRVLRRLRPQEFVNRTPETVFIFWG  
PPSKMQKPQGSILVRVIQRAGLVFPNMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHV  
HVGGMVPPNYCSQRRLQRMPIHYEYEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSHPSWT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

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**FIGURE 207**

GTAGCGCGTCTTGGGCTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCTGGAGCCAGGAGCGACGTCAC  
CGCCATGGCCAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTTGTATGCTTGG  
ATGTGCCCTTCCAATATACAACAAATACTGGCCCTCTTTGTTCTATTTTTTACATCCTTTCACCTATTCCATA  
CTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGAAGGAACCTGCCATCTTTCTTAC  
AACGGGCATTGTCTGTCTAGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGGAGCTTG  
TGCACTTGTTCTCACAGGAAACACAGTCATCTTTGCAACTATACTAGGCTTTTTCTTGGTCTTTGGAAGCAATGA  
CGACTTCAGCTGGCAGCAGTGGTTGAAAAGAAATTACTGAACATATTGTCAAATGGACTTCCTGTCAATTTGTTGGCC  
ATTCACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTTAGGTGCTCC  
CTTCTCACTTTTATTGTAAGCATACTATTTTCACAGAGACTTGCTGAAGGATTAAAAGGATTTTCTCTTTTGGAA  
AAGCTTGACTGATTTCACTTATCTATAGTATGCTTTTTTGTGGTGTCTGCTGAATTTAAATATTTATGTGTTT  
TTCTGTTAGGTGATTTTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCATTTGCATTGGT  
TAGGAATTCAGAATCCGCCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATTTATTTAGCCTCCATTA  
TTACAAAAAATTATAAAAAATAAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATGCAGACATACAGAC  
GGTTGGCATACTGTTATAGACTGTATACTCAGTGCAATATAGCTGCATTTATACCTCAGAGGGGCCAAGTGTTAA  
TGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTGAAAATTATTTTATGG  
AATTGCTACAGAGGAGTGCTTTTCTCTCAATTGTTAGAAGATTTATGTTAACTTTAAGGTAAGGGTGTAATA  
ACATTTTTGAGATAAGGTTTTTATTTATGTTTATTATTGTTAGAGTGAGTTGCAATGTGGGAAGAAATGACATTG  
AAATTCAGTTTTTTGAATCCTGTTTCTATTATAAGTGAAATTTGTGATCTCCTATCAACCTTTTCATGTTTTACC  
CTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTTGCATCATATATGCCAGAAAAC  
CTTCTCTGCTTCCTCTTTGACTTATTTGGTATGTTGTATATATTACATAAAATAACTTTTCAAATATAGTTT  
AATAACACTTAGAAGTGTTTACTTACCTGGAATAAATTGCTATGCCGTACATTAGAGTGCCCCCTCCCCTGCA  
AGGCCTTGCCATGATTAACAAGTAACCTGTTAGTCTTACAGATAATTATGCATTAAACAGTTTAAAGATTTAGACC  
ATGGTAATAGTAGTTCTTATTCTCTAAGGTTATATCATATGTAATTTAAAGTATTTTAAAGACAAGTTTCTGT  
ATACCTCTGAAGTGTGTTGATTTTGAAGTTCATCATGATAGATCTGCTGTTTCTTATAAAAGGCATTTGTTGTGT  
GAGTTAATGCAAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACATACCTGACCAAAAAATTTCCAGTAAC  
CAGGCATGATCAATTTATAGTGGTCGTTTACATCTAATAATTATCAGGACTTTTTTTCAGGAGTGGGTTATAAAAA  
CATTCAAGTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTGTATGTTTATTCAGTATACTTACATAAAAAAT  
ATTTGCCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGTTTTATGAAGTTTATTTCTCAAGAAAATG  
GGAATAAATTTGGGATTTGTTTCAGCTTTTTTACTAAAGATGCCTAAAGCCACAGGTTTATTGCTTAACCTTAAGC  
CATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCGGCGTGTGGCTGGAGCCTTCCCCTGGAGGC  
TGAAAGTGGCTTGTGGTATTATAATGTTTCAGATTTCAAGAGGAAGGTGCAGGTACACATGAGTTAGAGAGCTGGT  
GAGACAGTTGGGAACCTTTTGTGCTTGTGATCTACTGGACTTTTTTTTTTGCAGGAAGTGCATTCTCTGGTCCTTC  
CCTATTTTCTGTTCTGGATGTCAGTGCAGTGCAGTGTCTGTTTTATCCACTTGCCACAGACTTTTTCTAACA  
GCTGCGTATTATTTCTATATACTAATTGCATTGGCAGCATTGTGTCTTTGACCTTGATACTAGCTTGACATAGT  
GCTGTCTCTGATTTCTAGGCTAGTTACTTGAGATATGAATTTTCCATAGAATATGCACTGATACAACATTACCAT  
TCTTCTATGGAAAGAAAACCTTTTGATGATGAAACAATAAAGATTTTAAATATCTATTTTAAAAA

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**FIGURE 208**

MAGIKALISLSFGGGAI GLMFLMLG CALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAMSNACKELAI FLTT  
GIVVSAFGLPIVFARAH LIEWGACALVLTGNTVIFATILGFFLVFGSND DFSWQQW

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**FIGURE 209**

CTTGCAGAGAAAGAGTCTTTTGTGCAGCACCCCTTTAAAGGGTGACTCGTCCCACCTTGTGTTCTCTCTCCTGGTGC  
AGAGTTGCAAGCAAGTTTATCAGAGTATCGCCATGAAGTTTCGTCCCCTGCCTCCTGCTGGTGACCTTGTCTCTGCC  
TGGGGACTTTGGGTCAGGCCCCGAGGCAAAAGCAAGGAAGCACTGGGGAGGAATTCATTTCCAGACTGGAGGGA  
GAGATTCTTGCCTATGCGTCCCAGCAGCTTGGGGCAAGGTGCTGGAGAAGTCTGGCTTCGCGTCTGACTGCCGCA  
ACACAGACCAGACCTACTGGTGTGAGTACAGGGGGCAGCCCAGCATGTGCCAGGCTTTTGCTGCTGACCCCCAAC  
CTTACTGGAATCAAGCCCTGCAGGAGCTGAGGCGCCTTCACCATGCGTGCCAGGGGGCCCCGGTGCTTAGGCCAT  
CCGTGTGCAGGGAGGCTGGACCCAGGCCCATATGCAGCAGGTGACTTCCAGCCTCAAGGGCAGCCCAGAGCCCA  
ACCAGCAGCCTGAGGCTGGGACGCCATCTCTGAGGCCCCAAGGCCACAGTGAACTCACAGAAGCAACACAGCTGG  
GAAAGGACTCGATGGAAGAGCTGGGAAAAGCCAAACCCACCACCCGACCCACAGCCAAACCTACCCAGCCTGGAC  
CCAGGCCCGGAGGGAATGAGGAAGCAAAGAAGAAGGCCTGGGAACATTGTTGGAAACCCCTTCCAGGCCCTGTGCG  
CCTTTCTCATCAGCTTCTTCCGAGGGTGAACAGGTGAAAGACCCCTACAGATCTGACCTCTCCCTGACAGACAACC  
ATCTCTTTTATATTATGCCGCTTCAATCCAACGTTCTCACACTGGAAGAAGAGAGTTTCTAATCAGATGCAAC  
GGCCCAAATTCTTGATCTGCAGCTTCTCTGAAGTTTGGAAAAGAAACCTTCTTTCTGGAGTTTGCAGAGTTCAG  
CAATATGATAGGGAACAGGTGCTGATGGGCCAAGAGTGACAAGCATACACAACCTACTTATTATCTGTAGAAGTT  
TTGCTTTGTTGATCTGAGCCTTCTATGAAAGTTTAAATATGTAACGCATTCATGAATTTCCAGTGTTTCAGTAAAT  
AGCAGCTATGTGTGTGCAAAATAAAAGAATGATTTTCAGAAAAAAA

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**FIGURE 210**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59602
<subunit 1 of 1, 223 aa, 1 stop
<MW: 24581, pI: 9.28, NX(S/T): 0
MKEVPCLLLVTLSCSLGQAPRQKQGSGTGEFFHFQTGGRDSCTMRPSSLGQGAGEVWLR
VDCRNTDQTYWCEYRGQPSMCQAFAADPKPYWNQALQELRRLHHACQGAPVLRPSVCREA
GPQAHMQQVTSCLKGSPEPNQQPEAGTPSLRPKATVKLTEATQLGKDSMEELGKAKPTTR
PTAKPTQPGPRPGGNEEAKKKAWEHCKWPFQALCAFLISFFRG
```

**Important features:****Signal peptide:**

Amino acids: 1-19

**N-myristoylation sites:**

Amino acids: 38-44;51-57;194-200

**DNA photolyases class 1 proteins:**

Amino acids: 58-69

**Tyrosine kinase phosphorylation site:**

Amino acids: 64-71

**N-myristoylation sites:**

Amino acids: 38-44;51-57;194-200

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids: 4-15

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**FIGURE 211**

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCGGGTCCTGCTGTGGCTGCAGCTCTGCGCACTGACCCAGGCG  
GTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAACTGGAGCCAGAACCGGACCCCGTGCGCC  
GGCGGCGCCGTTGAGTTCCCGGCGGACAAGATGGTGTCTAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATG  
CTCCTGCCGCTGGATGGGGAACCTCGTCCTGGCTTCAGGAGCCGGATTGGGCGTCTCAGACGTGGGCTCGCACCTG  
GACTGTGGCGCGGGCGAACCTGCCGTCTTCGCGACTCTGACCGCTTCTCCTGGCATGACCGCACCTGTGGCGCT  
CTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGCCACGACGACGTCTTCTTTC  
CGCCTAGTGCCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAGCCCCGTGCGTGTCCGAGCATCTCGGCTCTGG  
GCCGACGTTACGCGCGACGAGGACCTGGCTGTTTTCTGGCGTCCCGCGCGGGCCGCCTACGCTTCCACGGGC  
CGGGCGCGCTGAGCGTGGGCCCCGAGGACTGCGCGGACCCGTGCGGCTGCGTCTGCGGCAACGCGGAGGCGCAGC  
CGTGGATCTGCGCGCCCTGCTCCAGCCCCCT

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**FIGURE 212**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59603
<subunit 1 of 1, 197 aa, 1 stop
<MW: 20832, pI: 8.74, NX(S/T): 2
MGVLGRVLLWLQICALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLV
QEGHAVSDMLLPDGEIVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDRTCGAL
GTRHLASSSWTPSACPAATTTSSFRLVPPSAWGSALALAPCVSAASRLWAGRSRATRTWL
FSWRPARAAYASTGRAR
```

**Important features:****Signal peptide:**

Amino acids 1-19

**N-glycosylation site:**

Amino acids 35-39

**Glycosaminoglycan attachment site:**

Amino acids 81-85

**N-myristoylation sites:**

Amino acids 82-88;118-124;153-159

**C-type lectin domain proteins:**

Amino acids 108-118



FIGURE 213

[illegible]

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**FIGURE 214**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCIIQSLALTWYSLSFIPFARDAVKKCFVCLA

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**FIGURE 215**

GGATTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAAGTGCAGGAGGCCCAGGACAGGCCCCACCC  
TGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGCAGAGAGGCCAAGCCCCCTTGCCCTTGGG  
TCACACAGCCAAAGGAGGCAGAGCCAGAAGTCAACAACAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACG  
AAAAGGCAGTCACCCGCAGGGCCAAGGTGGCTCCCGCTGAGAGGATGAGCAAGTCTTAAGGCACTTCACGGTCG  
TGGGAGACGACTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGC  
AGCCACCCACCCACACCAAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCCTGACGTTGCCCTGCCCCCTGGCCCCG  
CAGGAGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTTGAGCTCCACAGGTTTCAGGTCATCATCA  
TCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGCTTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCGACA  
AGAATAACTATGCTGCCATGGTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCT  
TTAAATTATTTGTCTTCCGCTGAGTTCTTTTACCACAAGTTTGAGATCCTGGATGCCCGTGGTGGTGGTCT  
CATTCATCCTGGACATTGTCTCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGCCTGCTGATTCTGCTCCGGC  
TGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGTTAAGACACGTTTCAAGACGGCAACTCTTAAGGT  
TAAAACAGATGAATGTACAATTGGCCGCCAAGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCCTGGACT  
GATGAGTTTGCTGTATCAACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTA  
CTCTCACACAGCCACCGTGAAGTCTCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAGCAGGCTGGC  
ATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTATCACTTCAGATTACAAATCACA  
CAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACCAAATCTATAAAGATATTCTGAAAATATGACAGAA  
TTTGACAAATAAAGCATAAACGTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 216**

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGGDYHAWNINYKKWENEEEEEEEEQPPPTPVSGEEGRAAAPDVA  
PAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELILDLDKIIQPKNNYAAMVFHYMSITILVFF  
MMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILDIVLLFQEHQFEALGILLILLRLWRVARIINGIIISVKTRSE  
RQLRLKQMNVQLAAKIQHLEFSCSEKPLD

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**FIGURE 217**

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGCTTCCCTGGGG  
CAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTGCACATCATTGGCTTTGGT  
ATTTCAAGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGC  
TGCACTTTTGAACCTGACATCAAACCTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTC  
CATGAGTTCAAAGAAGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTCAAGGCGGACAGCAGTGTGCT  
GATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGT  
TATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGGAAGTG  
AATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCACAGTGGTC  
TGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAAT  
GTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAAAATGAC  
ATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAAC  
TCAAAGGCTTCTCTGTGTGTCTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATG  
CTAAAATAATGTGCCTTGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAATATTTTAC  
CACCAGATATGACCTAGTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAG  
AGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAAGACATATTA  
GAAGTTGGGAAAATAATTCATGTGAAC TAGACAAGTGTGTTAAGAGTGATAAGTAAATGCACGTGGAGACAAGT  
GCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTG  
TCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCA  
CATCTTATATTCACAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAG  
GGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTCTCTTC  
CCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGTCGGGGACACCGATTT  
TATAAATAAAGTGAACCTTCTTTTAAACAA  
AAAAAAA

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**FIGURE 218**

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG  
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKRVQLTDAGTYKCYIITSKGKGNANLEYKTGAF  
SMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSC  
MIENDIAKATGDIKVTESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYMLK

FIGURE 219

[illegible]

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**FIGURE 220**

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMFPFLNQCGSLLYYLTL  
ASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISP EWVRTRPFPILP  
FPLQLFCFLVAIRVPFPWTVWRKTEAGVWD



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**FIGURE 221**

CTTCTGTAGGACAGTCACCAAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTGGAAGATGACAGCA  
ATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAAACTTTGCCAGTGGGAAGTACCTAGTGAAA  
CGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCTTGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTC  
CAGCACCATGAAGGGCATCCTCGTTGCTGGTATCACTGCAGTGCCTTGTTCAGCTGTAGAATCTCTGAGCTGCGT  
GCAGTGTAATTCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAGCTG  
TATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGTTCTGCTCAGCGGAGAA  
CTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCTGCTGAAGAACACTTTCATTTTGTAAAGCCA  
GTGCTGCCAAGGAAAGGAATGCAGCAACACCAGCGATGCCCTGGACCCCTCCCCTGAAGAACGTGTCCAGCAACGC  
AGAGTGCCCTGCTTGTATGAATCTAATGGAACCTTCTGTGCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACA  
GTGTGTCTTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTCCAACGT  
CAGTAACGCCACCTGTCAGTTCCTGTCTGGTGAAAACAAGACTCTTGGAGGAGTCATCTTTCGAAAGTTTGAGTG  
TGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACTTCCCACAACGTGGGCTCCAAAGCTTCCCTCTA  
CCTCTTGGCCCTTGCCAGCCTCCTTCTTCGGGGACTGCTGCCCTTGAGGTCTGGGGCTGCACCTTTGCCCAGCACC  
CCATTTCTGCTTCTCTGAGGTCCAGAGCACCCTGCGGTGCTGACACCCTCTTCCCTGCTCTGCCCCGTTTAA  
CTGCCCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTAAAGCACTGG  
TTCATTCACCTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 222**

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLET  
PVRLYQNMFCSAENCSEETHITAFTVHVSAAEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAECPACYESNGTSCRGKPKCYEEEQCV  
FLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENKTLGGVIFRKFEKANVNSLTPTSAPTTS  
HNVGSKASLYLLALASLLLRGLLP

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**FIGURE 223**

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCAGGGCTTGCCTCAC  
TGGCCACCCCTCCCAACCCCAAGAGCCCAGCCCCATGGTCCCCGCCGCCGCGCTGCTGTGGGTCTGTGCTGCTG  
AATCTGGGTCCCCGGGCGGCGGGGGCCCAAGGCCTGACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGC  
TTTGGGGGCCCCATGACCCGCAGCTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTA  
GAGGACGAGAATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCCACG  
GTGTCCACCGGCTTTAGCCGGTCTGTCGCCCATTAACGAGGAGGATGGGTCTTCAGAAGAGGGGGTTGTGATTAAAT  
GCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCAATACAGCGGGGAGTTCCAGCACGAGGTTT  
ATAGCCAATAGTCAGGAGCCTGAAATCAGGCTGACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGAC  
CTGCCAGGCTCGCAGGCCACCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCACCCCTCA  
CCCACAGCCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCACTGCAAG  
TCGGGCACCATGAGCCGAGCCGGTCTGGGAAGCTGCACGGCCTTCCGGGCGCCTTCGAGTTGGGGCGCTGAGC  
CAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTCCCTGCAACCGACTTCGGGAAGAGTGCCCCCTG  
GACACAAGTCTCTGTACTGACACCAACTGTGCCTCTCAGAGCACCACCAGTACCAGGACCACCCTACCCCCCTT  
CCCACCATCCACCTCAGAAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCAGCCCTGGCTTTTGGAAACGG  
GTCAGGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATAGACAGAAAC  
CAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCTCTTGCCCTTTCAATCCTAGCAC  
CCACTAGATATTTTACTACAGAAAACAAAACCTGGAAAACACAA

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**FIGURE 224**

MVPAAGALLWVLLNLGPRAAGAOGLTQTPTMQRVSLRFGGPMTRSyrSTARTGLPRKTRIILEDENDAMADAD  
RLAGPAAAEELLAATVSTGFSSAINEEDGSSEEGVINAGKDSTSRELPSATPNTAGSSSTRFIANSQEPEIRL  
TSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWSPSPPTAMPSPEDLRLVLPWGPWHCHCKSGTMSRSRSRK  
LHGLSGRLRVGALSQLRTEHKPCTYQQPCNRLREECPLDTSCTDTNCASQSTTSTRTTTTPFPTIHLRSSPSL  
PPASPCPALAFWKVRVIGLEDIWNLSVFTMQPIDRNQR

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**FIGURE 225**

CCCGGGTCGACCCACGCGTCCGGGGAGAAAGGATGCGCCGGCCTGGCGGGCGCGGTTGGTCCTGCTAGCTGGGGCAG  
CGGCGCTGGCGAGCGGCTCCAGGGCGACCGTGAGCCGGTGTAACCGCGACTGCGTACTGCAAGAGCAGA  
ACTGCTCTGGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCTGTC  
GGGACGACTGTAAGTATGAGTGTATGTGGGTACCGTTGGGCTCTACCTCCAGGAAGGTCACAAAGTGCCTCAGT  
TCCATGGCAAGTGGCCCTTCTCCCGGTTCTGTTCTTTCAAGAGCCGCGCATCGGCCGTTGGCCTCGTTTCTCAATG  
GCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCATGTACACACCTGTG  
TGGCCTTCGCCTGGGTGTCCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACCAGGGACACTGACCTCACAG  
AGAAAATGGACTACTTCTGTGCCTCCACTGTCATCCTACACTCAATCTACCTGTGCTGCGTCAGGACCGTGGGGC  
TGCAGCACCCAGCTGTGGTCAGTGCCCTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCTCCTACCTGA  
GCCATCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTGGTGTGGTGGC  
TGGCCTGGTGCCTGTGGAACAGCGCGGCTGCCTCACGTGCCCAAGTGCCTGGTGGTGGTCTTGCTGCTGCAGG  
GGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTGGATGCCCATGCCATCTGGCACATCA  
GCACCATCCCTGTCCACGTCTCTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTGAAGGAATCAGAGG  
ACAAGTTCAAGCTGGACTGAAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCGCCCTGCTGGCCTC  
CCTTCTCCCCCTAACCCCTTGAGATGATTTTCTTTTCAACTTCTTGAACCTGGACATGAAGGATGTGGGCCCAG  
AATCATGTGGCCAGCCACCCCTGTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGGAAGGCCTCCACGATC  
TGGGACTCGAGAGTGGGCAGCCCTCTACCTCCTGGAGCTGAACTGGGGTGGAACTGAGTGTGTTCTTAGCTCTA  
CCGGGAGGACAGCTGCCTGTTTCTCCCCACCAGCCTCCTCCACATCCCCAGCTGCCTGGCTGGGTCTGAAG  
CCCTCTGTCTACCTGGGAGACCAGGGACACAGGCCTTAGGGATACAGGGGGTCCCCTTCTGTTACACCCCCCA  
CCCTCCTCCAGGACACCACTAGGTGGTGTGGATGCTTGTCTTTGGCCAGCCAAGGTTACAGGCGATTCTCCCC  
ATGGGATCTTGAGGACCAAGCTGCTGGGATTGGGAAGGAGTTTACCCTGACCGTTGCCCTAGCCAGGTTCCCA  
GGAGGCCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCAGGGCAAGGATCCTGTGCTGCTGTCTGG  
TTGAGAGCCTGCCACCGTGTGTCGGGAGTGTGGGCCAGGCTGAGTGCATAGGTGACAGGGCCGTGAGCATGGGCC  
TGGGTGTGTGTGAGCTCAGGCCTAGGTGCCAGTGTGGAGACGGGTGTTGTGCGGGGAAGAGGTGTGGCTTCAAAG  
TGTGTGTGTGCAGGGGGTGGGTGTGTTAGCGTGGGTAGGGGAACGTGTGTGCGCGTGTGGTGGGCATGTGAGA  
TGAGTGAAGTCCCGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGATGAGGGAATCCTGTACCATCAATAAT  
CACTTGTGGAGCGCCAGCTCTGCCCAGACGCCACCTGGGCGGACAGCCAGGAGCTCTCCATGGCCAGGCTGCCT  
GTGTGCATGTTCCCTGTCTGGTGGCCCTTTGCCCCCTCCTGCAAACCTCACAGGGTCCCCACACAACAGTGCCC  
TCCAGAAGCAGCCCCCTCGGAGGCAGAGGAAGGAAAATGGGGATGGCTGGGGCTCTCTCCATCCTCCTTTTCTCCT  
TGCCCTTCGATGGCTGGCCTTCCCCTCCAAAACCTCCATTCCCCTGCTGCCAGCCCCCTTGCCATAGCCTGATTT  
TGGGGAGGAGGAAGGGGCGATTTGAGGGAGAAGGGGAGAAAGCTTATGGCTGGGTCTGGTTTCTTCCCTTCCCAG  
AGGGTCTTACTGTTCCAGGGTGGCCCCAGGGCAGGCAGGGGCCACACTATGCCTGTGCCCTGGTAAAGGTGACCC  
CTGCCATTTACCAGCAGCCCTGGCATGTTCTGCCCCACAGGAATAGAATGGAGGGAGCTCCAGAACTTTCCAT  
CCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTGTCTGCCCCTGACCCCTGTCCCTCTTTGAGGGA  
GGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTGGCCTGCGCTAGCTTCTTTTGATACTGAAAACCTTT  
AAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAATTCCAAGCCTCAAAAAAAAAAAAAAAAAA

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**FIGURE 226**

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGWTCRDDCKYECMWV  
TVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCRYRTFVPASSPMYHTCVAFWVSLNAW  
FWSTVFHTRDLDLTKMDYFCASTVILHSIYLCCVRTVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNL  
VANVAIGLVNVVWLLAWCLWNQRRLEPHVRKCVVVVLLQGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFS  
FLEDDSLYLLKESEDKFKLD

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

**N-glycosylation site.**

amino acids 40-44

**N-myristoylation site.**

amino acids 43-49

**CUB domain proteins profile.**

amino acids 285-302

**Amiloride-sensitive sodium channels proteins.**

amino acids 162-186

**FIGURE 227**

TTCGCGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCACCCCTTCCCCTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCTCGTGGGGTGCCTTGCACCCACGCGGACTCCCAGCTGGCGCGCCCTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCTTCCACCTGACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGCTTCGGCCCCGGCCTTCGCGCTTTTCTTGATCATGTGGCTGGGACCCGCTTCGCGTTATCATCTTGTGCGAGGGGCATTTTTCTGGCTGGTCTCCTGCTCCTGGCTCTGTGGTCTGTTTCTGTTGCTATGTGCTATGTGACCGAGCTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGTGCTGCTGTCTGTCTGCTCTACAGGAGGTGTTCCGCTTTGCCCTACTACAAGCTGCTTAAGAAGGCAGATGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACTTGGGCCAGGTGTGGTGGGATCCATGGAGACTCACCTATTACTTCTTGACTTTCAGCCTTCTGACAGCAGCATTATCTGCTCCATACCTTTTGGGAGTGTGTTCTTTGATGCCTGTGAGAGGACGGTACTGGGCTTTGGCCCTGGTGGTGGGAGTCACTTACCTGACATCGGAGCTGACATTCTGAACCCTGGTATGAGGCCAGCCTGCTGCCACTCTATGCAGTCACTGTTTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCAGCCTCTTGTTGAAGGACTGACTACCTGGACTGATCGCTGACAGATCCCACTGCTGTCCACTGCCATGACTGAGCCAGCCCCAGCCGGGTCCATTGCCACATCTCTGTCTCCTTCTCGTCGGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTTTACCAGGAGCAGCCTGGGTTTCAGCCAGTCACTGCTGGTGGGTTGAATCTGCACCTATCCCCACCACCTGGGGAGCCCCCTTGTGTCTCAGGACTCCCCCTGTGTGCTGCTGCTCTCACCCTGCCAAGACTCACCTCCCTCCCCCTGCGAGGCGCGCAGGAGGACAGTGGGTTGATGGTGTATTCTGCCCTGCGCATCCACCAGGAGTGGGGAACCTAGGGGGACCCCTGGGCCTGGGGTGGCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAAGTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAAGGATAGATGAGTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGAGTCTTTTCTCAGGCCCTGAGGGGGAACCAATTTTGGTGTGATAAATACCTAACTGCCCTTTTTCTTTTTTGGGTGGGGGAGGAGGATATATTGGAACCTCTTCAACCTCCTTGGGCTATATTTTCTCTCGAGTTGCTGCTCATGGCTGGGCTCAATTCGGTCCCTTCTCCTTGGTCCCAGACCTTGGGGGAAAGGAAGGAAGTGCATGTTTGGGAACTGGCATTACTGGAATAATGGTTTTAACCTCCTTAACCACAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGTGCTGTGGTGAGCTGGCCACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGGGAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAACTGTATCATTTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTTAATCAAGGTGATTGTGATTTTGACTAATAAAAAAAGAAATTTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 228**

MGAAVFFGCTFVAFGPALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDRSDARLQYGLLIFG  
AAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLSFGIISGVFSVINILADALGPGVVGIIH  
GDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMG  
LWAFITAGGSLRSIQRSLLCKD



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**FIGURE 229**

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTCCCAGGCTCCCGCG  
GCCGACCCCGCGCAACATGCAGCCACGGGCCGCGAGGGTTCCCGCGCGCTCAGCCGGCGGTATCTGCGGCGTC  
TGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGCCCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAG  
CCCTCTCCACGCTGGGCTCCCCAGCCTCTTACCACGCCGGGTGTCCCAGCGCCCTCACTACCCAGGCCTCA  
CTACGCCAGGCACCCCAAACCCCTGGACCTTCGGGGTTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACCTCGTGG  
ACGGCCACAATGACCTGCCCCAGGTCTTGAGACAGCGTTACAAGAATGTGCTTCAGGATGTTAACCTGCGAAATT  
TCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGTGGGTGCCAGTTCTGGTCAGCCTCCGTCT  
CATGCCAGTCCCAGGACCAGACTGCCGTGCGCCTCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCCT  
CCTACTCTGAACCTCGAGCTTGAGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCG  
TGNAGGGTGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCTACCTGA  
CACTTACCTTCACCTGCAGTACACCATGGGCAGAGATTCCACCAAGTTCAGACACCACATGTACACCAACGTCA  
GCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAACCGCCTGGGCATGATGATAGATTTGTCTTATG  
CATCGGACACCTTGATAAGAAGGGTCCTGGAAGTGTCTCAGGCTCCTGTGATCTTCTCCACTCAGCTGCCAGAG  
CTGTGTGTGACAATTTGTTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGA  
CACTGTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTGACCACATCA  
GGGCAGTCATTGGATCTGAGTTTCATCGGGATTGGTGAAATTATGACGGGACTGGCCGGTTCCCTCAGGGGCTGG  
AGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCTGAGTCGTASCTGGAGCGAGGAAGACTTCAAGGTG  
TCCTTCGTGGAACCTGCTGCGGGTCTTCAGACAAGTGGAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCG  
TGGAGGCTGAGTTTCCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGG  
CTACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCTCCCCATACCTTG  
TTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTCTGCTTGACACAGTCGGTCCCCGAGA  
GGTCACTGTGGCAAAGCCTCACAAGCCCCCTCTCCTAGTTCAATCACAAGCATATGCTGAGAATAAACATGTTA  
CACATGGAAAA

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**FIGURE 230**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817  
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown  
><MW: 53569.32, pI: 7.68, NX(S/T): 5  
MQPTGREGSRALSRRLRLRLRLRLRLRLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPSALTTPGLTTPGTP  
KTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSGQTS�DRLDGLVGAQFWSASVSCQSQD  
QTAVRLALEQIDLIHRMCASYSELELV TSAEGLNSSQKLACLIGVXGGHSLDSSLSVLR SFYVLGVRYLTLTFTC  
STPWAESSTKFRHHMYTNVSGLTSFGKVV EELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNL  
LNVPDDILQLLKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDVSTY  
PVLIEEELLSRXWSEELQGVLRGNLLRVFRQVEKVR EESRAQSPVEAEFPYQQLSTSCHSHLVPQNGHQATHLEV  
TKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359,  
357-362, 394-399, 427-432 and 472-477.**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

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**FIGURE 231**

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGATTGGCAAGCGCTGG  
CCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGTAGCTATTAGCCAATTCGGCAGGGGCC  
GCTTTTTAGAAAGCTTGATTTCTTTGAAGATGAAAGACTAGCGGAAGCTCTGCCTCTTTCCCAGTGGGCGAGGG  
AACTCGGGGCGATTGGCTGGGAACGTATCCACCCAAATGTCACCGATTTCTTCCTATGCAGGAAATGAGCAGAC  
CCATCAATAAGAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACTGGAGGCAAAGAGG  
GTTGCTCAACGCCCCGCCTCATTTGGAACCAATCAGATCTGGGACCTATATAGCGTGGCGGAGGCGGGGCGAT  
GATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCTTTCCCCGCCCTGAGACCCTGCAGCACCA  
TCTGTCATGGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCG  
GCCGCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGAAAGCGGCC  
CCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGTATGAGAAGAACCCAGACTCC  
CATGGTTATGACAAGGACCCGTTTTGGACGTCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATC  
CTGGTCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCCGCCGGAAGCTGAG  
AGGCTTGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCCAGCAAGATCCAG  
CTGCCAGAGGATGAGTGACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATT  
TGACCTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

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**FIGURE 232**

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPEDENLYEKNPDSHG  
YDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAERLVKYREANGLPIMESNCFDPSKIQLPEDE

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**FIGURE 233**

GCGGGGGCTATGCCGCTTGCTCTGCTCGTCTGTTGCTCCTGGGGCCCCGGCGGCTGGTGCCTTGCGAACCCTCA  
CGCGACAGCCTGCGGGAGGAACCTTGTCATCACCCCGCTGCCCTTCCGGGGACGTAGCCGCCACATTCCAGTTCCGC  
ACGCGCTGGGATTCGGAGCTTCAGCGGGAAGGAGTGTCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTG  
ATCTCCAAGTATTTCTCTACGGGAGCTGCACCTGTCATTACACAAAGGCTTTTGGAGGACCCGATACTGGGGGCCA  
CCCTTCTGTCAGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAATCT  
TGGAAGGAGCTCAGTAATGTCCTCTCAGGGATCTTCTGCGCTCTCTCAACTTCATCGACTCCACCAACACAGTC  
ACTCCCACTGCCCTCTCAAACCCCTGGGTCTGGCCAATGACACTGACCACTACTTTCTGCGCTATGCTGTGCTG  
CCGCGGGAGGTGGTCTGCACCGAAAACCTCACCCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCCTC  
TCTGTGCTGCTGAAGGCAGATCGCTTGTTCCACACCAGCTACCCTCCAGGCAGTGCATATCCGCCCTGTTTGC  
AGAAATGCACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCAGTTGTATTTGATGCCTTCATCAG  
GGGCAGGGAAAGAAAGACTGGTCCCTCTCCGGATGTTCTCCCGAACCTCACGGAGCCCTGCCCTGGCTTCA  
GAGAGCCGAGTCTATGTGGACATCACCACTACAACAGGACAACGAGACATTAGAGGTGCACCCACCCCGACC  
ACTACATATCAGGACGTATCCTAGGCACTCGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATC  
AACAACTCTCGAAACCTCAACATCCAGCTCAAGTGAAGAGACCCCCAGAGAATGAGGCCCCCCCAGTGCCCTTC  
CTGCATGCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTACAACACCCAC  
CCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCGGCTGTATGTGCACACCCCTCACC  
ATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCCACTACCAGCCTGCCAGGACCGGCTGCAACCCAC  
CTCCTGGAGATGCTGATTGAGCTGCCGGCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTG  
AAGTGGACCGAGTACACGCCAGATCCTAACCATGGCTTCTATGTGAGCCCATCTGTCTCAGCGCCCTTGTGCCC  
AGCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCCTCTCAACAGCCTGTTCCAGTCTCTGATGGC  
TCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCCGACACCGGACTTCAGCATGCCCTAC  
AACGTGATCTGCCTCAGTGCATGTGGTGGCCGTGTGCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTC  
CACATCGAGGAGCCCCGCACAGGTGGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCC  
CCACTCTGATTCTTGGCCCTTCCAGCAGCTGCAGCTGCCGTTTCTCTGCGGGAGGGGAGCCCAAGGGCTGTTTC  
TGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAGTGCCCTGGACCAGGTGAGGGCCTACAGCTGTGTTGT  
CCAGTACAGGAGCCACGAGCCAAATGTGGCATTGAAATTTGAATTAACCTAGAAATTCATTTCTCACCTGTAGT  
GGCCACCTCTATATTGAGGTGCTCAATAAGCAAAAGTGGTGGTGGCTGCTGTATTGGACAGCACAGAAAAGAT  
TTCCATCACACAGAAAGGTGGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGT  
GTAGTGGATGGAGTTTACTGTTTGTGGAATAAAAACGGCTGTTTCCGTGGAAAAAAAAAAAAA

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**FIGURE 234**

MPLALLVLLLLGPGGWCLAEPDRSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHYRLFPKALGQLISK  
YSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVSKSWKELSNVLSGIFCASLNFIDSTNTVTPT  
ASFKPLGLANDTDHYFLRYAVLPREVCTENLTPWKKLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNA  
RCTSISWELRQTLSVVFDAFITGQKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTY  
QDVILGTRKTYAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTHPYR  
AFPVLLLDTPVWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANSVTKVSIQFERALLKWT  
EYTPDPNHGFYVSPSVLSALVPSMVAAKPDWEESPLFNSLFPVSDGSNYFVRLYTEPLLVLNLTPTPDFSMPYNVI  
CLTCTVVAVCYGSFYNNLLTRTFHIEEPRTGGLAKRLANLIRRARGVPPL

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**FIGURE 235**

TGACGT CAGAAT CACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCCAGGAGCTGCAGGACAAGCACCAGGAGC  
CCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGTGGGCTACCCCTGGTGGTGG  
TTATGGGGGTCTGCCCCCTGGAGGGCCTTATGGACCACCAGCTGGTGGAGGGCCCTATGGACACCCCAATCCTGG  
GATGTTCCCCCTGGAACCTCAGGAGGACCATATGGCGGTGCAGCTCCCGGGGGCCCCCTATGGTCAGCCACCTCC  
AAGTTCCTACGGTGCCAGCAGCCTGGGCTTTATGGACAGGGTGGCGCCCCCTCCCAATGTGGATCCTGAGGCCTA  
CTCCTGGTTCCAGTCGGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAA  
CTGCAATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCAGGCCG  
CATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGAGAAGACCTCTCCAGCAGTATGACCG  
GGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCCAATGGGCTACAACCTGAGCCCCCA  
GTTACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCTGCCAATCCTGCCATGCAGCTTGACCGCTTCATCCA  
GGTGTGCACCCAGCTGCAGGTGCTGACAGAGGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCT  
CAGCTTCGAGGACTTCGTCACCATGACAGCTTCTCGGATGCTATTGACCCAACCATCTGTGGAGAGTGGAGTGCAC  
CAGGGACCTTTCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTTCTGTCCCTCTAGAAGAAC  
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCCTGCATCATAGCCACCAAATAGTGAGG  
ACCGGGGCTGAGGCCACACAGATAGGGGCCTGATGGAGGAGAGGATAGAAGTTGAATGTCCTGATGGCCATGAGC  
AGTTGAGTGGCACAGCCTGGCACAGGAGCAGGTCCTTGTAAATGGAGTTAGTGTCCAGTCAGCTGAGCTCCACCC  
TGATGCCAGTGGTGAGTGTTTCATCGGCCTGTTACCGTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAAC  
GAGCCCATTTTCTCCAAAGTGAATCTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCT  
GCCACACCCATAAATCCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTG  
GGCATCTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCCTGCCATGCTCTGCTCGGCTTCAGT  
CTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTTAATTTGCATTTTTTTTTCATTGGGGCCAAAAG  
TCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAACTCTGA

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**FIGURE 236**

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYGHPNPGMFPSG  
TPGGPYGGAAPGGPYGQPPSSYGAQQPGLYQGGAPPNVDP EAYSWFQSVDS DHSGYISMKELKQALVNCNWSS  
FNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDRDRSGSISYTELQQALSQMGYNLSPQFTQLL  
VSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREKDTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115



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**FIGURE 237**

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATCTCCCAGGCCT  
CTTTGCCCCGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACCAACTTGCCCTCAGCTCGGACA  
ACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCGCTCTGGACCCTAGGTCTAATGACTTGGCAAG  
GGTTCCTCTGAAGCTCAGCGTGCCTCCATCAGATGGCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCC  
TCCATCGTGGGGGCTGCCTGCCATGGATTCTTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGA  
GGACCGCCTGGGGGAAGCGCTGCCTGAAGAACTCTCTTACCTCTCCAGTGCTGCGGCCCTCGCTCCGGGCAGTGG  
CCCTTTGCCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGACTCGGA  
GTCCAGACGACTGCCCCGTTCTAATTCAGTGGGAGCCGGGGGAAAAATCCTTTCCCAACGCCCTCCCTGGTCTCT  
CATCCACAGGGTTCTGCCTGATCACCCCTGGGGTACCCTGAATCCCAGTGTGTCTGCGGGAGGTGGAGGCCCTGG  
GACTGGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGAATCTGGGGTATCAATAATCAACCCCCAGGTACCAG  
CTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAA  
TATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTCATCTATACCCAGGTATCAATAACCCATTTCTCCTGG  
AGTTCTCCGCCCTCCTGGCTCTTCTTGGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG  
GGGCTAGAGCACGATAGAGGGAAACCCAAACATTGGGAGTTAGAGTCTGCTCCCGCCCCTTGCTGTGTGGGCTCA  
ATCCAGGCCCTGTAAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCCTGCTCATCTCCAATAAAATA  
AAAGCACTTATGAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 238**

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSNFGTNLPQLGQPSSTGPSNSEHPQPALDPRSNDLARV  
PLKLSVPPSDGFPFAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAAEDRLGEALPEELSYLSSAAALAPGSGP  
LPGESSPDATGLSPEASLLHQDSESRRLPRNSNLGAGGKILSQRPPWSLIHRVLPDHPWGTLNPSVSWGGGGPGT  
GWGTRMPMPHPEGIWGINNQPPGTSGWNINRYPGGSGWNINRYPGGSGWNINRYPGGSGWNIHLYPGINNPFPFPGV  
LRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263, 259-264, 269-274, 270-275, 280-285, 281-286, 305-310

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**FIGURE 239**

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCCGCTGTGCCTGCTGTGCCCGCGCTGTGCGCG  
CTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCGGAGAGCTCAAGCGCCC  
AGCTCTGCCCCAGGAGCCCAGGCTGCCCCGTGAGTCCCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCCT  
GGGTGGTGTATCCCCCTTGGGGCTGCTGTTCCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACTCT  
CTTAGAGGAGCTGCTCAGCAAATACCAGCACAACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGAGGA  
CAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCTCCAACATGGAGTACAT  
GGTGAGCGCCGGCTCCGGCCGCAGAGGCTGGCACCGGGGGTGGGGCCTGGGCCACCAGCCTGCTCTGTTCCCCAG  
CCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGGCTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTG  
TTCTGTTTTGTTTGTGTTTGTGTTTGTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCA  
TGCCCTGAAACCTTAGACTCCCGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAGGCATGC  
ACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGTTGCCAGGCTGGTCTTGAA  
CTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTGCTAGGATTATAGGCATGAGTCACCCCTGTCTGG  
CTCTGGCTCTGTTCTTAACATTCTGCCAAAACAACACAGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTC  
ATGTCACCTCTTGGTAGTCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCC  
AGGGCTGGGCTTGTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTCCTTAGCCCG  
TGTGAGCCTCACTTCCACTTGGAGAGTCCCTCCTCGCGTGGTTGCCATGACTGTGAGATAAGTCGAGGCTGTGA  
AGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCTAGGCTTTGCTAACCGGGAAAGGAGCTAACGGTGACAGA  
AGACAGCCAAGGTCAACCCTCCCGGTGATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGAC  
CCCAAGCTCCAGTGTGAAACTTCCTTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAG  
GGTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTCAGCTATGAATGGCTTTTAAACAACC  
CACGTCCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATCCAAGTAGCCGGGCATGGTGGTGCG  
CACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAGGTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGC  
TTGAGCCTGGGAAGTCGAGGCTGCAGTGAGCTGAGATTGCACCCTGCACTCCAGCCTGGGTGACAGAGCAAGAC  
CCTGTCTCAAAAA

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## **FIGURE 240**

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILMLHNKLRGQVQPQAS  
NMEYMVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGRGGSRLCSVLFVCFETGSHSATDAGVQ  
WHNRHALKP

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 27-31, 41-45

**N-myristoylation site.**

amino acids 126-132, 140-146

**Amidation site.**

amino acids 85-89

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**FIGURE 241**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCC  
CTTGTCTCCTCTTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAG  
GAGTCTTTTCTGACAAATTCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCAT  
CTCCCTTCAGGGACCAGCGTCACCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATGAAGCCA  
TTGAAGCCTGTGTCTTCTTGGCCCGGGCTTTTGGCCGGGGATGCAGGAGGCAGGCCCGACCCCTGTCTTTCAG  
CAGGCCCCACCCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

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**FIGURE 242**

MSGGLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFELLEKLCLLLHLPSTSVTLHHARSQHHVVCNT

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**FIGURE 243**

GGCAAGTGGAACTGGCTTGGTGGATTTTGCTAGATTTTCTGATTTTAACTCCTGAAAAATATCCCAGAT  
AACTGTCATGAAGCTGGTAACTATCTTCCTGCTGGTGACCATCAGCCTTTGTAGTTACTCTGCTACTGCCTTCCT  
CATCAACAAAGTGCCCTTCCTGTTGACAAGTTGGCACCTTTACCTCTGGACAACATTCTCCCTTTATGGATCC  
ATTAAAGCTTCTTCTGAAAACTCTGGGCATTTCTGTTGAGCACCTTGTGGAGGGGCTAAGGAAGTGTGTAATGA  
GCTGGGACCAGAGGCTTCTGAAGCTGTGAAGAACTGCTGGAGGCGCTATCACACTTGGTGTGACATCAAGATAA  
AGAGCGGAGGTGGATGGGGATGGAAGATGATGCTCCTATCCTCCCTGCCTGAAACCTGTTCTACCAATTATAGAT  
CAAATGCCCTAAAATGTAGTGACCCGTGAAAAGGACAAATAAAGCAATGAATACATTA

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**FIGURE 244**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59855  
<subunit 1 of 1, 93 aa, 1 stop  
<MW: 10161, pI: 7.39, NX(S/T): 0  
MKLVTFLLVTISLCSYSATAFLINKVPLPVDKLAFLPLDNILPFMDPLKLLKTLGISV  
EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV
```

**Important features:****Signal peptide:**

Amino acids 1-18



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**FIGURE 245**

TGCTAGGCTCTGTCCCAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGATCCCTCTATGACT  
GCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAGCATGAAGCTCTTATCTTTGGTGGCTGTGGT  
CGGGTGTTTTGCTGGTGCCCCAGCTGAAGCCAACAAGAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACC  
TTATAGAAACATCAGTGGGCACATTTACAACCAGAATGTATCCAGAAGGACTGCAACTGCCTGCACGTGGTGGA  
GCCCATGCCAGTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAGCAC  
CACCACCATCAAGGTCATCATTGTCTATCTACCTGTCCGTGGTGGTGCCCTGTTGCTCTACATGGCCTTCCTGAT  
GCTGGTGGACCTCTGATCCGAAAGCCGGATGCATACACTGAGCAACTGCACAATGAGGAGGAGAATGAGGATGC  
TCGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGC  
CCAGCAGCGGTGGAAGCTGCAGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTTAGAT  
GGGCTGGTGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGGCTACTT  
CTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAAGCCTGTGGCATTTTTCCCTCCTTCTCCCTAACTTTAGAAATG  
TTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCTGATCTCTGTTGTCTTCTTGGGTCTTTGGGGTT  
GAAGGGAGGGGAAGGCAGGCCAGAAGGGAATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTC  
TCCTGGCTCCACTCTTGCCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGGAAGATAAAGCTGGGTC  
TTCAGGAACCTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTGAGCATGTGTTCCCTTCTGCAGTGGTTCTTATC  
ACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGC  
TGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACTGGAAGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCA  
CTGGGGCATGGAGTGGCCATGCATACTCTGCTGCCGTCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTC  
CTCTCCCCAGTGTCCACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGA  
ACACCACAGCCCCTGTACTTGGGTGCTCTTGTCCCTGAACCTCGTTGTACCAGTGCATGGAGAGAAAATTTTG  
TCCTCTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAATTTGTTTTATTTCTCTCA

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**FIGURE 246**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

&lt;subunit 1 of 1, 183 aa, 1 stop

&lt;MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKICPPYRNISGHIYNQNVSQKDCNCLHVVEPMPVPGHDVEAYCLL  
CECRYEERSTTTIKVIIIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMAAAAASLGGPRA  
NTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 90-112

**N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50

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**FIGURE 247**

AATTGTATCTGTGTAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTTCAAAAAACAACAGA  
CTAGTACTCTAAAGAACTCTTTAAACAATTAAGTGTAGGATTGCAGTTATGATTGGATATTATTTAATTCTGT  
TTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGCTATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTTG  
AAAATGAATGCTTAGTGGATCTGTGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAG  
TTCCCCTCCCCTCCGATTGTTCTAAATTAAGTGTGCTGTGCTGTGAAAAAGGCATGTATTTAAATCTGTAT  
GATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTTTTTTCTTGGCACTAAT  
CAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTAGTAAATAGAAACCTGTGTTTATTCTCAG  
GTATTTTAGAAACAACAGCCATCATTTTATTTTATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGG  
GCTATCAAATATTACTTCATTCAATATAAATAACAATAGTAGAAGTTGTTACTTAGATATGCTTTCTAGTTGCA  
TTTTCTCAGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTATCTTCA  
GATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATATTAATAAACCAAGTTCATATCTACCC

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**FIGURE 248**

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLPSDCSK

Important features:

Signal peptide:

amino acids 1-29

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**FIGURE 249**

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCTCGGGTCCCCGA  
ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCGCGACCCAAGTGAGGGGCCCCGTGTTGGGGTCCCTCCC  
TCCCTTTGCATTCCCACCCCTCCGGGCTTTGCGTCTTCTGGGGACCCCTCGCCGGGAGATGGCCCGGTTGATG  
CGGAGCAAGGATTGCTCTGCTGCCTGCTCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT  
TCGCGGGGCCAACTCAACTCCATCAAGTCTCTCTGGGCGGGGAGACGCTGGTCAGGCCGCCAATCGATCTGCG  
GGCATGTACCAAGGACTGGCATTCCGGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCTACCCTTGTTAGCAGT  
GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTCGGAGA  
AAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT  
ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC  
TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAAGGGCATGAAGGA  
GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA  
CCAGTGCTCCATCAGGGGGAAGTCTGTACCAAAACGCAAGAAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT  
TGCGACTGTGCGAAGGGCCTGTCTTGCAAAGTATGGAAAGATGCCACCTACTCCTCAAAGCCAGACTCCATGTG  
TGTGAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCGAGCTGTGAAGTTGTGTATTTAATGCATTATG  
CATGGTGGAAAATAAGGTTGAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAA  
AAAGGGAGAAAGAAAACATGAAGTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG  
CAACTTGTCTATGTAAATAATGTACACATTTGTGGAAAATGCTATTATTAAGAGAACAAGCACAGTGGAAATT  
ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCTTCAGATTGCTGATTGC  
TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAAATACTCCTAGAATAACTTGTTA  
TACAATAGGTTCTAAAAATAAAATTTGCTAAACAAGAAATGAAAACATGGAGCATTGTTAATTTACAACAGAAAAT  
TACCTTTTGATTGTAACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT  
TTCCAAATAATTGCAAAATAATGGCCAGTTGTTTAGGAAGGCCTTTAGGAAGACAAATAAAATAACAAACAAACAG  
CCACAAATACTTTTTTTTCAAATTTTAGTTTTACCTGTAATTAATAAGAACTGATACAAGACAAAACAGTTCC  
TTCAGATTCTACGGAATGACAGTATATCTCTTTATCCTATGTGATTCTGCTCTGAATGCATTATATTTTCCA  
AACTATACCCATAAATTGTGACTAGTAAATACTTACACAGAGCAGAATTTTCACAGATGGCAAAAAAATTTAA  
GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTAATTTCTTAAAGATTGGCCATAACCTATATTTT  
GATAGAATTAGATTGGTAAATACATGTATTACATACACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG  
CACTGGAGTAAGCAAGAAAATTTGGGAAAACTTTTCTGTTTGTTCAGGTTTTGGCAACACATAGATCATATGTCTG  
AGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT  
CATAATATTTACTATGCAGATGAATTCAGTGTGAGGTCTGTGTCCGTACTATCCTCAAATTTATTTTATAG  
TGCTGAGATCCTCAAATAATCTCAATTTCAGGAGGTTTCACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG  
TTTTATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAACCTCTGCAGCATCTG  
CTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCGAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTGTA  
ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATTTCTTGAAACCACTTTACTACTTTTTTTAACTT  
AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAATAAAAGGTTATCTTATAGTCGTGACTTTAACTTTTG  
TAGACCACAATTCATTTTTAGTTTTCTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG  
AGATTGAGTTTGAGCCTGTATATCTATTAAAAATTTCAACTTCCACATATATTTACTAAGATGATTAAGACTTA  
CATTTTCTGCACAGGTCTGCAAAAACAAAATTATAAACTAGTCCATCCAAGAACCAAGTTTGTATAAACAGGT  
TGCTATAAGCTTGTGAAATGAAAATGGAACATTTCAATCAAACATTTCTATATAACAATTATTATATTTACAAT  
TTGGTTTCTGCAATATTTTTCTTATGTCCACCCTTTTAAAAATTATTTTGAAGTAATTTATTTACAGGAAATG  
TTAATGAGATGTATTTTCTTATAGAGATTTCTTACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGAC  
TTTGTAATTTAGGAAAAATGTATAATAAGATAAATCTATTAAATTTTTCTCCTCTAAAACTGAAAAA  
AAAAAAAAAAAAAAAAAAAA

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**FIGURE 250**

MAALMRSKDSSCILLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLAFGGSKKGKNLGQA  
YPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRCNGICIPVTESILTPHIPALDGTRHRDR  
NHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRSSDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGL  
EIFQRCDCAKGLSCKVWKDATYSSKARLHVCQKI

**Signal peptide:**  
amino acids 1-25

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**FIGURE 251**

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAAGTGTTGGGATTAC  
AGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATGATTTCTTCAAATTCATGGCAAATATTTCC  
CTTCCCTTTAACTTCTTATGTGAGAATGAGGAAGGATAGCTGCATTTATTTAGTCAGTTTTCATTGCATAGTAAT  
ATTTTCATGTAGTATTTTCTAAGTTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTG  
AAAATACTTGATGTTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCTTTT  
AAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACATCACCAGCTCCCAGAT  
TTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACCCCAAGTACACAGCAGAATAGTACAAGTCA  
CCCTACAACCTACTACTTCTTGGGACCTCAAGCCCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAA  
ATCTCAACCTGAGCCATCCCCAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGT  
TCCTCCTCCTGGTTTGGAGTCCTTTCCTTCCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCCCTCCAC  
TGTGAACAAGCTTTTGCAGCTTCCCAGCAGCAGCATTTGAAAATATCTCTGTGTCTGTCCACCAGCCACAGCCCAA  
ACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAGATCCCAGCTTCTGCAGTGGAAATGCCTGGTTC  
AGCAGATGTCACAGGATTAAATGTGCAGTTTGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTCTGAATTTGG  
ATCAGCTCCAAGCAGTGAAAATAGTAATCAGATTTCCCATCAGCTTGTATTGGAAGTCTTTAAGTGAGCCTTTGAA  
TACATCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTTCCGTCATTACCTCCTGCAGTCTGAC  
AAGCTCATCACTGAATTTCTGCTAGTCCAGTAGCAATGTCTTCCTCTTATGACCAGAGTTCTGTGCATAACAGGAT  
CCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCAGGAACCATCATGAATGGACATGGTGGTGGTCTGAAG  
TCAGCAGACACTAGACAGTAAGTATAGCAGCAAGCTACTCTGTGTCATGGCTGGTGCCAACCAAACAGAGGAAGAG  
GATAGCTCACGTGATGTGGAACACACAGTTGGTCAATGGCTCATTCGTTAAAGCAGCCCTTTTGCTTTTTTG  
TTTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGTGGTGGTCTCATA  
TTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCATTTTAAAGATGCTTGGGCCAGGCGGG  
GTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCCAAGGCAGGCAGATTGCCAAGCTCAGGAGTTTGAGACC  
ACCCTGGGCAACATGGTGAAACTCTGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCC  
TGTAATCCCAGCTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCCGT  
CTGAAAAGA

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**FIGURE 252**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQQNSTSHPTT  
TTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPPPGLESFPSQAKLRESTPGDSPSTVNK  
LLQLPSTTIENISVSVHQFPQPKHIKLAKRRIPPASKIPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAP  
SSENSNQIPISLYSKSLSEPLNTSLSMSTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQ  
SPVSSSESAPGTIMNGHGGGRSQQTLDISKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

**Signal peptide:**  
amino acids 1-24



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**FIGURE 253**

GGGCGCCCGCTACTCACTAGCTGAGGTGGCAGTGGTTCACCAACATGGAGCTCTCGCAGATGTCGGAGCTCAT  
GGGGCTGTCGGTGTTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGGTAGCGCGGGGTGGCTGCGCGCGGG  
GGAGGAGAGGAGCGGCCGGCCCGCCTGCCAAAAAGCAAATGGATTTCCACCTGACAAATCTTCGGGATCCAAGAA  
GCAGAAACAATATCAGCGGATTCGGAAGGAGAAGCCTCAACAACACAACCTTCACCCACCGCCTCCTGGCTGCAGC  
TCTGAAGAGCCACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAATACCTGGCTACCTGTGCAGA  
TGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCCTGCAGCGAGAGCACCGCAGCATGAGAGCCAACGTGGA  
GCTGGACCACGCCACCCCTGGTGCCTTCAGCCCTGACTGCAGAGCCTTCATCGTCTGGCTGGCCAACGGGGACAC  
CCTCCGTGTCTTCAAGATGACCAAGCGGGAGGATGGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCTTAA  
AAAGCACAAGGCGCCTGTCTCGACATTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACAC  
CACTGTCTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACCAGATGAACAACACACACGC  
TGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCACCCAGATGTGAAGGTTTGGGAAGTCTGCTT  
TGGAAAGAAGGGGAGTTCCAGGAGGTGGTGCAGCCTTCGAACAAAGGGCCACTCCGCGGCTGTGCACCTCGTT  
TGCTTTCTCCAACGACTCACGGAGGATGGCTTCTGTCTCCAAGGATGGTACATGGAACTGTGGGACACAGATGT  
GGAATACAAGAAGAAGCAGGACCCCTACTTGCTGAAGACAGGCCGCTTTGAAGAGGCGCGGGTGCCGCGCCGTG  
CCGCTTGCCCTCTCCCCAACGCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCATCTCTACAATACCCG  
GCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCCAACTTGCTCTTTGACATCACTGG  
CCGCTTTCTGGCCTCCTGTGGGGACCGGGCGGTGCGCTGTTTCACAACACTCCTGGCCACCGAGCCATGGTGGA  
GGAGATGCAGGGCCACCTGAAGCGGGCCTCCAACGAGAGCACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGC  
CCAAGAGACCCTGAAGAGCCTGGGTGCCCTGAAGAAGTGACTCTCTGGGAGGGCCCGGCCAGAGGATTGAGGAGGA  
GGGATCTGGCCTCCTCATGGCACTGCTGCCATCTTTCCCTCCAGGTGGAAGCCTTTCAGAAGGAGTCTCCTGGTT  
TTCTTACTGGTGGCCCTGCTTCTTCCCATTGAACTACTCTTGTCTACTTAGGTCTCTCTTCTTCTTGGCTGGCTGT  
GACTCCTCCCTGACTAGTGGCCAAGGTGCTTTTCTCCTCCCAGGCCAGTGGGTGGAATCTGTCCCCACCTGGC  
ACTGAGGAGAATGGTAGAGAGGAGAGGAGAGAGAGAGAATGTGATTTTTGGCCTTGTGGCAGCACATCCTCAC  
ACCCAAAGAAGTTTGTAATGTTCAGAACACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTTGCAAGGATG  
GGAGACTGGGATAGCTTCCATCACAGAAGTGTGTTCCATCAAAAAGACACTAAGGGATTTCCTTCTGGGCCTCA  
GTTCTATTTGTAAGATGGAGAATAATCCTCTCTGTGAACCTCTTGCAAAGATGATATGAGGCTAAGAGAATATCA  
AGTCCCCAGGTCTGGAAGAAAAGTAGAAAAGAGTAGTACTATTGTCCAATGTCATGAAAGTGGTAAAAGTGGGAA  
CCAGTGTGCTTTGAAACCAAATTAGAAACACATTCTTGGGAAGGCAAAGTTTCTGGGACTTGATCATACATTT  
TATATGGTTGGGACTTCTCTCTTCGGGAGATGATATCTTGTTAAGGAGACCTCTTTTCAGTTCATCAAGTTCAT  
CAGATATTTGAGTGCCCACTCTGTGCCAAATAAATATGAGCTGGGGATTAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 254**

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQKQYQIRKEKPQOH  
NETHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWS TKDFLQREHRSMRANVELDHATLVRFSPDCRA  
FIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKKHKAPVIDIGIANTGKFIMTASSD TT VLIWSLKGQVLSTI  
NTNQMNNTTHAAVSPCGRFVASC GFTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKD  
GTWKLWDTDVEYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVHGEC  
IANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGH LKRASNESTRQRLQQQLTQAQETL KSLGALKK

**Important features:****Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

**Beta-transducin family Trp-Asp repeat protein.**

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

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**FIGURE 255**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCGGGCCAGGTGCCCC  
GTCGCAGGTGCCCCTGCCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCCTTCCTCGGCGCTGCCAACCC  
GCCACCCAGCCC**ATG**GCGAACCCCGGGCTGGGGCTGCTTCTGGCGCTGGGCCTGCCGTTCTGCTGGCCCGCTGG  
GGCCGAGCCTGGGGGCAAATACAGACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCC  
AGCTCCGATGGCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTC  
CTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCAGT  
AGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCTGCCTG  
CCCATC**TAG**GTCCCCCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCT  
GGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGA  
GGATGGGGCTATTCACCTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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**FIGURE 256**

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIVVFSLLAALLAVG  
LALLVRKLRKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI



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**FIGURE 258**

MGLFRGFVLLVLCLLHQSNTSFIKLNNGGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTYLFEATEKRFFFKN  
VSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEYIHFTPDLLLGKKQNEYGPPG  
KLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQF  
FPDKVQTEKASIMFMQSIDSVVEFCNEKTHNQEAPSLQNIKCNRSTWEVISNSEDFKNTIPMVTPPPPPVFSL  
KISQRIVCLVLDDKSGSMGGKDRNLNRMNQAAKHFLQLTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGL  
PTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMS  
KITGGSHFYVSDEAQNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFLITWNS  
LPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKM  
NKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNMGVYSRYFTAYTENGRYS  
LKVRAHGGANTARLKLRPPLNRAAYIPGWVNGEIEANPPRPEIDEDTQTTLDFSRASGGAFVVSQVPSLPLP  
DQYPPSQITDLATVHEDKIILTWTAPGDNFDVGKVQRYIIRISASILDLRDSFDDALQVNTTDLSPKEANSKES  
FAFKPENISEENATHIFIAIKSIDKSNLTSKVSANIAQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTL  
VLSVIGSVVIVNFILSTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592, 628-632,  
811-815, 832-836, 837-841, 852-856, 896-900

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**FIGURE 259**

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGCGACATGGCCGTTGTCTCAGAGGACGACTTTCAGCACAGTTCAA  
ACTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGCACTGCTTGAGAAGCTGCTGGACCGCC  
CGCCCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCTGTGGCACATACATCATCTTTCAGCCTGGGCATTGGCA  
GTCTACTGCCATGGAACCTTCTTTATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAG  
CCACCGGGGAGGACCCTGAGGGCTCAGACATCCTGAACACTTTTGAGAGCTACCTTGCCGTTGCCCTCCACCGTGC  
CCTCCATGCTGTGCCTGGTGGCCAACCTCCTGCTTGTCAACAGGGTTGCAGTCCACATCCGTGTCTGGCCTCAC  
TGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAAGTGGACACTTCCTCCTGGACCCGTTGGTT  
TTTTTGCGGTCACCATTTGTCTGCATGGTGATCCTCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCA  
TGACCGGCTCCTTTCCTATGAGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCG  
TGGCCTCATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCCTGACGGCCACCA  
TCTTCCTCGTGCTCTGCATGGGACTTACCTGCTGCTGTCCAGGCTGGAGTATGCCAGGTACTACATGAGGCCTG  
TTCTTGCGGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCAGGACTCCCTCAGTGCCCTTCGGTGGCCTCCA  
GATTCAATTGATTCCACACACCCCCCTCTCCGCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCT  
ACGTCTTCTTCATCACCAGCCTCATCTACCCGCGCTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCT  
CACTGTGGACCACCAAGTTTTTTCATCCCCCTCACTACCTTCCTCCTGTACAACCTTGTGACCTATGTGGCCGGC  
AGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCCAGGGTTCGTGCTCCTCCGGACCTGCC  
TCATCCCCCTCTTCGTGCTCTGTAACACAGCCCCGCGTCCACCTGAAGACTGTGGTCTTCAGTCCGATGTGT  
ACCCCGCACTCCTCAGTCCCTGCTGGGGCTCAGCAACGGCTACCTCAGCACCTGGCCCTCCTCTACGGGCCTA  
AGATTGTGCCCAGGGAGCTGGCTGAGGCCACGGGAGTGGTGTATGTCCTTTATGTGTGCTTGGGCTTAACACTGG  
GCTCAGCCTGCTCTACCTCCTGGTGCACCTCATCTAGAAAGGGAGGACACAAGGACATTGGTGCTTCAGAGCCTT  
TGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCCTAAAGTTTCACTTGGGGACAGAGAG  
CAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCAGTGAGCCACGTCCATGCCCATTCGGTGCAAGGCAGATA  
TTCCAGTCATATTAACAGAACACTCCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACA  
GCTGATGGTTAACATTCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTGCCCCTAGAGTTATTACAAA  
GCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCCAGCTGACAGCGAGATGCAA  
GCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGAAGTCCCCTGGCATGGTCAGTCCCTCAGGC  
CCAAGACTCAAGTGTGCACAGACCCCTGTGTTCTGCGGGTGAACAACTGCCCCTAACCAGACTGGAAAACCCAG  
AAAGATGGGCCTTCCATGAATGCTTCATTCCAGAGGGACCAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTCT  
GGCCTGGGTTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTCTTTCA  
GTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGCGTATTCAAAAA

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**FIGURE 260**

MAVVS EDDFQ HSSNSTY GTTSSSLRADQEALLEKLLDRPPPG LQRPEDRFCGTYIIFFSLGIGSLLPW NFFITAK  
EYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFLLVNRVAVHIRVLASLTVILAIFMVIT  
ALVKVDTSSWTRGFFFAVTIVCMVILSGASTVFSSSIYGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSD  
VRNSALAFFLTATIFLVLCMGLYLLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRP  
ILKKTASLGFCVTYVFFITS LIYPAVCTNIESLNKGSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVPGPN  
SKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLALLYGPKIVPRELAEATG  
VVM SFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252, 305-330,  
448-472



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**FIGURE 261**

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAACCAACACACCTGTTTA  
AAGAACCTAAGCACCATTAAAGCCCACTGGAAATTTGTGTCTAGTGGTTGTGGGTGAATAAAGGAGGGCAGAAAT  
GGATGATTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTACGTGGCCGGAATCATTCCCTT  
GGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGAAGTGTGTTGGGTGCTGGCCTTCTCTGTGGAAGTGTCT  
GGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAAGATATTCTTGAGGGAAAACACCACCAAGCAAGTGA  
AACACATAATGTGATTGCATCAGACAAAGCAGCAGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCA  
CACACAGCTGCATGCCATATTGGTGTGTTCCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGG  
TAACCTCCCATGTGCATTCTACTGACGATCCAGAACGAGCAAGGTCTAGCAATTCACAAATCACCACCACGCTGGG  
TCTGGTTGTCCATGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTT  
AATTGTGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCTGG  
CTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGTCATTGGCAGCACCAGTTATGTCCATGGTGACATA  
CTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTAGAGGTGAACGCCACGGGAGTGGCCATGCTTTTCTCTGC  
CGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGGCGGAATAGGGCACAGCCACAAGCCCGA  
TGCCACGGGAGGGAGAGGCCCTCAGCCGCTGGAAGTGGCAGCCCTGGTTCTGGGTGCTCATCCCTCTCATCCT  
GTCAGTAGGACACCAGCATTAATGTTCAAGGTCCAGCCTTGGTCCAGGGCCGTTTGCCATCCAGTGAGAACAGC  
CGGCACGTGACAGCTACTCACTTCCTCAGTCTCTTGTCTCACCTTGCGCATCTCTACATGTATTCCCTAGAGTCCA  
GAGGGGAGGTGAGGTTAAACCTGAGTAATGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTA  
TAGACATCCCATTGTGTTATCTTTTAAAGGCCCTTGACATTTTGCCTTTAATATTTCTCTTAACCCATTCTC  
AGGGAAAGATGGAATTTAGTTTAAAGGAAAAGAGGAGAACTTCATACTACAATGAAATAGTGATTATGAAATAC  
AGTGTCTGTAAATTAAGCTATGTCTCTTCTTCTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTTAACA  
TGGTCCCAACCATGTAAGACTGGTGTCTTAGCATCTATGCCATGCGTTGATGGAAGGTGATAGCACCACCTCA  
CTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGCAAGACACATTGAAAGCTC  
TCTTTATACTCAAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATTTAAACAGCTCCTTTGGCACGTGCCT  
CTCTGAATCCAGCCTGCCATTCATCAAATGGAGCAGGAGAGGTGGGAGGAGCTTCTAAAGAGGTGACTGGTATT  
TTGTAGCATTCCTTGTCAAGTTCCTCTTGCAGAATACCTGTCTCCACATTCCTAGAGAGGAGCCAAAGTCTAGT  
AGTTTCAGTTCTAGGCTTTCCTTCAAGAACAGTCAGATCACAAAGTGTCTTTGGAATTAAGGGATATTAAATTT  
TAAGTGATTTTTGGATGGTTATTGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAAAATGTATGGTTGTCC  
TTTTTTTTTGTTTTTTTTTTTTTTAAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGG  
TCAGCTTTGGCGACACTGTGTCTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTGTCCT  
ATTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCGTCTTTCTTTGCTTTTCTTCTAATTTTCCCTC  
TAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATATTTGTGTGGGATGAATTCCTATCAGGACAA  
CCACTTCTCGAACTGTAATAATGAAGATAATAATATCTTTATTTCTTTATCCCCCTTCAAAGAAATTACCTTGTG  
TCAATGCCGCTTTGTTGAGCCCTTAAATATACCACCTCCTCATGTGTAATTGACACAATCACTAATCTGGTAAT  
TTAAACAATTGAGATAGCAAAAGTGTGTTAACAGACTAGGATAATTTTTTTTTTTCATATTTGCCAAAATTTTGTAA  
ACCTGTCTTGTCAAATAAGTGTATAATATTGTATTATTAATTTATTTTACTTTCTATACCATTTCAAACACA  
TTACACTAAGGGGGAACCAAGACTAGTTTCTCAGGGCAGTGGACGTAGTAGTTTGTAACAAACGTTTCTATGAC  
GCATAAGCTAGCATGCCTATGATTTATTTCTTCAATTTGTCACTGGATCAGCAGCTGTGGAAATAAAGCTT  
GTGAGCCCTCTGCTGGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATT  
GCATACAATTTTACTACCAAGAGAAGGTATAGTATGAAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT  
GACTGGTGTGAGACTTGAGGTTTCATCTAGTCTTCAAACTATATGTTGCCTAGATTCTCTCTGGAACTGAC  
TTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAA

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## **FIGURE 262**

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHALYEDILEGKHHQAS  
ETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQIGNSHVHSTDDPEAARSSNSKITTTL  
GLVVHAAADGVALGAAASTSQTSLVLFVAIMLHKAPAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMT  
YLGLSKSSKEALSEVNATGVAMLFSAAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLI  
LSVGHQH

**Signal peptide:**  
amino acids 1-18

**Transmembrane domain:**  
amino acids 37-56, 106-122, 211-230, 240-260, 288-304

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**FIGURE 263**

CTCCTTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCGG  
GCAGGGGTGACAAACAGGTGTCATCTTTTGTATCTCGTGTGTGGCTGCCTTCCTATTTCAAGGAAAGAC  
GCCAAGGTAATTTTGAACCCAGAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAAACCCC  
AGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGTGG  
TTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCAGTGCTCAGAAGTGACTTGCCTGAGGGTG  
GACCAGAAGAAAGGAAAGGTCCCCCTCTTGTCTTGGCTGCACATCAGGAAGGCTGTGATGGGAATGAA  
GGTGAACAACTTGGAGATTTCACTTCAGTCATTGCTTCTGCCCTGCAAGATCATCCTTTAAAGTAGAGA  
AGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGAGCAACTCGTTCTAGAAGGAAATGGATGCAAGCAGC  
TCCGGGGGGCCCCAACCGCATGCTTCCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTGGGGGGCCCCGGCT  
TTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTCTGAAATGATGATGGTTTCGCCGGGGGCTGCT  
TGCCTGGATTTCCCGGGTGGTGGTTTTGCTGGTGTCTCCTCTGCTGTGCTATCTCTGTCTGTACATGT  
TGGCCTGCACCCCAAAGGTGACGAGGAGCAGCTGGCAGTGGCCAGGGCCAACAGCCCCACGGGGAAAG  
GAGGGGTACCAGGCCGTTCTCAGGAGTGGGAGGAGCAGCACCAGCACTACGTGAGCAGCCTGAAGCG  
GCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGGAATGGGCAGTACCAAG  
CCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTCCTGGCC  
TTCCTGCACCTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGC  
AGTGCCTTTTCGATAGCTTTACTCTACAGAAGGTGTACACAGCTGGAGACTGGCCTTACCCGCCACCCG  
AGGAGAAGCCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGGGAAGCCATTGAATCAGCCTTGGAGACC  
CTGAACAATCCTGCAGAGAACAGCCCCAATCACCGTCTTACACGGCCTCTGATTTTCATAGAAGGGAT  
CTACCGAACAGAAAGGGACAAAGGGACATTGTATGAGCTCACCTTCAAAGGGGACCACAAACAGGAAT  
TCAAACGGCTCATCTTATTTTCGACCATTCAGCCCCATCATGAAAGTGAAAAATGAAAAGCTCAACATG  
GCCAACACGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGGACAAGTTCGGGCAGTTTCATGCA  
GAATTTTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGGAAAG  
AAGAAATAAATGAAGTCAAAGGAATACTTGAACAACTTCCAAAGCTGCCAAGCTTTCAGGAATTTACC  
TTCATCCAGCTGAATGGAGAATTTTCTCGGGGAAAGGGACTTGATGTTGGAGCCCGCTTCTGGAAGGG  
AAGCAACGTCCTTCTCTTTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTA  
GGCTGAATACACAGCCAGGGAAGAAGGATTTTATCCAGTTCTTTTCAGTCAGTACAATCCTGGCATA  
ATATACGGCCACCATGATGCAGTCCCTCCCTTGGAAACAGCAGCTGGTCATAAAGAAGGAAATGGAT  
TTGGAGAGACTTTGGATTTGGGATGACGTGTGAGTATCGGTGAGACTTCATCAATATAGGTGGGTTTG  
ATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTCCACAGCAACCTC  
ATAGTGGTACGGACGCCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTTACATGGACGAGCT  
GACCCCCGAGCAGTACAAGATGTGCATGCAGTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTGG  
GCATGCTGGTGTTCAGGCACGAGATAGAGGCTCACCTTCGCAAAACAGAAACAGAAAGACAAGTAGCAAA  
AAAACATGAACCTCCAGAGAAGGATTTGTGGGAGACACTTTTTCTTTCTTTTGAATTTACTGAAAGTG  
GCTGCAACAGAGAAAAGACTTCCATAAAGGACGACAAAGAATTTGGACTGATGGGTGAGAGATGAGAA  
AGCCTCCGATTTCTCTCTGTTGGGCTTTTTACAACAGAAATCAAATCTCCGCTTTGCCTGCAAAAGT  
AACCAGTTGCACCCCTGTGAAGTGTCTGACAAAGGCAGAAATGCTTGTGAGATTATAAGCCTAATGGTG  
TGGAGGTTTTGATGGTGGTTTACAATACACTGAGACCTGTTGTTTTGTGTGCTCATTGAAATATTTCATG  
ATTTAAGAGCAGTTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA  
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTA  
TTATGATACTAGTGAGTACATTAAGTAAAAATAAATGGACCAGAAAAGAAAAGAAACCATAAATATCG  
TGTCAATATTTTCCCAAGATTAACCAAAAAATAATCTGCTTATCTTTTTTGGTTGCTTTTTTAACTGTCT  
CCGTTTTTTTTCTTTTATTTAAAAATGCACCTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTA  
CCACTTTGCAAGCCTTACAAGAGAGCACAAGTTGGCCTACATTTTATATTTTTTAAAGAGATACTTT  
GAGATGCATTATGAGAACTTTCAGTTCAAAGCATCAAATTCATGCCATATCCAAGGACATGCCAAATG  
CTGATTCGTGTCAGGCATGAATGTGAGGCATTGAGACATAGGGAAGGAATGGTTGTACTAATACAGA  
CGTACAGATACTTTCTCTGAAGAGTATTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATG  
ACACTTCTGCTTTACAGAAAAGGAACTCATTCAGACTGGTGATATCGTGATGTACCTAAAAGTCAG  
AAACCACATTTTCTCCTCAGAAGTAGGGACCGCTTTCTTACCTGTTTAAATAAACCAAGATATACCGT  
GTGAACCAACAATCTCTTTTCAAACAGGGTGTCTCCTCCTGGCTTCTGGCTTCCATAAGAAGAAATG  
GAGAAAAATATATATATATATATATATTGTGAAAGATCAATCCATCTGCCAGAATCTAGTGGGATG  
GAAGTTTTTGTACATGTTATCCACCCAGGCCAGGTGGAAGTAACTGAATTTATTTTAAATTAAGC  
AGTTCTACTCAATCACCAGATGCTTCTGAAAATTCGATTTTATTACCATTTCAACTATTTTTTAA  
AATAAATACAGTTAACATAGAGTGGTTTCTTCATTTCATGTGAAAATTATTAGCCAGCACCAGATGCAT  
GAGCTAATTAATCTCTTTGAGTCCTTGCTTCTGTTTGTCTCACAGTAACTCATTTGTTTAAAGCTTCAA  
GAACATTCAGCTGTTGGTGTGTTAAAAAATGCATTGTATTGATTTGTACTGGTAGTTTATGAAATTT  
AATTAACAACAGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

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**FIGURE 264**

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWEEQHRNYVSSL  
KRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDS  
FTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYE  
LTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMAANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY  
FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTRCRLNT  
QPGKKVFYPVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLIDIKGWGGED  
VHLYRKYLHSNLIVVRTPVRLFLWHEKRCMDLTPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQ  
KTSSKKT

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**FIGURE 265**

GGATGCAGAAAGCCTCAGTGTGCTCTTCCTGGCCTGGGTCTGCTTCCTCTTCTACGCTGGCATTGCCCTCTTCA  
CCAGTGGCTTCCTGCTCACCCGTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC  
TGCCATGGGGGAGCCAAGGGAAACCTGGGGCCTGCTGGATGGCTTCCCGATTTTCGCGGGTTGTGTTGGTGCTGA  
TAGATGCTCTGCGATTTGACTTCGCCCAGCCCCAGCATTACACGTGCCTAGAGAGCCTCCTGTCTCCCTACCCT  
TCCTGGGCAAATAAGCTCCTTGACAGAGGATCCTGGAGATTAGCCCCACCATGCCCGGCTCTACCGATCTCAGG  
TTGACCCTCCTACCACCACCATGCAGCGCTCAAGGCCCTCACCCTGGCTCACTGCCTACCTTTATTGATGCTG  
GTAGTAACCTCGCCAGCCACGCCATAGTGGAAAGACAATCTCATTAAGCAGCTCACCAGTGAGGAAGGCGTGATG  
TCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGCTTTCTCCAAAGCTTTCTTCTCCCATCCTTCA  
ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCTACCCACCATGGACAGTGGTGAATGGG  
ACGTGCTGATTGCTCACTTCCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCCTGAAATGGCCA  
AGAACTTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG  
CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTCTTTC  
TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC  
CCACGCTGGCCCTGCTGCTGGGCCTGCCATCCCATTTGGGAATATCGGGGAAGTATGGCTGAGCTATTCTCAG  
GGGGTGAGGATCCCAGCCCCACTCCTGTCTTAGCCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT  
CCCCATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT  
TCTCCAAGGCCCTGCTGACTACAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCGACTGTGA  
TTGCTGAGCTGCAGCAGTTCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTCC  
GCATGGCGGGGGTACTGCTCTCTTGGCTGCTTCTGCTTTATCTGCCCTGCTGGCATCTCAGTGGGCAATATCCC  
CAGGCTTTCCATTCTGCCCTCTACTCCTGACACCTGTGGCCTGGGGCCTGCTTGGGGCCATAGCGTATGCTGGAC  
TCCTGGGAACATTAGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAGCTCATTCTCCCTT  
TTCTGTGGAAAGCCTGGGCTGGCTGGGGTCCAAGAGGCCCTGGCAACCCTGTTTCCCATCCCTGGGCCCCGTCC  
TGTTACTCCTGCTGTTTCGCTTGGCTGTGTTCTTCTCTGATAGTTTGTGTAGCTGAGGCCAGGGCCACCCCT  
TCCTTTTGGGCTCATTCATCCTGCTCCTGGTTGTCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC  
TCACAATGCCCCGCTTGGCACTTCAGCCACAACAACCCCCACGGCACAATGGTGATGCCCTGAGGCTTG  
GAATTGGGTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTTGGCCAT  
CCTCTCCCTGGCTGAGTCTCTGCGCATCCATGGTGGGTGGTGCAGCCAAGAATTTATGGTATGGAGCTTGTGTGG  
CGGCGCTGGTGGCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCCGCTATGGTAATCTCAAGAGCCCCGAGCCAC  
CCATGCTCTTTGTGCGCTGGGGACTGCCCCAATGGCATTGGGTACTGCTGCCTACTGGGCATTGGCGTCCGGGG  
CAGATGAGGCTCCCCCGCTCTCCGGTCTGGTCTCTGGGGCATCCATGGTGTGCTCGGCTGTAGCAGGGC  
TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGCGAGGCGCTCCAA  
GGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAA  
TCTACCGACACATGCAGGAGGAGTTCCGGGGCCGGTTAGAGAGGACCAATCTCAGGCTCCCTGACTGTGGCTG  
CTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTACAGCCCTCACCCTGTTGGCCTTCCCACTTCTGCTGT  
TGATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTTTCTGCAGAGCTTCTTCTCTACATCTGCTTGTCTG  
CTGGGATACCGTCAACACCCCTGGTCTTTTACTGTGCCATGGCAGGCAGTCTCGGCTTGGGCCCTCATGGCCA  
CACAGACCTTCTACTCCACAGGCCACCAGCCTGTCTTCCAGCCATCCATTGGCATGCAGCCTTCGTGGGATTCC  
CAGAGGTCATGGCTCCTGTACTTGGCTGCCTGCTTTGCTAGTGGGAGCCAACACCTTGCCTCCCACCTCCTCT  
TTGCAGTAGGTTGCCCACTGCTCCTGCTCTGGCCTTTCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC  
CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCCGGG  
ATGCGCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCCTCAAGTACCTCTTTATCCTTGGTATTAGATTCT  
TGGCCTGTGCTTGGCAGCCTCCATCCTTCGAGGCATCTCATGGTCTGGAAGTGTGTTGCCCTAAGTTTCATAT  
TTGAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGATGAGAGTGGATGGTG  
CTGTGAGCTCCTGGTTCAGGCAGCTATTTCTGGCCAGCAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCT  
ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC  
TCTTACTATCATGCAGCCAGGGGCGCTGACATCTAGGACTTCATTATTTCTATAATTAGGACCACAGTGGAGTA  
TGATCCCTAACTCCTGATTGGATGCATCTGAGGGACAAGGGGGCGGCTCCGAAGTGAATAAAATAGGCCGG  
GCGTGGTGACTTGCACCTATAATCCAGCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCAGGAGTTCA  
AGACCAGCCTGTGGAACATAACAAGACCCGCTCTACTATTTAAAAAAAGTGAATAAAATGATAATAT

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**FIGURE 266**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

&lt;subunit 1 of 1, 1089 aa, 1 stop

&lt;MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLEFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGKPGACWMASRFSRVVLVLI  
DALRFDFAPQHQSHVPREPPVSLPFLGKLSSLRILEIQPHHARLYRSQVDPPTTTMQRLKALTTGSLPTFIDAG  
SNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLFPGAFSKAFFPSENVRLDLDVDNGILEHLYPTMDSGEWD  
VLIAHFLGVDHCGHKHGPHHPPEMAKKLSQMDQVIQGLVERLENDTLLVVAGDHGMMTNGDHGGDSELEVSAALFL  
YSPTAVFPSTPPEEPEVIPQVSLVPTLALLLGLPIPGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQQVS  
RFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRGARAMCIESWARFSLVR  
MAGGTALLAASCFCILLASQWAI SPGFPPFCPLLLTPVAWGLVGAIAYAGLLGTIELKLDLVLLGAVAAVSSFLPF  
LWKAWAGWGSKRPLATLFPIPGPVLLLLLFLRLAVFFSDSFVVAEARATPFLGSEFILLVVLHWEGQLLPKLL  
TMPRLGTSATNPFRHNGAYALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVA  
ALVALLAAVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAWALASGADEAPPRLRVLVSGASMLPRAVAGL  
AASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQEEFRGRLETKSQGPLTVAA  
YQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFLLLHLLAAGIPVTTPGPFTVPWQAVSAWALMAT  
QTFYSTGHQPVFPAIHWHAFAVGFPEGHGSCTWLPALLVGANTFASHLLFAVGCPLLLLPFLCESQGLRKRQQP  
PGNEADARVRPEEEEEPLMEMRLRDAPQH FYAALLQLGLKYLFI LGIQLACALAASILRRHLMVWVKVFAPKFIF  
EAVGFIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850, 1016-1034,  
1052-1070**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271

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**FIGURE 267**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGATCCAGAAACCCATG  
ATACCCTACTGAACACCGAATCCCCTGGAAGCCACAGAGACAGAGACAGCAAGAGAAGCAGAGATAAATACACT  
CACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTCTCTCACTCCCTCCCTCCCTCTCTCTGCTGCTCTAGTCCT  
CTAGTCCTCAAATCCCAGTCCCCTGCACCCCTTCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTG  
ATTTGGATCCTGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCAGCC  
TCTTACCCTGAGTGTGGAAACAATGCCCAGTCGCCCATCGATATTCAGACAGACAGTGTGACATTTGACCCTGAT  
TTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCAGCCTTTGGACCTGCACAACAATGGCCACACA  
GTGCAACTCTCTCTGCCCTCTACCCTGTATCTGGGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTG  
CACTGGGGTCAGAAAGGATCCCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTGCAGAGCTCCAC  
ATTGTACATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCCTGGCTGTCTG  
GGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAGTCACTTGCATGAAGTCAGG  
CATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAGAGCTGCTCCCCAAACAGCTGGGGCAGTACTTC  
CGCTACAATGGCTCGCTCACAACCTCCCCCTTGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAG  
ATTTCAATGGAACAGCTGGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTTAAGCTTCTGGTA  
CAGAACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTTCATCCAAGCAGGATCCTCGTAT  
ACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGTTGGCTGTCTCTGCCTTCTCCTGGCTGTTTATTTT  
ATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAAAGAGTGTGGTCTTCACCTCAGCACAAGCCACGACT  
GAGGCATAAATTCCTTCTCAGATACCATGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAATG  
GGGTGTAGGATCTGGCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCTCCTTCCCCTGGACATCTCTTAGAGA  
GGAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTAGGAGGAAATGAG  
GAAATCGCTGTGTTGTTAATGCAGAGANCAAACCTCTGTTTAGTTGCAGGGGAAGTTTGGGATATACCCCAAAGTC  
CTCTACCCCTCACTTTTATGGCCCTTCCCTAGATATACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTT  
GAAGTTGTATATTTTGTATCAATATATTTGGAATTAAAGTTTCTGACTTT

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**FIGURE 268**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNASPIDIQTDSVTFDPLPALQPHGYDQPGTE
PLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQINSEATFAELHIVHYDSDSYDSLSEA
AERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSV
LWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVG
CLCLLLAVYFIARKIRKKRLLENRKSVVFTSAQATTEA
```

**Important features of the protein:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69



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**FIGURE 269**

GTGGCGCTGGCGGTTGCTGTCAGCTGATTCCCGGGGTTGGTGGCAGCGCGGTTAGCAGCAATGGACTTTCTCCTG  
GGGAACCCGTTTCAGCTCTCCAGTGGGACAGCGCATCGAGAAAGCCACAGATGGCTCCCTGCAGAGCGAGGACTGG  
GCCCTCAACATGGAGATCTGCGACATCATCAACGAGACGGAGGAAGGTCCCAAAGATGCCCTCCGAGCAGTAAAG  
AAGAGAATCGTGGGGAATAAGAACTTCCACGAGGTGATGCTGGCTCTCACAGTCTTAGAAACCTGTGTCAAGAAC  
TGCGGGCACCCTTCCACGTGCTGGTGGCCAGCCAGGACTTCGTGGAGAGTGTGCTGGTGAGGACCATCCTGCCC  
AAGAACAACCCACCCACCATCGTGCATGACAAAGTGTCAACCTCATCCAGTCCCTGGGCTGACGCGTTCCGCAGC  
TCGCCCCATCTGACAGGTGTGGTCACCATCTATGAGGACCTGCGGAGGAAAGGCCTGGAGTTCCCCATGACTGAC  
CTGGACATGCTGTCACCCATCCACACACCCAGAGGACCGTGTCAACTCAGAGACACAATCAGGACAGGATTCTG  
TGGGCACTGACTCCAGCCAGCAAGAGGACTCTGGCCAGCATGCTGCCCCCTCTGCCCGCCCCGCCATACTCTCCG  
GTGACACGCCCCATAGCACCAACCCCGGAACAGATTGGGAAGCTGCGCAGTGAGCTGGAGATGGTGAGTGGGAACG  
TGAGGGTGATGTCGGAGATGCTGACGGAGCTGGTGGCCACCCAGGCCGAGCCCGCAGACCTGGAGCTGCTGCAGG  
AGCTCAACCGCACGTGCCGAGCCATGCAGCAGCGGGTCTTGAGTGATACCCTGCTCCGGGGCCATGCCCCAAGGA  
GCCCTTCAGAGCCCACTGCCAGTCGAGGCCTGGCTGGAGGCTGGCCACAGTGGAAATTCGCGGAGCCTATTG  
TCCCTACCTGCTCTGCTGCATGGGGCCCCATGGCTTTGGCTGGCCACTGAGGGTAGGGTGTGGAGGTGTGGAGG  
CCCCCTGAGGAGCTGCGCGGGCCCCAGGTACGAAGCTGCAACTCTGCGCGCAGTGGGCGAGATCTCATCAGCCCCA  
GGCTGCAGGTGAGGCTTCAGGGGATGCTGGGGCCCCACTGCCCCCTCCGCTGCCTTGCCCTCCATCCTTCCTCTGT  
TCCTTCTGGCCGGGCACCACAGCACTGGGGCTCACCTCTTGTTGATCCTCTTGTAAGTGGGAGAGGTGCCTTTTG  
TATCCCCAATTAAAGGTAGAAAACC

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**FIGURE 270**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62813
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23465, pI: 7.57, NX(S/T): 1
MDFLLGNPFSSPVGQRIEKATDGSLSQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNKNFHEVMLALTVLE
TCVKNCGHRFHVLVASQDFVESVLVRTILPKNNPPTIVHDKVLNLIQSWADAFRSSPDLTGVVTIYEDLRKGLE
FPMTDLDMLSPIHTPRGPCSTQRHNQDRILWALTPASKRTLASMLPLCPPRPYSPVTRP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-15

**N-glycosylation site:**

Amino acids 41-45

**N-myristoylation sites:**

Amino acids 6-12;23-29

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**FIGURE 271**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCGTCTGCC**AT**GGGGC  
TCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCTGATGCTGCCCCGTGAAGCCCCCGCAG  
GCTCCTGGGGGGCCCCAGATCATCGGGGGGCCACGAGGTGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCT  
TCGGGGGCCAACATCACTGCGGAGGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCC  
ACAGAGACCTCCGCACTGGCCTGGTGGTGTGGGCGCCACGTCCTGAGTACTGCGGAGCCCCACCCAGCAGGTGT  
TTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGACATCTGCCTGCTGCGGC  
TGAACGGCTCTGCTGTCTTGGGCCCTGCAGTGGGGCTGCTGAGGCTGCCAGGGAGAAGGGCCAGGCCCCCACAG  
CGGGGACACGGTGCCGGGTGGCTGGCTGGGGCTTCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGG  
CCAAGGTCCGAGTGCTGGACCCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCA  
CCCGCAGTGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCCCTGGTGTGCAGGAACCGGG  
CTCACGGCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGACGTGTACACGCAGGTGTCCG  
CCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCCCCAGCCCGGGCCCCCTGCCTGGGACCACCAGGC  
CCCCAGGAGAAGCCGCC**TGA**GCCACAACCTTGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCG  
TGGCTGGGGCCACGGGAAGCCTGATGTTTCAGGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACA  
TGCAAAGGGCAGAAGCAAACCCAGTAAATGTAACTGACAAAAAAAAAAAAAAAAAAGAAA

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**FIGURE 272**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGFLLRARWVVSAAHC
FSHRDLRTGLVVLGAHVLSTAEPTQQVFGIDALTTHPDYHPMTHANDICLLRLNGSAVLGPAVGLLRPLPGRRARF
PTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPDVCNSSWKGHLLTMLCTRSGDSHRRGFCSADSGGPLVCR
NRAHGLVSFSGLWCGDPKTPDVYTQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

**Signal peptide:**  
amino acids 1-30

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**FIGURE 273**

GAAGTTCGCGAGCGCTGGCTATGGGTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTGGCGCTCGGGACAG  
GAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGACCAGCGTGGCGCGCGCCCTGGCGCCCG  
AGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGCGCGGGGAGGAGCGCGGCTGCGGGACCTGACTAGATTCT  
ACGACAAGGTACTTTCTTTGCATGAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCAATTTACTCTCATCA  
AACGCCTGCAGTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGGATG  
GCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGGGCCCTGATGCGGCTGC  
AGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCGAGGTGTCTTTCAGAGAGTCACTGGCTCTGCCATCACTG  
ACCTGTACAGCCCCAAACGGCTCTTTTCTCTCACAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACA  
TGGGGGATTATTACCATGCCATTCCATGGCTGGAGGAGGCTGTCACTCTTCCGAGGATCTTACGGAGAGTGGA  
AGACAGAGGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAAATGTTT  
CGTGTGCCCTCAGCCTCTCTCGGGAGTTCTTCTCTACAGCCCAGATAATAAGAGGATGGCCAGGAATGTCTTGA  
AATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTTAGCTGAGGCTGTCTCCAGAGGCCCAATATACCCC  
ACCTGCAGACCAGAGACACCTACGAGGGGCTATGTACAGCCCTGGGTTCAGAGCCCACTCTCTACAGATCCCTA  
GCCTCTACTGTTCTATGAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCTCCACC  
TGGAGCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAACTTGCAGAAC  
CATGGCTACAGAGGTCACTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAGTACCGCATCAGCAAAGTGCCT  
GGCTGAAGGACACTGTTGACCCAAACTGGTGACCCTCAACCACCGCATTGCTGCCCTCACAGGCCTTGATGTCC  
GGCCTCCCTATGCAGAGTATCTGCAGGTGGTGAAGTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATG  
CTACGTCAACCAAGCAGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCT  
CGGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGAATGCAGCACTGT  
TTTGGTGAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCATGCTGGCTGTCTGTCTGCTGGTGGGAG  
ATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGGACAGGAATTCCGCAGACCCTGCAGCTCCAGCCCTGAAG  
ACTGAAGTGTGGCAGAGAGAAGCTGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTA  
GGAGAGGAGAAAAGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCACTTTGTCTGTGCTCGCAAATCAGAGGCAA  
GGGAGAGGTTGTTACCAAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAAGTCAGAGTAGGATGC  
ACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGGAGTTCACTACTCTCTGTGGGAACAGG  
ACATCTCAACAGTCTCAGGTTTCGATCAGTGGGTCTTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGG  
CAATGAGGACACCTGCAGGAGGGGCTAGCCTGACTCCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGC  
AGCCCAAGCAGGGAGTGTCCCCCTCCCAGAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTTTTTTAA  
GTTGAAAACAACCTTCTTTTCTTTTGTATGATGGTTTTTAAACACAGTCATTAAAAATGTTTATAAATCAAAA

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**FIGURE 274**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64849
><subunit 1 of 1, 544 aa, 1 stop
><MW: 61126, pI: 6.40, NX(S/T): 2
MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLLRRYLRGEEA
RLRDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGY
EKVEQDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVGTSAITDLYSPKRLFSLT
GDDCFQVGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRA
GNVSCALSLSREFLLYSPDNKRMAENVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDT
YEGLCQTLGSQLPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEA
QKIRELAEPWLQRSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRP
PYAEYLQVVNYGIGGHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIY
ANLSVPVVRNAALFWWNLHRSGEGSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSS
SPED
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-19

**Leucine zipper pattern:**

Amino acids 34-56;41-63

**Ribonucleotide reductase small subunit signature:**

Amino acids 340-356

**N-glycosylation sites:**

Amino acids 242-246;482-486

**Cell attachment sequence:**

Amino acids 27-30

**Tyrosine kinase phosphorylation site:**

Amino acids 189-198

**N-myristoylation sites:**Amino acids 4-10;135-141;153-159;164-170;241-247;303-309;309-315;  
457-463;473-479

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**FIGURE 275**

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCATCCTGGTGATCACC  
TTACTCCTGGACCAGACCAGCCACACATCCAGATTAAAAGCCAGGAAGCACAGCAAACGTCGAGTGAGAGAC  
AAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTCTGGACAGAAGTCAATGCCTTGAAGGAAATTCAGGCCCTG  
CAGACAGTCTGTCTCCGAGGCACTAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCAT  
GAGGCCAATGAAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCCCTC  
CAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGACATGGTCACGGAAGGC  
AAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGGACCGTGCACAGCCTAACGGTGGCAAGCGA  
GAAAACGTGTCTCTGTTCTCCCAATCAGCTCAGGGCAAGTGGAGTGATGAGGCCTGTCGCAGCAGCAAGAGATAC  
ATATGCGAGTTCACCATCCCTAAATAGGTCTTTCTCCAATGTGTCTCCTCCAAGCAAGATTTCATCATAACTTATAGG  
TTCATGATCTCTAAGATCAAGTAAAAATCATAATTTTTACTTTATTAATAAATTTGCAACACAAGATCAATGTCCAT  
AGCAATATGATAGCATCAGCCAATTTTGTAAACACATTTCTTTGGGATTTTGCCCTTCTGGGGTATAGGGGATC  
AGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCTAAACAGACTAAAATCTTTCTCTAGTCTTTT  
TCACTTGTAACAACCCAGTTTGTTTTCAAAAAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTT  
AGGCTACCTGAAAGATTTTCCCTTGGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCT  
AGGTGCTATATAATCCAAAACTTTTCAAGCCTGTGTCTCATTCTGTCCCATGCTGGCAATAATACCTTGTGAGCC  
CATTACCCTTATTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCTGCCATATCAGAACACAAACCCC  
TGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCCTACCCTTTTTTTTGGGAAGTTTCCAGCCGCAATTTGA  
AATGAAATGACAAGGTGTATATTGATCAATTTTCACTCCACCATTGCATTACAACCTCTAACTTAAATGGGTA  
ACCTAAGGCATATCAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTT  
TAGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTACATTTTCGTATATTTAT  
TTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTTGGGAAGCTGAAAACCTGAATTTAAAG  
AATGCTATCTTGAAAAATTGCATACGTCTGTGCAATTTTTTATTCTGCCTAGTGCTATTCTGCTTGTGTTAACTAG  
ATTGTACAAAATAACTTCATTGCTTAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTAGAAG  
CAAACAATTTTAAATATATTTTGTCTTCAAATAAATAGTGTGTTTAAACATTGAATGTGTTTTGTGAACAATATCC  
CACTTTGCAAACTTTAACTACACATGCTTGGAAATTAAGTTTTAGCTGTGTTTCATTGCTCAATAATAAGCCTGAA  
TTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 276**

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWTEVNALKEIQALQT  
VCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQDYGKRSLPGVNDFWLGINDMVTEGKF  
VDVNGIAISFLNWDRAQFNGGKRENCVLSQSAQGWSEACRSSKRYICEFTIPK



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**FIGURE 277**

GAGATAGGGAGTCTGGGTTTAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAGGAAGCCACCAGAC  
TCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCCACGAGCGCTGGCTGAGGGACCGAGCC  
GGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAGCGCCAGGATGCCGCGCGGGGACTCGGAGCAGGTGCGCT  
ACTGCGCGCGCTTCTCCTACCTCTGGCTCAAGTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGG  
CCCTGGTCTCTGTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCTTGAAAGTGCCTTCCTGG  
CTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTATGTTTCATGGTCTCCTTCATTGGTGTGCTGGCGTCCCTCC  
GTGACAACTGTACCTTCTCCAAGCATTATGTACATCCTTGGGATCTGCCTCATCATGGAGCTCATTGGTGGCG  
TGGTGGCCTTGACCTTCCGGAACCAGACCATTGACTTCCTGAACGACAACATTGGAAGAGGAATTGAGAATACT  
ATGATGATCTGGACTTCAAAAACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGTGTGGCGGGGAGGACTACC  
GAGATTGGAGCAAGAATCAGTACCACGACTGCAGTGCCCCCTGGACCCCTGGCCTGTGGGGTGCCCTACACCTGCT  
GCATCAGGAACACGACAGAAAGTTGTCAACACCATGTGTGGCTACAAAACATATCGACAAGGAGCGTTTCAGTGTGC  
AGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCATCTGGTTTCATGGACAACACACCATCATGGCGT  
GCATCCTCCTGGGCATCCTGCTTCCCCAGTTTCTGGGGGTGCTGCTGACGCTGCTGTACATCAGCCGGGTGGAGG  
ACATCATCATGGAGCACTCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCAGCGTGGAGGCGGCAGGCA  
CGGGATGCTGCTTGTGCTACCCCAATTAGGGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTCTGGGATAGC  
ACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCCACACTCAGTACTGACCAAAGCCAGG  
GCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTCCCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGC  
TTTCCCCGAGGCAGCTCTGGAATCTGTGCCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTCTCCAGGCCTGGG  
CTACAGGGGAGGGAGAGCCTGAGGCTCTGCTCAGGGCCCATTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCA  
AGGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGGGCATCTGGGGAA  
GGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGCCTCTTCTCAGCCTCCCAGGTGCCTT  
GAGCCCTCTTGCAAGGGCGGCTGCTTCCTTGAGCCTAGTTTTTTTTTACGTGATTTTTGTAACATTCTTTTTTT  
GTACAGATAACAGGAGTTTCTGACTAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCAAC  
CAGTTTGTTAATCAAACAATAAAAACATGTTTTGTTTTGTTTTTAAAAA

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**FIGURE 278**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAPAIILILLGVVMFM
VSFIGVLASLRDONLYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFLNDNIRRG IENYYDDLDFKNIMDFVQK
KFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPTCCIRNTTEVVNTMCGYKTIDKERFSVQDVIIYVRGCTNAVII
WFMDNYTIMACILLGILLPQFLGVLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN
```

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

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**FIGURE 279**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACACCTGGGAAGAT  
GGCCGGCCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATCCAAGCCACCCTCAGTCCCAC  
TGCAGTTCTCATCCTCGGCCCAAAGTCATCAAAGAAAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAG  
CATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCT  
GGTGAACACCGTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGTGCAGGTGAAGCC  
CTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCCTGGTCAA  
GACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGCCCCAC  
CCGCTGGTCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTGTGTATAAGCTCTCCTTCCT  
GGTGAACGCCTTAGCTAAGCAGGTGATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTG  
TCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTCCTCAG  
CATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAA  
GTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGA  
CAACATCCCGTTCAGCCTCATCGTGAGTCAGGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA  
ATTCATGGTCCTGTTGGACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGA  
AAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTTTTTTATAGA  
CCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCAGTGAAGCCCTCCGCCCTTTGTT  
CACCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAA  
CATCAGCTCTGATCGGATCCAGCTGATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCAT  
CACTGAGATCATCCACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTATTGGT  
GAAGGCCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCCTTGTG  
GAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGGGTCCCAGCTGGGAGT  
ATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTGCCTGTGAAAA

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**FIGURE 280**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881  
><subunit 1 of 1, 484 aa, 1 stop  
><MW: 52468, pI: 7.14, NX(S/T): 3  
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDNATSILQQLPLLSAMREKPAGGIPVLGS  
LVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVEFHMTTEAQATIRMDTSASGP  
TRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISL  
SIDRLEFDLLYPAIKGTIQLYLGAKLLDSQGVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAAVLSPE  
EFMVLLDSVLPESAHLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPL  
FTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSL  
VKALGFEEAESSLTkdALVLTpasLWKpSSpVSQ

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

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**FIGURE 281**

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTCCCCGCGTTCT  
CTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCTGCCCACCGCTGCTTCCTGGC  
CCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTC  
CTTTTCGTCTCCCTTCCTCCGACTCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAGGATGGTTCCCGAGGT  
GAGGGTCCTCTCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCGAGA  
CATGTTCTGCCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCT  
GATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTCCA  
CTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCG  
GGCCCCACCAAAGTCCTGCCAGCACAAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTT  
CCCCTCCCGCTGCCCAACCAAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAACTG  
CCCCGAACCAGGCTGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGA  
GCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGC  
TGGGAGAAAGAGAGGCCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT  
CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGG  
CGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCTTGCCCTGCATCCTATG  
CACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTACCCCGAGAA  
AGTGGCTGGGAAGTGCTGCAAGATTTGCCAGAGGACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAG  
GTGTCCCAAGGCACCGGGCCGGGTCTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGC  
CCTGGAACACGAGGCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCA  
GAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGC  
AAGACTTCAGAAAGAGGCACAGCACTTCGACTGCTCGCTGGCCCCACGAAGGTCACTGGAACGTCTTCCTAG  
CCCAGACCCTGGAGCTGAAGGTCACGCCCAGTCCAGACAAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCA  
GATATGAGCTGTATAATTGTTGTTATTATATATTAATAAATAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAA  
AAAAAA

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**FIGURE 282**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSEGAHVSCYRLH
CPPVHCPQPVTTEPQQCCPKVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELFP SRLPNQCVLCSTEGQIYC
GLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVRHPQDPCSSDAGRKRGP GTFAPTGLSAPLSF
IPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPC
RHPEKVAGKCKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIY LWKLVKDE
ETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPGAEGHGQSRQSDQDITKT
```

**Signal peptide:**  
amino acids 1-25

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**FIGURE 283**

GCGATGGTGC GCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCAACGAGGAGAAGAT  
GACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGCCATGAGGAGCCTGCCGAGCCTGGGCG  
GCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCGCCGTCGCTCAGCCGCCTCGGCGGGGAATGTCACCGGTG  
GCGGCGGGGCGCGGGGCGAGGTGGACGCGTCGCGGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCTTA  
GGGCGACGGCTCCACAGGCCAGGCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTGCGA  
CTTCTCCAGCCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTCCACACCCCTTCAGGCGC  
CGCTCGGCCCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACTTCGACCACCTCTCAGGCGCCGACCAGACCCG  
CGCCGACCACCCCTTCGACGACCACCTGGCCCGGCGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGA  
CTCCCCGACCCCGACCCCGATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGG  
CCCCCTCTTCGCTCTCCAGAGTATGTATGTAAGTCTGTGGTTGGAAGCCTGAATGTGAATCGCTGCAACC  
AGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACCTGCAAAGAGGGCTTTTACC  
TAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCCACATGGAGCTCTCAGCATACCGTGCAACAGGT  
AAGCAACAGAGGTTGAACTGAAGTTTATTTATTTTAGCAAGGGAAAAAAAGGCTGCTACTCTCAAGGACCA  
TACTGGTTTTAAACAAAGGAGGATGAGGGTCATAGATTTACAAAATATTTATATACTTTTATTCTTACTTTAT  
ATGTTATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAGCACTAGAGTCGCCAA  
TTTTTCTCTGGGATAATTTCTGTAAATTTTATGGGAAAAAATTATTGAAGAATAAATCTGCTTTCTGGAAGGGCT  
TTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTTATGTTTATTAATATACCATTGGAGTTTGAGGAAAT  
TTGTTGTTTGGTTTATTTTCTCTCTAATCAAAATTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGG  
GGTACCCTAATTTATTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTTGAGACCAAAA  
GTAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGAATAATGTACTGT  
TATCTAAGCATTTGCCCTGTACTGCACTGAAAGTAATTATTCTTTGACCTTATGTGAGGCACTTGGCTTTTTGTG  
GACCCCAAGTCAAAAACTGAAGAGACAGTATTAATAATGAAAAAATAATGACAGGTTATACTCAGTGTAACC  
TGGGTATAACCCAAGATCTGCTGCCACTTACGAGCTGTGTTCCCTTGGGCAAGTAATTTCTTTCACTGAGCTTGT  
TTCTTCTCAAGGTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACCTCAATAAATT  
CTGGTTTGTTTTAAATTTCAAAGGAATATTATGACTGAAATGAGAGAACATGTTTTAAGAACTTTTAGCTCCTTG  
ACAAAGAAGTGCTTTATACTTTAGCACTAAATATTTAAATGCTTTATAAATGATATTATACTGTTATGGAATAT  
TGTATCATATTGTAGTTTATTAATAATGTAGAAGAGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTT  
GGGAGGCCAAGCGGGTGGATCACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCT  
CTACTAAAAATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGC  
AGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGTGAG  
AGAGGGGAGACTCTGTCTTAAAAA

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**FIGURE 284**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSPLGGLALLCCAAAAA VASAASAGNVTGGGGAAGQVDASPGPGLRGEPSHPFPRATAPTAQAPRTGPPRA
TVHRPLAATSPAQSPETTP LWATAGPSSTTFQAPLGPSPTTPPAAERTSTTSQAPTRPAPTTLSTTTGPAPTPV
ATTVPAPTTTPRTPTDLPSSSNSSVLPTPPATEAPSSPPPEYVCNCSVVGSLNVNRCNQT TGQCECRPGYQGLHC
ETCKEGFYLN YTSGLCQPCDCSPHGALSIPCNR
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.



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**FIGURE 285**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCCGCTGCTCTGGGGG  
AGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCCGTGACGGTGACGGAAGGCCTGTGT  
GTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATTACCTGGCCCAGTAGTTCATGGCTACTGG  
TTCCGGGAAGGGGCCAATACAGACCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAG  
ACTCGGGACCGATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGAAGA  
AGTGATGCGGGGAGATACTTCTTTTGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCT  
GTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCAGGCACCCTGGAGTCCGGCTGCCCCAGAAT  
CTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCC  
CCCCGACCCCTCCACCACCCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACACAGCCTC  
ACCTGTCAGGTGACCTTCCCTGGGGCCAGCGTGACCAGAACAGACCGTCCATCTCAACGTGTCTTACCCGCCT  
CAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCA  
CTCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGC  
CTGAGCTGGAGAGGCCTGACCCTGTGCCCCCTCAGGCCCTCAAACCCGGGGGTGCTGGAGCTGCCCTTGGGTGCAC  
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCC  
CTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGTGGTTCGGGGGAGCTGGAGCCACAGCCCTGGTCTTCTTG  
TCCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAGGCCAGCAGCGGCGTGGGAGAT  
ACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTCAGCCTCTCAGGGGCCCCTGACTGAACCTTGGGCAGAAGAC  
AGTCCCCAGACAGCCTCCCCAGCTTCTGCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTC  
AGCTTCCAGATGGTGAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATC  
CACAGATGAGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGAGAAGTCAGAGGC  
TGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATGTGCAGAGTGAAGAGC  
ACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCCTCCCTTTTATTTTAACTAAAAG  
ACAGACAAATTCCTA

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**FIGURE 286**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWFREGANTDQDAPVA  
TNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNYKHHRLSVNVTALTHRPNILI  
PGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVSPLDPSTTRSSVLTLPQPQDHGTSLTCQVTFPGASVTTN  
KTVHLNVSYPQNLMTVFQGDGTVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPS  
NPGVLELPWVHLRDAAEFTCRAQNPLGSQQVYLNVSLSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSRCK  
KSARPAAGVGDTGIEDANAVRGASQGPLTEPWAEDSPDPPPASARSSVGEDELQYASLSFQMKPWDSRGQE  
ATDTEYSEIKIHR

**Signal peptide:**  
amino acids 1-15

**Transmembrane domain:**  
amino acids 351-370

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**FIGURE 287**

CGCGAGCTGAGAGGAGCAGGTAGAGGGGCAGAGCGGGACTGTCTGCTGCTGGGGGAGCCGCCAGGAGGCTCCTCAG  
GCCGACCCAGACCCCTGGCTGGCCAGGATGAAGTATCTCCGGCACCCGGCGGCCCAATGCCACCCCTCATTCTGGCC  
ATCGGCGCTTTTACCCCTCCTCCTCTTCAGTCTGCTAGTGTACACACCCACCTGCAAGGTCCAGGAGCAGCCACCG  
GCGATCCCCGAGGCCCTGGCCTGGCCCCACTCCACCCACCCGCCAGCCCCGGCCCCGTGCCATGCCAACACCTCT  
ATGGTCAACCCACCCGGACTTCGCCACGCAGCCGCAGCAGTTCAGAACTTCCTCCTGTACAGACACTGCCGCCAC  
TTTCCCCTGCTGCGAGACGTGCCCCCTCTAAGTGCAGCGCAGCCGGTCTTCCTGCTGCTGGTGATCAAGTCCTCC  
CCTAGCAACTATGTGCGCCGCGAGCTGCTGCGGCGCACGTGGGGCCGCGAGCGCAAGGTACGGGGTTTGCAGCTG  
CGCCTCCTCTTCTGGTGGGCACAGCCTCCAACCCGCACGAGGCCCGCAAGGTCAACGGGCTGCTGGAGCTGGAG  
GCACAGACTCACGGAGACATCCTGCAGTGGGACTTCCACGACTCCTTCTTCAACCTCACGCTCAAGCAGGTCCCTG  
TTCTTACAGTGGCAGGAGACAAGGTGCGCCAACGCCAGCTTCGTGCTCAACGGGGATGATGACGTCTTTGCACAC  
ACAGACAACATGGTCTTCTACCTGCAGGACCATGACCCTGGCCGCCACCTCTTCGTGGGGCAACTGATCCAAAAC  
GTGGGCCCCATCCGGGCTTTTTGGAGCAAGTACTATGTGCCAGAGGTGGTGACTCAGAATGAGCGGTACCCACCC  
TATTGTGGGGTGGTGGCTTCTTGCTGTCCCGCTTCACGGCCGCTGCCCTGCGCCGTGCTGCCCATGTCTTGGAC  
ATCTTCCCCATTGATGATGTCTTCTGGGTATGTGTCTGGAGCTTGAGGGACTGAAGCCTGCCTCCCACAGCGGC  
ATCCGCACGTCTGGCGTGCAGGCTCCATCGCAACACCTGTCTCCTTTGACCCCTGCTTCTACCGAGACCTGCTG  
CTGGTGCACCGCTTCCTACCTTATGAGATGCTGCTCATGTGGGATGCGCTGAACAGCCCAACCTCACCTGCGGC  
AATCAGACACAGATCTACTGAGTCAGCATCAGGGTCCCCAGCCTCTGGGCTCCTGTTTCCATAGGAAGGGCGAC  
ACCTTCTCTCCAGGAAGCTGAGACCTTTTGGTCTGAGCATAAGGGAGTGCCAGGGAAGGTTTGAGGTTTGATGA  
GTGAATATTCTGGCTGGCGAACTCCTACACATCCTTCAAAACCCACCTGGTACTGTTCCAGCATCTTCCCTGGAT  
GGCTGGAGGAACCTCAGAAAATATCCATCTTCTTTTGTGGCTGCTAATGGCAGAAGTGCTGTGCTAGAGTTCC  
AACTGTGGATGCATCCGTCCCGTTTGAGTCAAAGTCTTACTTCCCTGCTCTCACCTACTCACAGACGGGATGCTA  
AGCAGTGCACCTGCAGTGGTTTAAATGGCAGATAAGCTCCGTCTGCAGTTCAGGCCAGCCAGAACTCCTGTGTC  
CACATAGAGCTGACGTGAGAAATATCTTTAGCCCAGGAGAGAGGGTCTGATCTTAACCCCTTCTCCTGGGTCTC  
AGACAACTCAGAAGGTTGGGGGGATACCAGAGAGGTGGTGAATAGGACCGCCCCCTCCTTACTTGTGGGATCAA  
ATGCTGTAATGGTGGAGGTGTGGGCAGAGGAGGGAGGCAAGTGTCTTTGAAAGTTGTGAGAGCTCAGAGTTTCTG  
GGGTCTCATTAGGAGCCCCCATCCCTGTGTTCCCAAGAATTACAGAGAACAGCACTGGGGCTGGAATGATCTTT  
AATGGGCCCCAAGGCCAACAGGCATATGCCTCACTACTGCCTGGAGAAGGGAGAGATTACAGTCTCCAGCAGCCT  
CCCTCACCCAGTATGTTTTACAGATTACGGGGGGACCGGGTGAGCCAGTGACCCCTGCAGCCCCAGCTTCAGG  
CCTCAGTGTCTGCCAGTCAAGCTTCACAGGCATTGTGATGGGGCAGCCTTGGGGAATATAAAATTTTGTGAAGAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 288**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65413

&lt;subunit 1 of 1, 372 aa, 1 stop

&lt;MW: 42515, pI: 8.92, NX(S/T): 6

MKYLRRHRPNATLILAIGAFTLLLFSLVSPPTCKVQEQQPAIPEALAWPTPPTRPAPAPCHANTSMVTHPDFAT  
QPQHVQNFLLYRHCRRHFLLQDVPPSKCAQPVFLLLVIKSSPSNYVRRELLRRTWGRERKVRGLQLRLLFLVGTA  
SNPHEARKVNRLLLELEAQTHGDILQWDFHDSFFNLTLKQVLFLOWQETRCANASFVLNGDDDDVFAHTDNMVFYLO  
DHDPGRHLFVGQLIQNVGPIRAFWSKYYVPEVVTQNERYPYCGGGGFLLSRFTAAALRRAAHVLDIFPIDDVFL  
GMCLELEGLKPASHSGIRTSGVRAPSQHLSSFDPFCFYRDLVLVHRFLPYEMLLMWDALNQPNLTCGNQTQIY

**Important features:****Type II transmembrane domain:**

Amino acids 15-34

**N-glycosylation sites:**

Amino acids 10-14;64-68;184-188;202-206;362-366;367-371

**TonB-dependent receptor proteins signature 1:**

Amino acids 1-32

**N-myristoylation sites:**

Amino acids 308-314;316-322

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**FIGURE 289A**

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGCGAGAGGCAGCCTCCTCCAGGAGCGGGGCCCT  
GCACACCATGCCCCCGGGTGGGCAGGGGTGGCGCGCGCCGTGCGCGCCCCGCTGGCGCTGGCCTTGGCGCTGGC  
GAGCGTCTGAGTGGGCTCCAGCCGTGCGCTGCCCCACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCA  
CGGGCTGGGCCTCCGCGCGGTTCTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATAT  
CACCAGGATCACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCATCTGGAAGACAACCAGGTGAG  
CGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACAAGAATAAGCTGCAAGT  
CCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTAGATTTGAGTGAAAACCAGATCCAGGGGAT  
CCCAGGAAGGCGTTCCGCGGCATCACCAGTGTGAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGA  
AGATGGAGCCTTCCGAGCGCTGCGCGATTGGAGATCCTTACCTCAACAACAACAACATCAGTCGCATCCTGGT  
CACCAGCTTCAACCACATGCCGAAGATCCGAACCTGCGCCTCCACTCCAACCACCTCTACTGCGACTGCCACCT  
GGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCTGCATGGCTCCTGTGCATTT  
GAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTGTGCCAGCCCCCCTCGGAGCCCCCATCCTG  
CAATGCCAATCCATCTCCTGCCCTTCGCCCTGCACGTGCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTT  
GATGGAGATTCTGCCAATTTGCCGGAGGGCATCGTCGAATACGCCTAGAACAGAACTCCATCAAAGCCATCCC  
TGCAGGAGCCTTCAACCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGATATTGCTCC  
AGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCTGTATGGGAACAAGATCACCGAGATTGCCAAGGG  
ACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTCAATGCCAACAAGATCAACTGCCTGCGGGTGAACAC  
GTTTCAGGACCTGCAGAACCTCAACTTGCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTT  
CGCCCCCTCTGCAGTCCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCT  
GGCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGGCCGCTGCAGCAGCCCGCGCGACTCGCCAACAA  
GCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGGATTACCGCAGCAGGTTCCAGCAGCGA  
GTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCTGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCT  
GGTCCGCATCCCAAGCCACCTCCCTGAATATGTACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGA  
GGCCACTGGCATCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTGCG  
AGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCTGGAGACCGTGCACGG  
GCGCGTGTTCCTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGAGTAACCTTGATCAGCTGTGTGAGTAATGA  
CACCTTTGCCGGCCTGAGTTCGGTGAGACTGCTGTCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGC  
CTTACCACGCTTGTCTCCCTGTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTG  
GCTCGGCAAGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCCTAGGTGCCAGAAGCCATTTTTCTCAAGGA  
GATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAGTAGCTGCCAGCTGAGCCC  
GCGCTGCCCCGAGCAGTGCACCTGTATGGAGACAGTGGTGCGATGCAGCAACAAGGGGCTCCGCGCCCTCCCCAG  
AGGCATGCCCAAGGATGTGACCGAGCTGTACCTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGC  
CCTCCGACACCTGACGCTTATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACAT  
GTCTCACCTTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCTTCAACGGGCTGCG  
GTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTCCTGAAGGCTCCTTCAACGACCTCACATC  
TCTTTCCATCTGGCGCTGGGAACCAACCCACTCCACTGTGACTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAA  
GGCGGGGTACAAGGAGCCTGGCATCGCCGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCAC  
CCCAACCCACCGCTTCCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAG  
CCCGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCCTGCCCC

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**FIGURE 289B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCAGCATGGAGGCACC  
TGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGCCCTCTGGGCTTTGAGGGGCAGCGGTGTGAG  
ATCAACCCAGATGACTGTGAGGACAACGACTGCCAAAACAATGCCACCTGCGTGGACGGGATCAACAACCTACGTG  
TGTATCTGTCCGCCTAACTACACAGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTC  
TGTCAGCATGAGGCCAAGTGCATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGGAAG  
CTCTGTGAGACAGACAATGATGACTGTGTGGCCACAAGTGCCGCCACGGGGCCCAGTGCCTGGACACAATCAAT  
GGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCCTTCTGTGAACACCCCCACCCATGGTCTACTGCAG  
ACCAGCCCATGCGACCAGTACGAGTGCCAGAACGGGGCCCAGTGCATCGTGGTGCAGCAGGAGCCACCTGCCGC  
TGCCACCAGGCTTCGCCGGCCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTG  
GAACTGGCCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAACGGCATC  
CTTCTCTACAAAGGAGACAATGACCCCCTGGCACTGGAGCTGTACCAGGGCCACGTGCGGCTGGTCTATGACAGC  
CTGAGTTCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGAATGATGGGCAGTTTCACAGTGTGGAGCTGGTG  
ACGCTAAACCAGACCTGAACCTAGTAGTGGACAAAGGAACCTCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCA  
GCAGTGGGCATCAACAGCCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGC  
ACGGACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAGGACTTCAAG  
GCCCTCCCACCACAGTCCCTGGGGGTGTACCAGGCTGCAAGTCCCTGCACCGTGTGCAAGCACGGCCTGTGCCGC  
TCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCCAGGCTGGACCGGCCCCTCTGCGACCAGGAGGCCCGG  
GACCCCTGCCTCGGCCACAGATGCCACCATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCC  
GAGGGCTATGGAGGGGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTACCAT  
GGGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGCGAGCACTGCCAA  
CAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCAGAAAGGTTATGCATCATGTGCCACA  
GCCTCCAAGGTGCCATCATGGAATGTCGTGGGGGCTGTGGGCCCCAGTGCTGCCAGCCCACCCGAGCAAGCGG  
CGGAAATACGTCTTCCAGTGACGGACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACCTTAGAGTGC GGCTGC  
CTCGCGTGTTCCTAAGCCCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCCAT  
GTGGGACCCCCTGGTGATTCAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGAAGAGAATATTAAGTA  
TATTGTAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 290**

MAPGWAGVGAAVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRNAERLDLDRNNITR  
ITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNKNKLQVLPELLFQSTPKLTRLDLSENQIQGIPR  
KAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEILTNNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAW  
LSDWLRQRRTVGQFTLCMAPVHLRGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLME  
IPANLPEGIVEIRLEQNSIKAIPAGAFTQYKKLRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAKGLF  
DGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTIKGLFAPLQSIQTLHLAQNPFFVCDCHLKWLD  
YLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDIYRSRFSSECFMDLVCPEKCRCEGTIVDCSNQKLV  
IPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPNLRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRV  
FRGLSGLKTLMLRSNLISCVSNDTFAGLSSVRLSLYDNRIITITPGAFTTLVSLSTINLLSNPFNCNCHLAWLG  
KWLRRRIIVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLRALPRGM  
PKDVTLEYLEGNHLTAVPRELSALRHLTLIDLSNNSISMLTNYTFSNMHLSTLILSYNRLRCIPVHAFNGLRSL  
RVLTLLHGNDISSVPEGSFNDLTSLSHLALGTNPLHDCSLRWLSEWVKAGYKEPGIARCSSPEPMADRLLLTPT  
HRFQCKGPVDINIVAKCNACLSSPCKNNGTCTQDPVELYRCACPYSGKDCVTPINTCIQNPCQHGGTCHLSDS  
HKDGFSCSCPLGFEGQRCEINPDDCEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVPELNLCQHEAK  
CIPLDKGFSCCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDITINGYTCTCPQGFSGPFCEHPPPMVLLQTS  
PCDQYECQNGAQCIVVQEQPTCRCPGFGPRCEKLITVNFVGKDSYVELASAKVRPQANISLQVATDKDNGILLYKGD  
NDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHSVELVTLNQTLNLVVDKGTPKSLGKLQKQPAVGINS  
PLYLGGIPTSTGLSALRQGTDRPLGGFHGCIHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDS  
VVCECRPGWTGPLCDQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHIS  
DQGEFYCLCQPGFSGEHCQQENPCLGQVVREVIRROKGYASCATASKVPIMECRGGCGPQCCQPTRSKRRKYVFQ  
CTDGSSFVEEVERHLECGCLACS

**Signal peptide:**

amino acids 1-27

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**FIGURE 291**

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCAGACTCAACTGAGA  
AGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCTCCGGCAGGCTTTGAGGATGAAGGCTG  
CGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAGGCGCCGAGTCCAAAATCTACACTCGTTGCAAACTGGCAA  
AAATATTCTCGAGGGCTGGCCTGGACAATTACTGGGGCTTCAGCCTTGGAAGCTGGATCTGCATGGCATATTATG  
AGAGCGGCTACAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCAACA  
GCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTGCGCTGCTCAGCCTTGATCACTG  
ATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGAGACACAAGGAATGAAGTATTTGGCAAGGCT  
GGAAGAAACATTGTGAGGGCAGAGACCTGTCCGAGTGGAAAAAAGGCTGTGAGGTTTCCTAAACTGGAAGTGGAC  
CCAGGATGCTTTGCAGCAACGCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCT  
CCCAATATTCCTTCTCAAACCTTGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCATTTAAATGTC



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**FIGURE 292**

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAPTVLDDGSIDYGIF  
QINSAWCRRGKLENNHCHVACSALITDDLTDALICARKIVKETQGMNYWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**  
amino acids 1-19

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**FIGURE 293**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTACCCAAGGAAAG  
TGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTCTCATAGCGACCAACCAGAGGA  
TGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGC  
AAGGAAATCAAAGACGAATGTCCTAGTGCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTTATCTAC  
CAGACCTTCTGTGACATGACCTCTGGGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATGCCT  
GGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAAC  
TGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACTACGAC  
ATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTG  
CTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCA  
GTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCCCCGGTGATCCCTGTGGTCTATGATTTTGGCGACGCC  
CAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCAGGATTTGTTTCAGTTCAGGGTATTT  
AATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATT  
GGTGGAGGAGGATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT  
GGAATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTT  
TGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTACCCAGTAGCTAGA  
ATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

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**FIGURE 294**

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSIPRSCKEIKDECPSAFDGLYFLRTENGVIYQTFCDMTSG  
GGGWTILVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIW  
HVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYGEKGCWTDNGPVIPIVVDYFGDAQKTASYSP  
YQREFTAGFVQFRVFNNERAAANALCAGMRVTGCNTEHHCIGGGGYFPEASFPQCGDFSGFDWSGYGTHVGYSSS  
REITEAAVLLFYR

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**FIGURE 295**

CAGGCCATTTGCATCCCACTGTCCTTGTGTTCCGGAGCCAGGCCACACCGTCCTCAGCAGTGTGCATGTGTTAAAAA  
CGCCAAGCTGAATATATCATGCCCCCTATTAAAACTTGTACATGGCTCCCCATTGGTTTTTGGAGAAAAGTTCAAG  
CTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTTCAGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGT  
CACTTCCCAGATCTGCTTCTCACCAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATA  
GAGGAATACACCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAAACA  
TTCAAGTCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTCTAAATGTCACCAGCTTTGACTCAGTTGTT  
CCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGCTGCTCTCCATCAACAGATACGAAAGGAAG  
AAAAATCTGACTTTTGGCACTGGAAGCCCTAGTACAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTT  
CATCTGATCGTGGCAGGTGGTTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATG  
GTCCAACAGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCCCTCCTC  
CACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCCTCTGGAAGCCATGTACATG  
CAGTGCCAGTCATTGCTGTTAATTGGGTGGACCTTGGAGTCCATTGACCACAGTGTACAGGGTTTTCTGTGT  
GAGCCTGACCCGGTGCACCTTCTCAGAAGCAATAGAAAAGTTTCATCCGTGAACCTTCCTTAAAGCCACCATGGGC  
CTGGCTGGAAGAGCCAGAGTGAAGGAAAAATTTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACC  
AAACTGCTGGTATTAATCAGATTGTTTTTAAGATCTCCATTAATGTCAATTTTTATGGATTGTAGACCCAGTTTTGA  
AACCAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAACTTGAGTCTTGAATGTGAGCCA  
CTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAAAACCATGTCTTTTATGCTATAATCATTCCAAATTT  
TGCCAGTGTAAAGTTACAAATGTGGTGTCAATCCATGTTTCAGCAGAGTATTTTAATTATATTTCTCGGGATTAT  
TGCTCTTCTGTCTATAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAGTGTGTATCATTATCA  
AAGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCCAGATTCAATCCACCGAAGTGT  
TCACTGTCTGTTAGGGAATTTTTGTTTGTCTTTCCTGCTTTGCTGGATCCATAGCGAGAGTGCTCTGTATTTTT  
TTTAAGATAATTTGTATTTTTTGCACACTGAGATATAATAAAAGGTGTTTATCATAAAAA

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**FIGURE 296**

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRRLARRRKKILFYCHFPDLLLLTKRDSFLKRLYRAPIDWIEEYTTG  
MADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLDDLVPKGKKFLLLSINRYERKKNLTLA  
LEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVEHYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCV  
LYTPSNEHFGIVPLEAMYMQCPVIAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRAR  
VKEKFSPEAFTEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

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**FIGURE 297**

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCATGTTGGACTTCGCGATCTTCGCCGTTACCTTC  
TTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGACAAGCTGCAGGAATTCCAGGGATTACT  
CCAACGAAGAAAAAGATGGTAATCTTCCAGATATTGTGAATAGTGGAAGTTTGATGAGTTCCTGGTTAATTTG  
CATGAGAGATATGGGCCTGTGCTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTA  
CTGAAGCAGCATATCAATCCCAATAAGACATCGGACCCTTTTGAACCATGCTGAAGTCATTATTAAGGTATCAA  
TCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAAATGGTGTGACTGATTCTCTGAAG  
AGTAACTTTGCCCTCCTCTAAAGCTTTTCAAGAAGTATTATTAGATAAATGGCTCTCCTACCCAGAGACCCAGCAC  
GTGCCCCCTCAGCCAGCATATGCTTGGTTTTTGTATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAA  
GATGATCAGGAAGTCATTGCTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGAT  
GGGTCACTTGATAAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTTTTAAGG  
AACATCATAAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTCCTTAGTACAAGGGAACCTT  
AATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGGCCAGTTGCATAATAACTGCAAAATTTGTGTACC  
TGGGCAATCTGTTTTTTAACCACCTCTGAAGAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGA  
AATGGTCCTGTTACTCCAGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAAACTGTTGAACT  
GCCAACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATTCCTAGAGAG  
ACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCCATCTCCACACAAGTTTGATCCA  
GATCGGTTTTGATGATGAATTAGTAATGAAAACCTTTTCTCACTTGGATTCTCAGGCACACAGGAGTGTCCAGAG  
TTGAGGTTTGCATATATGGTGACCACAGTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAG  
GGACAGGTTATTGAAACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGA  
TATTAAAATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAAAAATCTATGTTG  
AATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTACTTAA

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**FIGURE 298**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVSFWFGR  
RLVVS LGTV DVLKQHINPNKTS DPFETMLKSLRYQSGGGSVSENHMRKKLYENGVTDSLKSNFALLLLKLSEELL  
DKWLSYPETQHVP L SQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHGTWVSEIGKGFLDGS LDKNMTRKKQYE  
DALMQLESVLRNIIKERKGRNFSQHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLT TSEE VQK  
KLYEEINQVFGNGPVTPEKIEQLRYCQHVLCE TVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP  
NTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLSVEGQVIETKYELVTSS  
REEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

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**FIGURE 299**

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGACCGCCGCCCTT  
GTCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACGCTCCTGGCGCATCTGGTGGT  
CGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTA  
TGACAAGCAGGACATTCACTGGTGGCCGCGCTCTCTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTT  
CCTCTCAGGAGTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGC  
CCTGTCTTCTTCATATTCGAGCGTTGGGAGTGCCTACGTATTGGTACATTTTTGTCTTCTGCAGTGGCCTTCC  
AGCTGTCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCTTCTTGATTACCTTCATGACG  
GGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTT  
TTCCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATT  
GTATTTAGTGCTTTGTAATAAAATATGTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACAATTAAA  
AAAAAAAA



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**FIGURE 300**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPFTFTPEEYDKQDIQLVAALSVTLGLFAVELAGFLSGV  
SMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALFVTVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

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**FIGURE 301**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGACTCGCTGCTGC  
TTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATGGTCTCCCGGCTCAGAGGAC  
CCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCC  
CGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCC  
CCCAACCGCCCGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCC  
AACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTC  
CACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAGAGTTC  
CACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTA  
GAACGGGGCCGCCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCA  
GCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTATCGGCTG  
GTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGATACCCCCTACTACCCATCTGGGTGACCCGGGGCAGGC  
CACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGG  
GTTGGGCCTCAGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG  
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTG  
GGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCCTGTGGGCAG  
GCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTTCTTGCCATCCTGAGGAAAGATA  
GCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAG  
GAGCCAGTCAGCAGGGTGGGGTGGGGCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTC  
GTGTGCTGAGCATGGCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCT  
CCAGCCAGGCCACCCCTTTCCAAAATCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATGGCACA  
CCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATCCGCGTGCTGTGTGTC  
CCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCGAGAGGGGTCCCTCAACAGTCAGCC  
TCACCTGTGAGACCGGGGTCTCCCGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGC  
CGGGCCGAGAGCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGA  
AACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

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**FIGURE 302**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

&gt;&lt;subunit 1 of 1, 252 aa, 1 stop

&gt;&lt;MW: 28127, pI: 8.91, NX(S/T): 5

MQLTRCCFVFLVQGSlyLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTLLGLLAPPGEA  
WGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVP  
PSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAF  
YSTDYRLVQKVC PDYNYHS DTPYYPSG

**Important features of the protein:****Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

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**FIGURE 303**

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCCCTTTATGTCT  
TCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTTCTGGTTGGTGTCTCTACTGA  
TTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACAAAGATGGACCAACACAGAAATATCTGCTGA  
TCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCA  
GTGAAGGTTTGAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGG  
GCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCA  
TTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGTATTCT  
GGGGCATTGTATTTTTTGATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGC  
TGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCA  
TGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGA  
ACTTTCTTCTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTA  
GAGGAAGCACAACTGTGCCTTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

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**FIGURE 304**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658

&gt;&lt;subunit 1 of 1, 257 aa, 1 stop

&gt;&lt;MW: 28472, pI: 9.33, NX(S/T): 0

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDGPTQKYLLIFG  
AFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGP GTVGIHG  
DSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGT  
WAFLAAGGSCRSCLKLCLLCQDKNFLLYNQRSR

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

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**FIGURE 305**

[illegible]

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**FIGURE 306**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

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**FIGURE 307**

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAAGAAAAATTTTTTGG  
GGGACCAAGTTTTTGAGGATTAATGTGAGAAATGGAGACGAGATCAGCAAATGAGTCAACTAGTGAATTCAAACA  
ACTTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCTTCAATCGGCCTGTGGATGTCTGGTCCCATCTGTCAATC  
TGCAGGCATTTAAATCCTTCCTGAGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTT  
TAGACAATGAAGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGGCTT  
ACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCTGACCTGGCGAGGAGGGTGA  
AGATTGGACATTCTGTTTAAAAACGGCCGATGTATGTACTGAAGTTCAGCACTGGGAAAGGCGTGAGGCGGCCGG  
CCGTTTGGCTGAATGCAGGCATCCATTCCCGAGAGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGA  
TTGTATCTGATTACCAGAGGGATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTGTTGCCTGTGG  
CCAATCCTGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCAGAAATCCTGGAA  
GCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAGGGAGCCAGCGACAACCCCTT  
GCTCCGAAGTGTACCATGGACCCACGCCAATTCGGAAGTGGAGGTGAAATCAGTGGTAGATTTCATCCAAAAAC  
ATGGGAATTTCAAGGGCTTCATCGACCTGCACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCA  
AAAAGGCCCCAGATGCCGAGGAACCTGACAAGGTGGCGAGGCTTGGCGCCAAAGCTCTGGCTTCTGTGTGCGGGCA  
CTGAGTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGGCGTATGACA  
ACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGCTTCCTCCTGCCAGCTAACCAGA  
TCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGACCATCATGGAGCATGTGCGGGACAACCTCTACTAGG  
CGATGGCTCTGCTCTGTCTACATTTATTTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTT  
CCTACCTGTGTGAGTCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAG  
TCGTGTGTCTGCGGCTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCTGCTGTTTTTGTATG  
AGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACTCAGCATCACCCCTTCTCTGGGTGGCAT  
GTCTCTCTCTACCTCATTTTTAGAACCAGAAACATCTGAGATGATTCTCTACCCCTCATCCACATCTAGCCAAGC  
CAGTGACCTTGCTCTGGTGGCACTGTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTT  
CCTTTAATTTCTCGCAGTCTTCCTGGAAAATATTTTCCTTTGAGCAGCAAATCTTGTAGGGATATCAGTGAAGGT  
CTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTTGCTCTTGTGGCCAGGCTGGAGTGTGA  
TGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCTCTTGAGTAGC  
TTGGTTTATAGGCGCATGCCACCATGCCTGGCTAATTTTGTGTTTTTAGTAGAGACAGGTTTCTCCATGTTGGT  
CAGGCTGGTCTCAAACCTCCCAACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTG  
AGCCACTGTGCGGGCCCGTCCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCTTCACTGTGC  
TGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTTCAGTGTGACCAGGATGGCGGGAGGG  
GATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAAGTGACCATCTAAATTGCAGGATGGTGAAATT  
ATCCCCATCTGTCTAATGGGCTTACCTCCTCTTTGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTAC  
AGGTCTAAATCACTCATCTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTGTGCTGTGGTGTATCCT  
GTGTTTCCTTGCTCTGGTTTGT  
TTTTGTATCCTTGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCTGCCTCTGTTTTCATTTACCT  
CAGCACGTACCATCTGTCTTTTGTGTTGTGTTTTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTG  
TCTTAACCTCCTGCCTAGGATTTGTACAGCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAA  
AAAAA



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**FIGURE 308**

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNRFPVDVLVPSVSLQA  
FKSFLRSQGLEAYVTIEDLQALLDNEDEMQHNEGQERSNNFNFGAYHSLEAIYHEMDNIAADFPDLARRVKIG  
HSFENRPMYVLKFSTGKGVRPAVWLNAGIHSREWISQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANP  
DGYVYTQTQNRLWRKTRSRNPGSSCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDVFIQKHGN  
FKGFIDLHSYSQLLMYPYGYSVKKAPDAEELDKVARLAALASVSGTEYQVGPTCTTVYPASGSSIDWAYDNGI  
KFAFTFELRDTGTYGFLLPANQIIPAEETWLGLKTIMEHVRDONLY

**Signal peptide:**

amino acids 1-16

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**FIGURE 309**

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGCCTGAGTCCAAGAT  
TCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTATCTCTTCACCTTCAAGTCCC  
CTTTCTCAAGAATCCTCTGTCTTTGCCCTCTAAAAGTCTTGGGTACATCTAGGACCCAGGCATCTTGCTTCCAGC  
CACAAAGAGACAGATGAAGATGCAGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGC  
AACAAATTCCAATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCAC  
CAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGG  
GGTCAGCATAGTCACCAACTCTGAGTTCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAGTTCAG  
CACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCAC  
CAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCCACCAACTCTGGGTCCAGTGTGACCTCCAGTGG  
AGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAG  
CACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC  
CAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAG  
GGCCAGCACTGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCACAGCCAC  
CAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG  
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCACAGCCACCAACTCTGACTCCAG  
CACAACTCCAGTGGGGCCGGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCCAC  
CAATTCTGAGTCCAGCACACCCTCCAGTGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGG  
GGCCAACACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAG  
CACAACTCCAGTGGGGTCCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC  
CAACTCTGACTCCAGCACAACTCCAGTGAGGCCAGCACAGCCACCAACTCTGAGTCTAGCACAGTGTCCAGTGG  
GATCAGCACAGTCCACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCAACACAGCCACCAACTCTGGGTCCAG  
TGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGAATGCACACAACTTCCCATAGTGCATCTACTGCAGT  
GAGTGAGGCAAAGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGC  
CGTGGGGCTCTTTGCTGGGCTCTTCTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGT  
CTACCACCCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG  
GTGGAGTCTTAACCTGGTTCTGGAGGAGACAGTATCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCC  
**CTG**AGCAGCCCCGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCACCCAAGACCTGGTTTCTTTT  
CATTATCCCAGGAGACCCCTCCCAGCTTTGTTTGGATCCTGAAAATCTTGAAGAAGGTATTCCTCACCTTTCT  
TGCCTTTACAGACACTGGAAAGAGAATACTATATTGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACAC  
ACACGACAAAGAGAAGCTGTGCTTGCCCCGGGGTGGGTATCTAGCTCTGAGATGAACTCAGTTATAGGAGAAAAC  
CTCCATGCTGGACTCCATCTGGCATTCAAAATCTCCACAGTAAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 310**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATIS  
GSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESS  
TPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTS  
SGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGA  
GTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTA  
TNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNS  
ESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESS  
TVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGS  
LVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAP  
HRPRWSPNWFWRPVS SIAMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

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## FIGURE 311A

CTAAGCCGGAGGATGTGCAGCTGCGGCGGGCGGCGCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACC  
GCCCCAGCCAGCCGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCCGCGCTCGTCGCCGCGC  
TGCCCGCCCCCGCTCCCCGCGCGAGCGGGAGGAGCCGCCGCCACCTCGCGCCCGAGCGCCCGCTAGTCGCGCGC  
CGGGCATGGTCCCCCTCTTAAAGGCGCAGGCCGCGGCGGGCGGGGGCGGGTGTGCGGAACAAAGCGCCGGCGCGGGG  
CCTGCGGGCGGGCTCGGGGGCCGCGATGGGCGCGGCGGGCCCCGCGGCGGGCGGGCGCTGCCGGGGCGGGCCCTCG  
CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGGCAGCGGGCTGAGGCGCGCGCGGAGCCTGCGCGGGCGGGCGGC  
GGCGGCGGGCGGGCGGCCGCGGGCGGAGCGGCGCGGGCATGGCGCGCGCGGGCGGGCGCGCCTGGCTCAGCGTGC  
TGCTCGGGCTCGTCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG  
GCCCCAGGGCGCGCGCCAGCCCCGAGGGCTGCCGCTCCGGGACGGCGGGCGGCTTCCAGGGCGGGCGGGCGCGCG  
GCGATGCGCGCGGGGCGCAGCTCTGGCCGCCCGGCTCGGACCCAGATGGCGGGCGCGGACAGGAACCTTCTCT  
TCGTGGGAGTCAAGCCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTACAGAACATGGTCCAAGACAA  
TTCCTGGGAAAGTTCAGTTCTTCTCAAGTGAGGGTTCGACACATCTGTACCAATTCAGTAGTGCCACTACGGG  
GTGTGGACGACTCTACCCGCCCCAGAAGAAGTCTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA  
AGTATGAATGGTTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAAGTCTCTGAGGAGTT  
TGAACAGCAGCGAGCCCCCTCTTCTTGGGCGAGCAGGCTGGGCACCACGGAAGAAATGGGAAAAGTGGCCCTGG  
AGCCTGGTGAGAACTCTGCATGGGGGGGCTGGCGTGATCATGAGCCGGGAGGTGCTTCGGAGAATGGTGCCGC  
ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGGAAGGTGTGTCGGGAGGTTTG  
CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTATGAGAATTACGAGCAGAACAAAAGGGGT  
ACATTAGAGATCTCCATAACAGTAAATTCACCAAGCTATACATTACACCCCAACAAAACCCACCCTACCAGT  
ACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAAATACAGCTGCACCCGCAAA  
TTGTCTGATGAGCAAATACAGCAACACAGAAATTCATAAGAGGACCTCCAGCTGGGAATCCCTCCCTCCTTCA  
TGAGGTTTTAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAAATACTTGTATTGCGCAG  
TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAAGCCTTGGACGACATTGTATGCAGGTCA  
TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATATTGACTTCAAAGAGATCCAGTACGGCTACCGCC  
GGGTGAACCCCATGTATGGGGCTGAGTACATCCTGGACCTGCTGCTTCTGTACAAAAGCACAAGGGAAGAAAA  
TGACGGTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC  
TGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTTTCTCTCAAACCTCCCTGAAGA  
AGCTCGTCCCTTTAGCTCCCTGGGTGGAAGAGTGAGCACAAGAACCACAAAGATAAAAAGATAAACAATACTGA  
TTCCTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAACTTTGAGAAGACGTGTCTTATCCCCAATC  
AGAACGTCAAGCTCGTGGTTCTGCTTTTCAATTCGACTCCAACCCTGACAAGGCCAAACAAGTTGAACTGATGA  
GAGATTACCGCATTAAGTACCCTAAAGCCGACATGCAGATTTTGCCTGTGTCTGGAGAGTTTCAAGAGCCCTGG  
CCCTGGAAGTAGGATCCTCCAGTTTAAACAATGAATCTTTGCTCTTCTGCGACGTCGACCTCGTGTCTTACTA  
CAGAATTCCTTCAGCGATGTGAGCAATACAGTTCTGGGCCAACAAATATATTTTCCAAATCATCTTCAGCCAGT  
ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCATTTTGCCTTTACTCAGAAAAGTGGCTTCT  
GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTTGTCCGAGTGGGTGCTTTGATGTTTCCA  
TCCAAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC  
AGGAAGTAGGAGTAGTCCACGTCCACCATCCTGTCTTTTGTGATCCCAATCTTGACCCCAACAGTACAAAATGT  
GCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA  
GTTACAGTAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTAATGTCCAGCTTTGCTGGAAAAGACGTTTT  
TAATTATCTAATTTATTTTCAAAAATTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC  
AAGTGGTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTTTGCCTTTGAA  
CACATCTTCTGCTGAACATTATGTAGCAGACCTGCTTAACTTTGACTTGAAATGTACCTGATGAACAAAAGTTT  
TTTAAAAAATGTTTTCTTTTGGACCTTTGCTCCAGTCTTATGGCAGAAAACGTGAACATTCTGCAAGTAT  
TATTGTAACAAAACACTGTAACCTGGTAAATGTTCTGTTGTGATTGTTAACATTCCACAGATTCTACCTTTTGT  
GTTTTGTTTTTTTTTTTACAATTGTTTTAAAGCCATTTCAATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA  
GCTGTTTCATCATTTGCTTTCAGGAGAGCTTTCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGC  
CACGTAGGTTTTTTGTTTGTGTTTTGTTTCTTTTTTGGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAATG  
CAGTGGCGCAATCTGGCTCACTTTAACCTCCACTTCCCTGGTTCAAGCAATCCCCTGCCTTTGCCTCCCGAGT  
AGCTGGGATTACAGGCACACACCACGCCCAGNTAGTTTTTTTGTATTTTTAGTAGAGACGGGGTTTTACCAT  
GCAAGCCCAGCTGGCCACGTAGGTTTTAAAGCAAGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG  
TGATAGTTTCAATTCGGCCTAAATAGACCTGGCATTAAATTTCAAGAAGGATTGGCATTCTCTTCTTGACCTT  
CTCTTTAAAGGTTAAATATTAATGTTTGAATGACAAAGATGAATTATTACAATAAATCTGATGTACACAGACT  
GAAACATACACACATACACCCTAATCAAAACGTTGGGGAAAAATGTATTTGGTTTTGTTCTTTTATCCTGTCTG  
TGTTATGTGGGTGGAGATGGTTTTTATTCTTTTATTACTGTTTTGTTTTATCCTTTGTATCTGAAATACCTTTAA

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**FIGURE 311B**

TTTATTTAATATCTGTTGTTTCAGAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTATTTATGTGTATCGG  
GAGTGTGTTTAGTCTGTTTTATTGTCAGTAAACCGATCTCCAAAGATTTCCTTTTGGAAACGCTTTTCCCTCC  
TTAATTTTATATTCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGGG  
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT  
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG  
CCTGATGCTCATTGGAATAAACCAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTGTCTCATT  
ATTCCTGTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAACTTAAACACGAAAAA

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**FIGURE 312**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGARG
DARGAQLWPPGSDPDGGPRDRNFLEFVGVMTAQKYLQTRAVAAAYRTWSKTIPGKVQFFSSEGSD
TSVPIPVVPLRGVDDSYPPQKKSEFMMMLKYMHDHYLDKYEFMRADDDVYIKGDRLNENFLRSLN
SSEPLFLGOTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYTTTHED
VEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPPYQYRL
HSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQREEILEWEEF
LTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQYGYRRVNP
MYGAEYILDLLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKRINQESGSL
SFLSNSLKKLVPPFQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTCLIPNQNVKL
VLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQFNNESSLFFC
DVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFTQKTGFWRNYGF
GITCIYKGD LVRVGGFDVSIQGWGLEDDVLFNKVVQAGLKTFRSQEVGVVHVHHPVFCDPNLD
PKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

**Signal peptide:**

amino acids 1-23

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**FIGURE 313**

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCGCGACGGAGGTTGTGACCCC  
TACGGAGCCCCAGCTTGCCACGACCCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTCA  
GGTGGGAGGCTGGAACATATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCA  
ACAAATGGATGATGTGATATATGCATTCCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCAT  
GGTCAATTAACGAGGCAGTTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCT  
TTGGAATCATGGTGTGATGGAAGGGATTTACTTTATACTGACTCTGTTTTGGGGAAGCTTTT  
TTGGAAGCATTTTTCATGCTGAGTCCCTTTTTTACCTTTGATGTTTGTAAACCCATCTTGGTATC  
GCTGGATCAACAACCGCCTTGTGGCAACATGGCTCACCCCTACCTGTGGCATTATTGGAGACCA  
TGTTTGGTGTAAAAGTGATTATAAAGTGGGATGCATTTGTTCCCTGGAGAAAGAAGTGTCAATTA  
TCATGAACCATCGGACAAGAATGGACTGGATGTTCCCTGTGGAATTGCCTGATGCGATATAGCT  
ACCTCAGATTGGAGAAAAATTTGCCTCAAAGCGAGTCTCAAAGGTGTTCCCTGGATTTGGTTGGG  
CCATGCAGGCTGCTGCCTATATCTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTCCG  
AAGACATGATTGATTACTTTTGTGATATTCACGAACCACTTCAACTCCTCATATTCCCAGAAG  
GGACTGATCTCACAGAAAACAGCAAGTCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTC  
AGAAATATGAATATGTTTTACATCCAAGAACTACAGGCTTTACTTTTGTGGTAGACCGTCTAA  
GAGAAGGTAAGAACCTTGATGCTGTCCATGATATCACTGTGGCGTATCCTCACAACATTCCTC  
AATCAGAGAAGCACCTCCTCCAAGGAGACTTTCCCAGGGAAATCCACTTTCACGTCCACCGGT  
ATCCAATAGACACCCTCCCCACATCCAAGGAGGACCTTCAACTCTGGTGCCACAAACGGTGGG  
AAGAGAAAGAAGAGAGGCTGCGTTCCCTTCTATCAAGGGGAGAAGAATTTTTATTTTACCGGAC  
AGAGTGTCAATCCACCTTGCAAGTCTGAACTCAGGGTCCTTGTGGTCAAATTGCTCTCTATAC  
TGTATTGGACCCTGTTTCAAGCCCTGCAATGTGCCTACTCATATATTTGTACAGTCTTGTTAAGT  
GGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGAGAATATTTGGTGGACTGGAGA  
TCATAGAAGTTCATGTTACCGACTTTTACACAAACAGCCACATTTAAATTCAAAGAAAAATG  
AGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTGGAAATGTTCTAAACCTT  
TCTAAGCTCAGATGCATTTTTCATGACTATGTGCAATATTTCTTACTGCCATCATTATTTGT  
TAAAGATATTTTGCACCTAATTTTGTGGGAAAAATATTGCTACAATTTTTTTTAAATCTCTGAA  
TGTAAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTTGGGCCAGAATA  
TTATTAAACAATCATCAGGCTTTTAAA

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**FIGURE 314**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFGIMVSWKGIYFILTLFWGSFFGSI FML  
SPFLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDADFVPGERSVIIMNHRTR  
MDWMFLWNCLMRYSYLRLEKICLKASLKGVPFGFWAMQAAAYIFIHRKWKDDKSHFEDMIDYF  
CDIHEPLQLLI FPEGTDLTENSKSRSNFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLD  
AVHDITVAYPHNIPQSEKHLLOGDFPREIH FHVHRYPIDTLPTS KEDLQLWCHKRWEEKEERL  
RSFYQGEKNFYFTGQSVIPPCKSELRVLVKLLSILYWT L FSPAMCLLIYLYSLVKWYFIITI  
VIFVLQERIFGGLEIIELACYRLLHKQPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377



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**FIGURE 315**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGA  
CCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACAGG  
AATATCC**ATG**GCTTTTGTGCTCATTGTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTG  
GCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTG  
CTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGGTTCTTCAGGAATCAGTTCCA  
TGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCG  
AGGGAGAAGTGAAGTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGCTAAAAAA  
CATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTTCAAGTTCCTCTCATTTCATCGTGGGATA  
GGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCATCGTGGGATA  
TGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCTCCAGCCACAGCCAA  
GTGGAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAG  
CCTGTATGATGTGGAGATCTCATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCAT  
CCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCA  
GCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGTGCCCTGTGTGGTGT  
TGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCAGGCGGAACTGGACTG  
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCT  
GGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTGAACCCATAGAAA  
AGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCA  
GGGTTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGACAAAATGTAGGGTGGTATGT  
GGGAGTGTGTGCGGATGACGTAGACAGGGGGAAGAACAATGTGACTTTGTCTCCCAACAATGG  
GTATTGGGTCCCTCAGACTGACAACAGAACATTTGTATTTTACATTCAATCCCCATTTTATCAG  
CCTCCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCTGGACTATGAGGGTGGGACCAT  
CTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGCTGACATGTCAGTTTGAAGG  
CTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAGGGGACTCCCATATTCAT  
ATGTCCAGTGTCTGGGGAT**TGA**GACAGAGAAGACCCTGCTTAAAGGGCCCCACACCACAGACC  
CAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGCCCCAGCTTCCTCTCCGGAGCCTGCGC  
ACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCCTGAGCCCTGCA  
GCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCTGTGGGAGTCAGAAGCC  
ATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAACCTCCATC  
CAGCTAAGCGATCTTGAACAAGTCACAACCTCCAGGCTCCTCATTTGCTAGTCACGGACAGT  
GATTCCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTTTGA  
GGGCACAGTGTGTTGCTAATGATGTGTTTTTATATTATACATTTTCCACCATAAACTCTGTTT  
GCTTATTCCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACAC  
CTGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTTCACTGATTCTATAAGCCAG  
CATTACCTGATACCAAACAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCA  
TATCCCTCATTAACACAGACACAAAAATCTAAATAAAATTTTAAACAAATTAACTAAACAAT  
ATATTTAAAGATGATATATACTACTCAGTGTGGTTTGTCCCACAAATGCAGAGTTGGTTTAA  
TATTTAAATATCAACCAGTGAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAA  
AAAAA

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**FIGURE 316**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLVSFYELVSGWQVTPGPKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAV
VHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEAT
WELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLY
DVEISIIIVQENAGSILCSIHAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALCGVVM
GMIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAP
QEVPHSEKRFRTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYW
VLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLL
RPYIQHAMYDEEKGTPIFICPVSWG
```

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

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**FIGURE 317**

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTTC  
TGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGGAAGCGGCA  
GGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCACCA  
GGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGGCATT  
TGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTGATGGG  
GCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTTATATATACTGTACATTCTATTTAAGGT  
AAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAATCATTGT  
CTACATTAAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTAAATCCTGC  
CTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTTCAGTTTCACATAAGAATGTTTACTCAA  
TGTTTAAGTGTTTTGCCCCAAAATTCACAACCAAGGCAGAACTAGGACTTGAACATGGAT  
CTTTTGGTTCCTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

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**FIGURE 318**

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPPTPEGKLGRFPPMMHHHQAPSDGQTP  
GARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRILILHQ

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**FIGURE 319**

CCTTCACAGGACTCTTCATTGCTGGTTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTAG  
GAAAAGAGTTTGTGGGAACCCCTGGGTATCGGCCTCGTCATCTTCATATCCCTGATTGTCCCT  
GGCAGTGTGCATTGGACTCACTGTTCAATTATGTGAGATATAATCAAAAGAAGACCTACAATTA  
CTATAGCACATTGTCAATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGGCTTCTAA  
CAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAATCTCC  
ATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGGAGTGTT  
GGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAGATAAAAT  
TGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAGATCCTCA  
CTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGG  
AACACGAAGAAGTAAACTCTAGGTGAGTCTCAGGATCGTTGGTGAGCAGAAAGTAGAAGA  
GGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTT  
AATTAATGCCACATGGCTTGTGAGTCTGCTCACTGTTTTACAACATATAAGAACCCTGCCAG  
ATGGACTGCTTCCTTTGGAGTAACAATAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAAT  
AATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCTCTTGCAGAGCTTTC  
TAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGATGCATCCTATGAGTT  
TCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAATGATGGTTACAGTCA  
AAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTTGCAATGAACCTCAAGC  
TTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGC  
ATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTGAGATGCTAGAGATATCTGGTACCTTGC  
TGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAGCCTGGTGTTTATACTAGAGT  
TACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATC**TAA**GAGACAAAAGCCTCATGGAA  
CAGATAACATTTTTTTTTTGTGTTTTTGGGTGTGGAGGCCATTTTTAGAGATACAGAATTGGAGA  
AGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAACTGTTTGCTTGATGCATGTATTTT  
CTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCAGATCAACTCTGTCATCTGTGA  
GCAATAGTTGAACTTTATGTACATAGAGAAATAGATAATAACAATATTACATTACAGCCTGTA  
TTCATTTGTTCTCTAGAAGTTTTGTGAGAATTTGACTTGTTGACATAAAATTTGTAATGCATA  
TATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTCAGCTCCTCTCATTTTCAGCAAATATCCA  
TTTTCAAGGTGCAGAACAAAGGAGTGAAAGAAAATATAAGAAGAAAAAAATCCCCTACATTTTA  
TTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGTGGAATATTAGAAATGATCATATTTCATTAT  
GAAAGGTCAAGCAAAGACAGCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACATA  
GTTAAGGAAGTCCAGAAAGAAGCCAAGATATATCCTTATTTTCATTTCCAAACAACTACTATG  
ATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCTATAATAATTATACAACTTCATGCAATG  
TACTTGTTCTAAGCAAATTAAGCAAATATTTATTTAACATTGTTACTGAGGATGTCAACATA  
TAACAATAAAATATAAATCACCCA

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**FIGURE 320**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

&gt;&lt;subunit 1 of 1, 423 aa, 1 stop

&gt;&lt;MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTDK  
LYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFH  
STEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQS  
LRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAHCFTTYKNPARWTASFGVTIK  
PSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTYNAVHRVCLPDASYEFQPGDVMFVTG  
FGALKNDGYSQNHRLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSGGPLV  
SSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

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**FIGURE 321**

CCGGGCTCCTGGGTGAGGCCGGCAAGTTTGGAGCGTGGTCAGACAATAGGGGCGTGGCTACGG  
CTCGCGGAGCGCAACCAACGCTCTAGACCAGACCTGGGCTCGAGACCATAACTGTTTGGCTTT  
AACAGTACGTGGGCGGCCGGAATCCGGGAGTCCGGTGACCCGGGCTGTGGTCTAGCATAAAGG  
CGGAGCCCAGAAGAAGGGGCGGGGTATGGGGAGAAGCCTCCCCACCTGCCCCGCAAGGCGGCA  
TCTGCTGGTCCTGCTGCTGCTCCTCTCTACCCTGGTGATCCCCCTCCGCTGCAGCTCCTATCCA  
TGATGCTGACGCCCAAGAGAGCTCCTTGGGTCTCACAGGCCTCCAGAGCCTACTCCAAGGCTT  
CAGCCGACTTTTCTGAAAGGTAACCTGCTTCGGGGCATAGACAGCTTATTCTCTGCCCCCAT  
GGACTTCCGGGGCCTCCCTGGGAACTACCACAAAGAGGAGAACCAGGAGCACCAGCTGGGGAA  
CAACACCCTCTCCAGCCACCTCCAGATCGACAAGATGACCGACAACAAGACAGGAGAGGTGCT  
GATCTCCGAGAATGTGGTGGCATCCATTCAACCAGCGGAGGGGAGCTTCGAGGGTGATTTGAA  
GGTACCCAGGATGGAGGAGAAGGAGGCCCTGGTACCCATCCAGAAGGCCACGGACAGCTTCCAC  
ACAGAACTCCATCCCCGGGTGGCCTTCTGGATCATTAAGCTGCCACGGCGGAGGTCCCACCAG  
GATGCCCTGGAGGGCGGCCACTGGCTCAGCGAGAAGCGACACCGCCTGCAGGCCATCCGGGAT  
GGACTCCGCAAGGGGACCCACAAGGACGTCCTAGAAGAGGGGACCGAGAGCTCCTCCCACTCC  
AGGCTGTCCCCCGAAAGACCCACTTACTGTACATCCTCAGGCCCTCTCGGCAGCTGTAGGGG  
TGGGGACCGGGGAGCACCTGCCTGTAGCCCCATCAGACCCTGCCCCAAGCACCATATGGAAA  
TAAAGTTCTTTCTTACATCTAAAAA

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**FIGURE 322**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68879  
><subunit 1 of 1, 242 aa, 1 stop  
><MW: 27007, pI: 8.68, NX(S/T): 2  
MGEASPPAPARRHLLVLLLLLSTLVIPSAAAPIHDADAQESSLGLTGLQSLLOGFSRLFL  
KGNLLRGIDSLFSAPMDFRGLPGNYHKEENQEHQLGNNTLSSHLQIDKMTDNKTGEVLIS  
ENVVASIQPAEGSFEGDLKVPRMEEKEALVPIQKATDSFHTELHPRVAFWIILPRRRSH  
QDALEGGHWLSEKRHRLQAIRDGLRKGTHKDVLEEGTESSSHSRLSPRKTHLLYILRPSR  
QL

**Important features of the protein:****Signal peptide:**

Amino acids 1-30

**N-glycosylation sites:**

Amino acids 97-101;112-116

**N-myristoylation sites:**

Amino acids 80-86;132-138;203-209;216-222



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**FIGURE 323**

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCC  
TGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGGCC  
CAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTC  
TCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTAC  
GCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGG  
GACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTG  
ACTTACTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTGTCTGTTTCTTATCATTGTGGGG  
ATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGT  
TTGCTTGTCAATTTTCTGTGTAGAAGTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATG  
GTTCCAGTACAATGGTCAGATATGGTCACCTTTGAAAGCCAGGATGACAAATTATGGATTACCT  
AGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTA  
GTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCAGATTCTGCTGTGTT  
AGAGAATTCCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGACCTTTATCAAGAG  
GGTTGTGGGAAGAAAATGTATTCCTTTTTCAGAGGAACCAACAACCTGCAGGTGCTGAGGTTT  
CTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGG  
GCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTCCTTGAAGAATGACAAC  
TCTCAGCACCTGTCATGTCCCTCAGTAGAAGTGTGAAACCAAGCCTGTCAAGAATCTTTGAA  
CACACATCCATGGCAAACAGCTTTTAATACACACTTTGAGATGGAGGAGTTATTAAAAAGAAATG  
TCACAGAAGAAAACCAAACTTGTTTTATTGGACTTGTGAATTTTGTGACTACATACTATGTG  
TTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA  
TGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTTAGTC  
CCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTACTGAAC  
ACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAACGAGTCACA  
TATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGTATATAAAGTACT  
AATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTACTCAGCGATCTATTCT  
TTCTGATGCTAAATAAATTATATATCAGAAAACCTTCAATATTGGTGACTACCTAAATGTGAT  
TTTTGCTGGTTACTAAAATATTCTTACCCTTAAAAGAGCAAGCTAACACATTGTCTTAAGCT  
GATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGATTTTCAGTTCT  
GATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTAA  
GCCTTTCCTGTTAATAAAGCTTTACTATTCTGTCCTGGGCTTATATTACACATATACTGTTA  
TTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGA  
ATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTTCAGAA  
AGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTGGACACTAAACACTTTTTAAAA  
AGCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATCTACAGA  
AAATAGTGTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAAACATGTGACAATTTAG  
AGATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTT  
TTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTAT  
TTTGTATTCTCAGAATATGGAAAGAAAATTTAAATGTGTCAATAAATATTTTCTAGAGAG  
TAA

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**FIGURE 324**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

&gt;&lt;subunit 1 of 1, 305 aa, 1 stop

&gt;&lt;MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVV  
HPVMIAVCCFLIIVGMLGYCGTVKRNLALLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWS  
DMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGC  
SKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDR  
REPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

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**FIGURE 325**

AGCAGTGCATTGCTGGAGCGAGGAGAAGCTCACGAATCAGCTGCAGGTCTCTGTTTTGAAAAA  
GCAGAGATACAGAGGCAGAGGAAAAGGGTGGACTCCTATGTGACCTGTTCTTAGAGCAAGACA  
ATCACCATCTGAATTCCAGAAGCCCTGTTTCATGGTTGGGGATATTTTCTCGACTGC**ATG**GAAT  
CAGAAAGAAGCAAAAGGATGGGAAATGCCTGCATTCCCCTGAAAAGAATTGCTTATTTCTTAT  
GTCTCTTATCTGCGCTTTTGCTGACTGAGGGGAAGAAACCAGCGAAGCCAAAATGCCCTGCCG  
TGTGTACTTGTACCAAAGATAATGCTTTATGTGAGAATGCCAGATCCATTCCACGCACCGTTC  
CTCCTGATGTTATCTCATTATCCTTTGTGAGATCTGGTTTTACTGAAATCTCAGAAGGGAGTT  
TTTTATTACGCCATCGCTGCAGCTCTTGTTATTCACATCGAACTCCTTTGATGTGATCAGTG  
ATGATGCTTTTATTGGTCTTCCACATCTAGAGTATTTATTCATAGAAAACAACAACATCAAGT  
CAATTTCAAGACATACTTTCCGGGGACTAAAGTCATTAATTCACCTTGAGCCTTGCAAACAACA  
ATCTCCAGACACTCCCAAAAGATATTTTCAAAGGCCTGGATTCTTTAACAAATGTGGACCTGA  
GGGGTAATTCATTTAATTGTGACTGTAAACTGAAATGGCTAGTGGAATGGCTTGCCACACCA  
ATGCAACTGTTGAAGACATCTACTGCGAAGGCCCCCAGAATACAAGAAGCGCAAAATCAATA  
GTCTCTCCTCGAAGGATTTGATTGCATCATTACAGAATTTGCAAAGTCTCAAGACCTGCCTT  
ATCAATCATTGTCCATAGACACTTTTTCTTATTTGAATGATGAGTATGTAGTCATCGCTCAGC  
CTTTTACTGGAAAATGCATTTTCTTGAATGGGACCATGTGGAAAAGACCTTCGGAATTATG  
ACAACATTACAGGCACATCCACTGTAGTATGCAAGCCTATAGTCATTGAAACTCAGCTCTATG  
TTATTGTGGCCAGCTGTTGGTGGCTCTCACATCTATAAGCGAGACAGTTTTGCAAATAAAT  
TCATAAAAATCCAGGATATTGAAATCTCAAAATCCGAAAACCCAATGACATTGAAACATTCA  
AGATTGAAAACAACTGGTACTTTGTTGTTGCTGACAGTTCAAAAGCTGGTTTTACTACCATTTAC  
AAATGGAACGGAAACGGATTCTACTCCCATCAATCCTTACACGCGTGGTACAGGGACACTGAT  
GTGGAATATCTAGAAATAGTCAGAACACCTCAGACACTCAGAACGCCTCATTTAATTCTGTCT  
AGTAGTTCCCAGCGTCCTGTAATTTATCAGTGGAACAAAGCAACACAATTATTCACTAACCAA  
ACTGACATTCCTAACATGGAGGATGTGTACGCAGTGAAGCACTTCTCAGTGAAAGGGGACGTG  
TACATTTGCTTGACAAGATTCATTGGTGATTCCAAAGTCATGAAATGGGGAGGCTCCTCGTTC  
CAGGATATTCAGAGGATGCCATCGCGAGGATCCATGGTGTTCAGCCTCTTCAAATAAATAAT  
TACCAATATGCAATTCTTGGAAGTGATTACTCCTTTACTCAAGTGTATAACTGGGATGCAGAG  
AAAGCCAAATTTGTGAAATTCAGGAATTAAATGTTTCAGGCACCAAGATCATTACACATGTG  
TCCATTAATAAGCGTAATTTTCTTTTTGCTTCCAGTTTTAAGGGAAATACACAGATTTACAAA  
CATGTGCATAGTTGACTTAAGCGC**ATG**AGACACCAAATCTGTGGCTGCCATCAGAAATTTTCT  
ACAGTACATGACCCGGATGAACTCAATGCATGATGACTCTTCTTATCACACTTGCAAATGAAT  
GCCTTTCAAACATTGAGACTGCTAGAACCAAGCACTACCAGTATCTCCATCCTTAAGTGTCCA  
GTCCAGTGATGTGGGAAGTTACCTTTTATAAGACAAAATTTAATTGTGTAAGTGTCTTTGCA  
GTGAAGATGTGTAAATAAGCGTTTAAATGGTATCTGTTACTCCAAAAGAAATATTAATATGTA  
CTTTTCCATTTATTTATTCATGTGTACAGAAACAACCTGCCAAATAAAATGTTTACATTTTCTT  
TCATA

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**FIGURE 326**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68882
><subunit 1 of 1, 557 aa, 1 stop
><MW: 63818, pI: 8.61, NX(S/T): 3
MESERSKRMGNACIPLKRIAYFLCLLSALLLLEGGKPAKPKCPAVCTCTKDNCENARS
IPRTVPPDVISLSFVRSGFTEISEGSFLFTPSLQLLLFTSNSFDVISDDAFIGLPHLEYL
FIENNNIKSISRHTFRGLKSLIHLSLANNNLQTLPKDIFKGLDSLTVNVDLRGNSFNCDCCK
LKWLVEWLGHNTATVEDIYCEGPPEYKKRKINSLSSKDFDCIITEFAKSQDLPYQSLSID
TFSYLNDEYVVIAQPFRTGKCIFLEWDHVEKTFRNYDNITGTSTVVCKPIVIETQLYVIVA
QLFGGSHIYKRDSFANKFIKIQDIEILKIRKPNDIETFKIENNWFVVDSSKAGFTTIY
KWNNGNGFYSHQSLHAWYRDTDVEYLEIVRTPQTLRTPHLILSSSSQRPVIYQWNKATQLF
TNQTDIPNMEDVYAVKHFSVKGDVYICLTRFIGDSKVMKWGGSSFQDIQRMPSRGSMTVFQ
PLQINNYQYAILGSDYSFTQVYNWDAEKAKFVKFQELNVQAPRSFTHVSINKRNFLFASS
FKGNTQIYKHVIVDLA
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-34

**Transmembrane domain:**

Amino acids 281-306

**N-glycosylation sites:**

Amino acids 192-196;277-281;422-426

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 310-314

**Tyrosine kinase phosphorylation sites:**

Amino acids 228-235;378-385

**N-myristoylation sites:**

Amino acids 172-178;493-499

**Amidation site:**

Amino acids 33-37

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**FIGURE 327**

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCCCTCTGATAAAGCCC  
CTACCAGTGCTGATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAAAAAGTGCTTGA  
AAGAGAAGGGGACAAAGGAACACCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTC  
CAGAAGG**ATG**CCTCCATTCCTGCTTCTCACCTGCCCTCTTCATCACAGGCACCTCCGTGTCACC  
CGTGGCCCTAGATCCTTGTTCTGCTTACATCAGCCTGAATGAGCCCTGGAGGAACACTGACCA  
CCAGTTGGATGAGTCTCAAGGTCTCCTCTATGTGACAACCATGTGAATGGGGAGTGGTACCA  
CTTCACGGGCATGGCGGGAGATGCCATGCCCTACCTTCTGCATACCAGAAAACCACTGTGGAAC  
CCACGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAAGGCGACGGCATTGTGCAACGCCA  
GGCTTGTGCCAGCTTCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAAAGTCAAGGCTTG  
CCCTGGAGGCTACTATGTGTATCGTCTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGG  
TCATTTTTATGACATCTGCGACGAGGACTGCCATGGCAGCTGCTCAGATACCAGCGAGTGCAC  
ATGCGCTCCAGGAACCTGTGCTAGGCCCTGACAGGCAGACATGCTTTGATGAAAATGAATGTGA  
GCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCCTACCGCTGTGAGTG  
TGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAA  
TAACAATGGTGGCTGCAGCCACTCTTGCCCTGGATCTGAGAAAGGCTACCAGTGTGAATGTCC  
CCGGGGCCTGGTGCTGTCTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAAATCAAA  
TGCCATTGAAGTGAACATCCCCAGGGAGCTGGTTGGTGGCCTGGAGCTCTTCTTGACCAACAC  
CTCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACATCCTCTTCTCTCTCAAGACATGTGG  
TACAGTGGTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGACAGGTCTACCCAA  
GCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTGAC  
CTGCGAGTTTCCACGCCGTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCC  
ACTGGAAATCATGAGCCGAAATCATGGGATCTTCCCATTCACCTCTGGAGATCTTCAAGGACAA  
TGAGTTTGAAGAGCCTTACCGGGAAGCTCTGCCCACCCTCAAGCTTCGTGACTCCCTCTACTT  
TGGCATTGAGCCCGTGGTGCACGTGAGCGGCTTGGAAGCTTGGTGGAGAGCTGCTTTGCCAC  
CCCCACCTCCAAGATCGACGAGGTCTGAAATACTACCTCATCCGGGATGGCTGTGTTTCAGA  
TGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGGTCCCTGTCTT  
CAAGTTTGTGGGCAAAGACCACAAGGAAGTGTCTGCACTGCCGGTTCTTGTCTGTGGAGT  
GTTGGACGAGCGTTCCCGCTGTGCCCAGGGTTGCCACCGGCGAATGCGTCGTGGGGCAGGAGG  
AGAGGACTCAGCCGGTCTACAGGGCCAGACGCTAACAGGCGGCCCGATCCGCATCGACTGGGA  
GGACT**TAG**TTTCGTAGCCATACCTCGAGTCCCTGCATTGGACGGCTCTGCTCTTGGAGCTTCTC  
CCCCACCGCCCTCTAAGAACATCTGCCAACAGCTGGGTTTCACTTCCACTGTGAGTTCAG  
ACTCCCAGCACCAACTCACTCTGATTCTGGTCCATTCAAGTGGGCACAGGTACAGCACTGCTG  
AACAAATGTGGCCTGGGTGGGGTTTCATCTTTCTAGGGTTGAAAATAAATGTCCACCCAGAA  
AGACACTCACCCCATTTCCCTCATTTCTTTCTTACACTTAAATACCTCGTGTATGGTGAATC  
AGACCACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAAATTAAACAG  
TTACTGAAATTATGACTTAAATACCCAATGACTCCTTAAATATGTAAATTATAGTTATACCTT  
GAAATTTCAATTCAAATGCAGACTAATTATAGGGAATTTGGAAGTGTATCAATAAAACAGTAT  
ATAATTTT

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**FIGURE 328**

MPPFLLLTCLFETGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFT  
GMAGDAMPTFCIPENHCGTHAPVWLNGLISHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPG  
GYVYRLTKPSVCFHVYCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQN  
NGGCSEICVNLKNSYRCECGVGRVLRSDGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRG  
LVLSEDNHTCQVPVLCKSNAIEVNIPRELVGGLFLTLNTSCRGVSNGTHVNILFSLKTCGTV  
VDVVDNKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVTCEFPRLYTISEGYVPNLRNSPLE  
IMSRNHGIFPFTLEIFKDNEFEEPYREALPTLKLRLDSLYFGIEPVVHVSGLESLVESC FATPT  
SKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRVLVCGVLD  
ERSRCAQGCCHRRMRRGAGGEDSAGLQGQTLTGGPIRIDWED

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

**Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

**N-myristoylation sites.**amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

**ZP domain proteins.**

amino acids 431-457

**Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

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**FIGURE 329**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCT  
GCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACC  
TGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACC  
GGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCG  
ATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCA  
TCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGGTGATTC  
TGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTG  
ACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAG  
GGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCA  
CAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTA  
GGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAA  
TCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCC  
TGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGG  
AGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCTAGCATCCAGTACGACAAACAGCACGTCT  
GTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACTGCTTCAGGAAACATA  
CCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGCAGCTTCCCATCCCTGG  
CTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACATCGCCC  
TCATGAAGCTGCAGTTCCCCTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCT  
TTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGA  
ATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGT  
GCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGG  
AAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGGCCCTGATGTACCAATCTGACCAGT  
GGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAAGGAGTAT  
ACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG**TAAT**GTCT  
GCTGCCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCTGGGGATCCCCCAA  
AGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCATTTCTT  
GGAGCAGCAAAGGGCCTCAATTCCCTGTAAGAGACCCCTCGCAGCCCAGAGGCGCCAGAGGAAG  
TCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACT  
GAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTACTGAATGGAAGC  
AGGCTGTCTTGTAAAAGCCCAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCA  
GCCCTGTCCGTCTTACCCATCCCCAAGCCTACTAGAGCAAGAAACCAGTTGTAATATAAAAT  
GCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTTCATTGTTATTACAGCTATGG  
CCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAAAAAAAA

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**FIGURE 330**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVVLIVILDKYYFL
CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSA
CFDNFTEALAEACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPGCLSGSLVSLHCL
ACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWVLTAAHCFRKHTDVFNWK
VRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTP
ATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC
QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

**Transmembrane domain:**  
amino acids 32-53 (typeII)



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**FIGURE 331**

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCTGCTGGC  
TCCAGGACTTTGGCCATCTATAAAGCTTGGCA**ATG**AGAAATAAGAAAATTCTCAAGGAGGACG  
AGCTCTTGAGTGAGACCCAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTTCGAAATCA  
ATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTTCTCCCTAGCTGTGGTGGTCATCTACC  
TGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGCGCGGC  
TCCGGGTCTTGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGTCCTTCT  
CCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTGCAAGTCC  
TGCAGGCCCCAATCACCCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGTAGACAACCT  
TCACTCAGAACCAGGGATGTTTCAGAATCAAAGGTGAACAAGGCGCCCCAGGTCTTCAAGGTC  
ACAAGGGGGCCATGGGCATGCCTGGTGGCCCTGGCCCGCGGGACCACCTGCTGAGAAGGGAG  
CCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGGCCACCGGGAG  
TCAAGGGAGAGGCGGGCCTCCAAGGACCCAGGGTGCTCCAGGGAAGCAAGGAGCCACTGGCA  
CCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATTGGCCCCAAAAGGGG  
AAACTGGAATAAGGGAGAGAAAGGAGACCTGGGTCTCCCAGGAAGCAAAGGGGACAGGGGCA  
TGAAAGGAGATGCAGGGGTTCATGGGGCCTCCTGGAGCCCAGGGGAGTAAAGGTGACTTCGGGA  
GGCCAGGCCCACCAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGATCAAGGACAACCTGGAC  
TGCAGGGTGTTCCGGGCCCTCCTGGTGCAGTGGGACACCCAGGTGCCAAGGGTGAGCCTGGCA  
GTGCTGGCTCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGAGTCCAGGAGCCACAGGCC  
TGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGAAGAAAAGGAGAATCAGGAG  
TTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGGGCTGGCAGGTCCCAAGGGAG  
CCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAGGATCTTCTGGGGAGCAAGGAG  
TAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCCGTCAGGATTGTCGGCAGTAGTA  
ACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGGGACAATTTGCGATGACGAGTGGC  
AAAATTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTACTCCAAAGGAAGGGCCCTGTACA  
AAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAATGTTTCACTGTCGGGGCACGGAGAGTA  
CCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCATGACTGCAGCCACGAGGAGGACGCAG  
GCGTGGAGTGCAGCGT**TGA**CCCCGGAACCCCTTTCACTTCTCTGCTCCCAGGTGTCCTCGGG  
CTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGTTCCCTGGGGACAACCTGAGCAGCCTCTGG  
AGAGGGGCCATTAATAAAGCTCAACATCATTGA

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**FIGURE 332**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886  
><subunit 1 of 1, 520 aa, 1 stop  
><MW: 52658, pI: 9.16, NX(S/T): 3  
MRNKKILKEDELLSETQQAAFHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGLL  
VVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLQLQSAHPGEHLAQGASRLQVLQAQLTWVRVS  
HEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRDGAT  
GPSGPQGPFGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGEKGDL  
GLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPAGKGDQGPGLQGVPPGAV  
GHPGAKGEFPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGTGLQGGQGRKGESGVPGPAGVKGEQ  
GSPGLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGRAEVYYSG  
TWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLNDNVQCRGTESTLWSCTKNSWG  
HHDCSHEEDAGVECSV

**Transmembrane domain:**

amino acids 47-66 (type II)

**N-glycosylation sites.**

amino acids 43-47, 83-87, 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 432-440

**N-myristoylation sites.**amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,  
400-406, 441-447, 475-481, 490-496, 515-521**Amidation site.**

amino acids 360-364

**Leucine zipper pattern.**

amino acids 56-78

**Speract receptor repeat**

amino acids 422-471, 488-519

**Clq domain proteins.**

amino acids 151-184, 301-334, 316-349

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**FIGURE 333**

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTGAGGGGCTG  
CCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATACCATGTTCT  
CCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCTGGC  
TGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCAACTG  
CTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGTGGGAG  
GCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTCAGCGAGCCTAGAGAGGGCAGACTA  
TCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGAAGACCGG  
GGCACTTGTGGGTGTCAGAGCCCCTCAGCC**ATG**TTGGGAGCCAAGCCACACTGGCTACCAGGT  
CCCCTACACAGTCCCGGGCTGCCCTTGTTCTGGTGCTTCTGGCCCTGGGGGCCGGGTGGGCC  
CAGGAGGGGTGAGAGCCCGTCTGTGGAGGGGGAGTGCCTGGTGGTCTGTGAGCCTGGCCGA  
GCTGCTGCAGGGGGGGCCGGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGCGAGTGGCATT  
GCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGCACCAGTGGGGCC  
ATCTACTTCGACCAGGTCTTGGTGAACGAGGGCGGTGGCTTTGACCGGGCCTCTGGCTCCTTC  
GTAGCCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCATGTGGTGAAGGTGTACAACCGCCAA  
ACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCATCTCAGCCTTTGCCAATGATCCT  
GACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGACCCTGGGGACCGAGTG  
TCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACTCAAGTTTCTCTGGCTTC  
CTCATCTTCCCTCTCT**AG**AGGACCCAAGTCTTTCAAGCACAGAATCCAGCCCCTGACAACCTTT  
CTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAGACTCCCTCTGGCTCCTATC  
CCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAGTTTAAGAGAAGAGTAGAGCTGTGGC  
ATCTCCAGACCAGGCCTTTCCACCCACCCACCCCCAGTTACCCTCCAGCCACCTGCTGCATC  
TGTTCCCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCAAGAAGGAAGATCTGCACTACTT  
TGCGGCCTCTGCTCCTCCGGTTCCCCCACCCAGCTTCCTGCTCAATGCTGATCAGGGACAGG  
TGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCCAGATGGACAAGCCTCAGCGTACCCTG  
CAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATCTCAGCCAGCACCGTCAGAAGCTGAG  
CCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCACAGGCAGAAGGGTGGGAAGGGCCTGGA  
GTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTGTCTAGACTGAACATGGTACACATTCTG  
CATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCTGGCTGTCTTCTATGCTGGATCCCAGAT  
GGAATCTGGCCCTTACCTCCCCACCTGAGATTAGGGTGAGTGTGTTTGCTCTGGCTGAGAGCA  
GAGCTGAGAGCAGGTATACAGAGCTGGAAGTGGACCATGGAAAACATCGATAACCATGCATCC  
TCTTGCTTGCCACCTCCTGAAACTGCTCCACCTTTGAAGTTTGAACCTTTAGTCCCTCCACAC  
TCTGACTGCTGCCTCCTCCTCCCAGCTCTCTCACTGAGTTATCTTCACTGTACCTGTTCCAG  
CATATCCCCACTATCTCTCTTCTCCTGATCTGTGCTGTCTTATCTCCTCCTTAGGCTTCCT  
ATTACCTGGGATTCCATGATTCATTCCTTCAGACCTCTCCTGCCAGTATGCTAAACCTCCC  
TCTCTCTTTCTTATCCCGCTGTCCCATTTGGCCAGCCTGGATGAATCTATCAATAAAACAAT  
AGAGAATGGTGGTCAGTGAGACACTATAGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGA  
TCGGGTGTTACAGGTACAAGTAGGTATGTTGCAGAGGAAAATAAATATCAAAGTGTATACTAA  
AATTAAAAA

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**FIGURE 334**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLERGECLVVCEPGRAAAGGPGGAA
LGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVYSF
RFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRGNLL
GGWKYSSFSGFLIFPL
```

**Signal peptide:**  
amino acids 1-32

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FIGURE 335

[illegible]

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**FIGURE 336**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRSK
VEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIYFTWLVFDWNTPKKGGRSQW
VRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFPGIR
PYLATLAGNFRMPVLRREYLMMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSMPGKN
AVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFAPCIFH
GRGLFSSDTWGLVPYSPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDKHKTKFG
LPETEVLEVN
```

**Important features of the protein:****Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

**FIGURE 337**

[illegible]

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**FIGURE 338**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFFVVSGLVINVFQLCTLALWPVSKQLYRRLNCRLAYSLWSQLVM
LLEWWSCTECTLFQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKKEL
LYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSM
EVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKKYEAD
MCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLNFLSWA
TILLSPLFSFVLGVFASGSPLLIITFLGFVGAASFGVRRLLIGESLEPGRWRLQ
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169



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**FIGURE 339**

GATATTCTTTATTTTAAAGAATCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCCTGGGGCAG  
CCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTTGC  
TTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCGGCT  
TACGCCTGATACGGCCCTGGGTAGAAAGGGAAGGGAAGATAAACTTTTATACAAATGGGGATA  
GCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCCTGGGATCTGCCTATACCTTCTTTTCTC  
TAACCTGGCATAACCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAAAGTATT  
TAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGTACATGTG  
GTGTTCTCTTGTTCGTTCTG**TAA**TGTGGTATGCCATGGGGTCTTGCACAAGCCTTTCCTCTT  
TGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTCATCCTGCAG  
ATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCATCTTGTTTAAT  
GCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTATCTTTATGTGC  
GTTTGTGGTTGTATGGGTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGCTGCGTGAGGGTC  
AAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCTCATGTTTTAGAGA  
CTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCAGATGGTGTAGGGCC  
CAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGATGCAGGTCCTGATTC  
AGTAGGCCCAGGTTGGGCATCTCTAACAACTCCCACGTGATGCTGATGCTGGTCTTATGAAC  
TATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGCTCACACCTATGATCCCA  
GCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATTTCAAGACTAGCCTGGCCA  
ACATGGTGGAAACCCCATCTGTACTAAAAATACACAAATTAGCTGGGCATGGTGGCACATGCCT  
GTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTGAACCTGGGAGGCGGAGGTTG  
CAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGACAGAGTGAGACTCTATGTCCAA  
AAAAAAAAAA

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**FIGURE 340**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHS LQCPGAATRH IHL CVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRRE
GKINFY TNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWSGP
CPPGQLHCTCGVLLSFL
```

**Important features of the protein:****Signal peptide:**

amino acids 1-28

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**FIGURE 341**

CGCCATGGCCGGGCTATCCCGCGGGTCCGCGCGCGCACTGCTCGCCGCCCTGCTGGCGTCGACG  
CTGTTGGCGCTGCTCGTGTGCCCCGCGCGGGTTCGCGGCGGCCGGGACCACGGGGACTGGGAC  
GAGGCCTCCCGGCTGCCGCCGCTACCACCCCGCGAGGACGCGGCGCGCGTGGCCCGCTTCGTG  
ACGCACGTCTCCGACTGGGGCGCTCTGGCCACCATCTCCACGCTGGAGGCGGTGCGCGGCCGG  
CCCTTCGCCGACGTCCTCTCGCTCAGCGACGGGCCCCCGGGCGCGGGCAGCGGCGTGCCCTAT  
TTCTACCTGAGCCCGCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTACACTG  
ACCATGACTTTGGCACAGACCAACTTCTGCAAGAAACATGGATTTGATCCACAAAGTCCCCTT  
TGTGTTACATAATGCTGTCAGGAACGTGACCAAGGTGAATGAAACAGAAATGGATATTGCA  
AAGCATTCGTTATTCATTCGACACCCTGAGATGAAAACCTGGCCTTCCAGCCATAATTGGTTC  
TTTGCTAAGTTGAATATAACCAATATCTGGGTCTTGGACTACTTTGGTGGACAAAAATCGTG  
ACACCAGAAGAATATTATAATGTCACAGTTCAGTGAAGCAGACTGTGGTGAATTTAGCAACAC  
TTATGAAGTTTCTTAAAGTGGCTCATAACACACTTAAAAGGCTTAATGTTTCTCTGGAAAGCGT  
CCCAGAATATTAGCCAGTTTCTGTC

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**FIGURE 342**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269  
><subunit 1 of 1, 220 aa, 1 stop  
><MW: 24075, pI: 7.67, NX(S/T): 3  
MAGLSRGSARALLAALLASTLLALLVSPARGRGGRDHGDWDEASRLPPLPPREDAARVAR  
FVTHVSDWGALATISTLEAVRGRPFADVLSLSDGPPGAGSGVPYFYLSPLQLSVSNLQEN  
PYATLTMTLAQTNFCKKHGFDPQSPLCVHIMLSGTVTKVNETEMDIKHSLEFIRHPMKT  
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTVQ

**Important features of the protein:****Transmembrane domain:**

Amino acids 11-29

**N-glycosylation sites:**

Amino acids 160-164;193-197;216-220

**N-myristoylation sites:**

Amino acids 3-9;7-13;69-75;97-103

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**FIGURE 343**

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGAT  
TATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTCAGCAACTAAAAAGCCACAG  
GAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTACATT  
AAAATCTGTTTTTTGTTCTCTTGTAACCTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACT  
GTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGT  
CCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAAC  
TGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTAGCTGCGG  
CTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGAT**TG**ACAAGCCCCGAAGATTTTCATAGGCG  
ATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGG  
GCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCCGCCATCTAACCTTTT  
CATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACCTCTGTCCCAAGGAACCCAGAGCT  
TGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGA  
CTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACTTG  
TGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGC  
ATTGAGTGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACTCGGGACTCACCTCTG  
GGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTGAAGGGCAACTGCAGGC  
CGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAGCCAGGGGCAGCCGCTG  
GGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCCTCCTTCCCTCTGAGAGGCCCTCCTATGT  
CCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATGGCTCAGTGTGGCCAGGA  
GGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCGAACACGGAAATGCCTCCAGT  
AAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCTCAATTTAAATCATGTTCTAGT  
AATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTTCAAATGATCTCCAAGGGCCCT  
TATACCCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCAAACCTAAGAACCAGGTGCA  
TTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACATTTTGGGAGGCCGAGGCG  
GGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTC  
TACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATCCCAGCTACTCGGG  
AGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACAGGAGAATCACT  
TCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTATGGTTATTT  
GTAA

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**FIGURE 344**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTAS
PCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
```

**Signal peptide:**  
amino acids 1-15

FIGURE 345

[illegible]

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**FIGURE 346**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

&gt;&lt;subunit 1 of 1, 671 aa, 1 stop

&gt;&lt;MW: 74317, pI: 7.61; NX(S/T): 0

MPHAFKPGDLVFAMKGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYDK  
CKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDDEDRGVM  
AVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSEEN  
SESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPVAMAR  
SASSSSSSSSSSSDSDSVKPPRRGRKPAEKPLPKPRGRKPKPERPPSSSSSSSDSDSDEVDRISE  
WKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGDELREDD  
EPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKKSAKKPQSSSTEPARKPGQKEKRVRPPEKQQ  
AKPVKVERTRKRSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNALEELG  
TLQVTSQILQKNTDVVATLKKIRRYKANKDVMEKAAEVYTRLKSRVLGPKIEAVQKVNKAGME  
KEKAEKLAGEEELAGEEAPQEKAEDKPSTDLAPVNGEATSQKGESAEDKEHEEGRDSEEGPR  
CGSSEDLHDSVREGPDLDPRGSDRQERERARGDSEALDEES

**Signal peptide:**

amino acids 1-13



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**FIGURE 347**

GTGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA  
ACACCATTGAAAGAGAACATTGTTTTTCATCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA  
TTTTACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTCCAGTCACTGGCACTTTGAAGCA  
AAATATTTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCTTTTTGGGTTTCATC  
AGAAGGACTGGATTTTCAAACCTCTTCTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACCACAT  
CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTAAGAAGATTATTGGCCTGCTGCAAGGAACGGGTGGA  
ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAATTTTCATCAGAGTACTTCAGCCCTATAACAA  
AACTCACATATATGTGTGTGGAAGTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA  
GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTTCGATCCTCAGCAGCC  
TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAGATACTGCATT  
CACTCGATCCCTTGGGCTACTCATGACCACCACTACATCAGAACTGACATTTTCAGAGCACTACTGGCTCAATGG  
AGCAAAATTTATTTGGAACCTTTCTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTTTCG  
TGAATCATCTCAAGAAAGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGAAGAATGATGT  
AGGAGGACAACGCAGCCTGATAAACAAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG  
TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT  
AGTATATGGAGTCTTTACTACAACCAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATAGCATGGCTGACAT  
CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAT  
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCAGA  
TGATGTCATCAGTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGAGGACCAACGTT  
CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTTCATTGCAGAAGATGGCCAGTACGA  
TGTAATGTTTCTTGAACAGACATTGGAACGTCTCTCAAAGTTGTGAGCATTTCAAAGGAAAAGTGGAAATATGGA  
AGAGGTAGTGCTGGAGGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTGTCTCTGAAGCA  
GCAACAATTTGACATTTGGTTCCCGAGATGGATTAGTTGAGCTCTCCTTGCACAGATGCGCACTTATGGGAAAGC  
TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCTGGGATGGAATGCATGCTCTCGATATGCTCCTAC  
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAATAATATGGCGACCCAATCACCAGTGCTGGGACATCGAAGACAG  
CATTAGTCATGAAACTGCTGATGAAAGGTGATTTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC  
TAAATCCCAACAAGCAACTATTAATGGTATATCCAGAGGTGAGGGGATGAGCATCGAGAGGAGTTGAAGCCCGA  
TGAAAGAATCATCAAACGGAATATGGGCTACTGATTGGAAGTTGCAGAAGAAGGATTCTGGGATGTATTACTG  
CAAAGCCCAGGAGCAGACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCATTGAGAATGAACAGATGGA  
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCGAGGTCAAGGATCTATTGGCTGAGTCACGTTGAGATACAAAGA  
CTACATCCAAATCCTTAGCAGCCAAACTTCAGCCTCGACCACTGCGAACAGATGTGGCACAGGGAGAGCG  
GAGACAGAGAAACAAGGGGGGCCAAAGTGAAGCAGATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCA  
CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTAGTTTTCTACTTAATTTAAAGAAAAGAATTCCTTACC  
TATAAAAACATTGCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTTGCTAAGG  
CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAATTCATTTGAACAGTTTT  
CCAAGAACAATCTTGACAAGCAAAGTATAAGAATTATCCTAAAAATAGGGGGTTTACAGTTGTAAATGTTTTA  
TGTTTTGAGTTTTGGAATTTATGTGATGTAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGTATAAGGT  
GCTTTATTCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT  
CATTCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTGAGACACAATTAAGACAACCTCCCATATC  
AACAGGAACCTTTCTCAGTGAGCCATTCACTCCTGGAGAAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC  
TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT  
ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA  
GCTCTACAGGGACAGAATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTTAAATAAACAAGGAAAACA  
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT  
AAATTTCTGGCTTTGGGGAAAACCTCATATCCCCATGAAAAGGAACAATCACAAATAAAGTGAGAGTAATGTAA  
TGGAGCTCTTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAATCTAGATTATAACA  
AACTGCTAGCAAAATCTGAGGAAACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTTATAACC  
AATGATATTTTCAATATATATTTCTCTCTTTTAAAAAATATTTATCATACTCTGTATATTATTTCTTTTACTGC  
CTTTATTTCTCTCTGTATATTGGATTTTGTGATTATATTTGAGTGAATAGGAGAAAACAATATATAACACACAGA  
GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATATTTGTTGAATAACAGAACGAGTGTAAATTTTAAAC  
AACGGAAGGGTTAAATTAACCTTTTGACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAATT  
GTAGTATTGTTTTGTAATTTAACAATAAATAAGCCTGCTACATGT

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**FIGURE 348**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

&gt;&lt;subunit 1 of 1, 777 aa, 1 stop

&gt;&lt;MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTYKDLLLSNSCIPFLG  
SSEGLDFQTLTLLDEERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDANT  
ECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFDPPQ  
PFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHHYIRTDISEHYWLNAGAKFIGTFFIPDT  
YNPDDDKIYFFFRESSQEGSTSDKTIILSRVGRVCKNDVGGQORSLINKWTTFLKARLICSIPGS  
DGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGPYAHKES  
ADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDVISFIKRHSVMYKSVYPVAGGPTEK  
RINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEELQIFKHSS  
IILNMELSLKQQQLYIGSRDGLVQLSLHRCPTYGKACADCCCLARDPYCAWDGNACSRYPATSK  
RRARRQDVKYGDPITQCWDIEDSISHETADEKVIIFGIEFNSTFLECIPKSQQATIKWYIQRSG  
DEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTNLNVIENEQMENTQ  
RAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRNKGGPKWKHMQEM  
KKKRNRRHHRDLDELPRAVAT

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

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**FIGURE 349**

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTCATCCTGGAGCATGCCCCACCGCGGGGAGCAGA  
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC  
CTCAGCAGTTTTAGCCAGCAGGGACTGATCAGGTGTGTCTCTGGAGTGGGGAGCAGAAGCGTGGCTGGCAAGA  
GTGGCCTGGAGAAAGAGGTTTACGCGCTTGACCAGCCGAGCTGCCCCGTGACTACAAGATCCAGACCATGGGCATC  
GGGTGAGGTGGGGGGGCACAGGTGTCATGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG  
AGCCATTGAGGGTGTCTGAGCTACAGAGGGGAGGGAAGGTATTTTAAGGTACAGTGTGGCACAATAGTTAA  
GAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTTCTTCTGTGCTTCTTAGTTCTGTAGCCCCAGGT  
AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT  
AGGGAAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG  
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT  
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCGAGAGAGCATCCGCCGGGCACAGGTGAGCC  
AGGTGAAGGGGGCTGCCCCGGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA  
TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGCGGCTCAGTGAGGCTCGGCTGTCCCAGAGGGACCTCTCTC  
CAACCGCTGAGGATGCTGAGCTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCCC  
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCCGACACGTCGACAGCTGGTATTTTCGCTATCAGGCAGGGCTGAGGATG  
AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTCATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA  
ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCCAGAGAGCAGCC  
AAGACAGTGACAATCCCTGCGGGGCAGAGCCACAGCATTCCTGGCACAGGCCCTGTACAGCTACACCGGACAGA  
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCCGGGCCCCAAGATGGAGTAGATGACG  
GCTTCTGGAGGGGAGAAATTGGGGGCGGTGTTGGGGTCTTCCCTCCCTGCTGGTGGGAAGAGCTGCTTGGCCCCC  
CAGGGCCACCTGAACCTCTCTGACCCTGAACAGATGCTGCCGTCCCCTTCTCTCCAGCTTCTCCCCACCTGCAC  
CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCCTGG  
ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCCGGCTAAAGCCCCGGATCCTGGCCACC  
CAGATCCCCTCACCTGAAGGCCAGGGAAGCCTTGACCCCCAGTGATGCTGTCTTCTTCAAGCTGTTCAGA  
CCACACCATCAATGATCCAGAGCAACACAGCCAAAGCTGGAATCGCCCTTATTTCCACCCCTCACCTCCAAGGGT  
GGAAACTTGCCCCCTCCCATTTCTAGAGCTGGAAACCCACTCCTTTTTTTTCCATTGTTCTATCATCTCTAGGACC  
GGAATACTACCTTCTCTTCTGTCTGATGCCCTATCTAGGGTGGTGAATGCCTGAAATCTCTGGGGCTGGAAACC  
ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTTCCCCACCTGGCTCCATGACCCACCCCACTCTGGATG  
CCAGGGTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG  
CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCCTGGGCCTCTTGTG  
CTAAGAGGGGAGGGGGCTACGGTGCTATTGCTTTAGGGGCCACACGGGCAGGGGCTGCTCCAGCTGCCAC  
GCTCTATCATATGGAGCGAGGTGTTGGGGAAGGCGGGGCAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAC  
TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC  
AGCTGGGGGGCAGTGCTGTCCAGTGGAGGGGAGGGCTTTCACGCCCCACCCACCCCTGGCCCTGCCAGCTGGTAG  
TCCATCAGCACAAATGAAGGAGACTTGAGAGAAGGAAGAATAACACTGTTGCTTCTGTTCAAGCTGTGTCCAGC  
TTTTCCCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGGATTTATAGCAAAGGCTAAGCCTGC  
AGTTTACTCTGGGGGTTAGGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA  
TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG  
TCAACAATGAGAGACCAGGAGTAGGTCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCCAGCCCAGTGC  
AGTCCCCGGCTGTGTTTTCTACCTGGTGATCAGAAGTGTCTGGTTTGGCTGGCTGCCCATTTGCCCTCTTGTAGTGG  
GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTTGGCTCTGCAGAAGCTCTGGGGTTCCCTTCAAGTG  
CACGAGGGGTTAGGCTGCTGTCCCTGAGTCTCCATTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC  
TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCCAGACCCCTGACCACCCCTG  
GGTCTGTCCCCCACCAGAGCCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT  
TCTCAATGTGTGTACCCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG  
GCCCTCCCCCTGTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCCTTCTC  
AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAGACCAAGGCCCACTT  
TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTCCCTGGAGCACCTGCCCACTGCCCA  
CAGAGAACACAGTGGTCTCCCTGTCCGGGGGCGGCTTTTTCTTCTTGGAGCGTCCCTGACGGACAAGTGGAG  
GCCTCTTGTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC  
CGTCTGCAAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTTCCCT  
TCATGTTTTGTTTCTTACGTTCTTTACGATGCTCCTTAAACCCCAAGCCCCAATTTCCCCAAGCCCCATTT  
TTCTTGTCTTTATCTAATAAACTCAATATTAAG

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**FIGURE 350**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRAQ
VSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELSDF
EECEETGELFEEPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEWVKA
RNQHGEVGVFPERYLNFPDLSLPESQSDNPGAEPTAFLAQALYSYTGQSAEELSFPEGAL
IRLLPRAQDGVDDGFWRGEGGRVGVFPSSLVEELLGPPGPPPELSDPEQMLPSPSPPSFSPPA
PTSVLDGPPAPVLPDGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

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**FIGURE 351A**

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA  
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCACAGAGAGTCTACAGAGGGAGAGGCCAGAGAAGCTGCAGA  
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG  
GCACCTCTCCCAAGCCCAAGGACTAAGTTTTCTCCATTTCCCTTAACGGTCCTCAGCCCTTTGAAAACCTTTGCC  
TCTGACCTTTGGCAGGAGTCCAAGCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTGGAGGACTTTGGT  
GCCCTAGACGGCCTCAGTCCCTCCAGCTGCAGTACCAGTGCCATGCTCCAGACAGGCTCGCATCCCGGGAGGGG  
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCAACCTGCCTCCTGCTCCCCATTGTGCCGCTCTCCTGGCTGGTGTG  
GCTGCTTCTGCTACTGCTGGCCTCTCTCCTGCCCTCAGCCCGGCTGGCCAGCCCCCTCCCCGGGAGGAGGAGAT  
CGTGTTCAGAGAAGCTCAACGGCAGGCTCCTGCCTGGCTCGGGCGCCCCCTGCCAGGCTGTTGTGCCGCTTGCA  
GGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGGCTGACAGTGCAGTA  
CCTGGGCCAGGCGCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC  
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGAGCCCTGTTAGGCGTGTACAATATCGGGGGGCTGAACCTCA  
CCTCCAGCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCCTACGCCGAAGAGTCC  
TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGAAGCCCCAGCCCCAGACCCGAAGAGCCAA  
GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGATTCCACGGTGC  
GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAAGGCCTTCAAGCACCCAGCATCCGCAATCC  
TGTGAGCTTGGTGGTGAATCGGCTAGTGATCCTGGGGTCAAGCGAGGAGGGGGCCCCAAGTGGGGCCAGTGCTGC  
CCAGACCTTCGCGAGCTTCTGTGCCTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACCTTTGA  
CACAGCCATTCTGTTTACCCGTGAGGACCTGTGTGGAGTCTCCACTTGCAGACAGCTGGGTATGGCTGATGTGGG  
CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGATGATGGGCTCCAGTCAGCCTTCACTGCTGCTCA  
TGAAGTGGGTGATGCTTCAACATGCTCCATGACAACTCCAAGCCATGCATCAGTTTGAATGGGCCTTTGAGCAC  
CTCTCGCCATGTGATGGCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGCCCGCTT  
CATCACTGACTTCTGAGCAATGGCTATGGGCAGTGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCCTGT  
GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCGGGCCCCGACTCACGCCATTGTCC  
ACAGCTGCCCGCCCTGTGCTGCCCTCTGGTGTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAACA  
CTCGCCCTGGGCCGATGGCACACCCCTGCGGGCCCGCACAGGCCCTGCATGGGTGGTGGCTGCCCTCCACATGGACCA  
GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGGTCTTGGGGACCATGGGGTGAATGCTCTCGGACCTG  
TGGGGGTGGTGTCCAGTTCTCCTCCGAGACTGCACGAGGCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG  
CCGCCGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA  
GTGTGCTGCCATAACACCGCACCGACCTCTTCAAGAGCTTCCCAGGGCCCCATGGACTGGGTTCCTCGCTACAC  
AGGCGTGGCCCCAGGACCAAGTGCAAACTCAGCTGCCAGGCCCGGCACTGGGCTACTACTATGTGCTGGAGCC  
ACGGGTGGTAGATGGGACCCCTGTTCCCGGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATCCTGCTGG  
CTGTGATCGCATCATTGGCTCCAAGAAGAAGTTTGACAAGTGCATGGTGTGCGGAGGGGACGGTCTGGTTGCAG  
CAAGCAGTCAGGCTCCTTCAGGAAATTCAGGTACGGATACAACAATGTGGTCACTATCCCGCGGGGGGCCACCCA  
CATTCTTGTCCGGCAGCAGGGAACCCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA  
TGCCCTCAATGGTGAATACAGCTGATGCCCTCCCCACAGATGTGGTACTGCCTGGGGCAGTCAGCTTGGCCTA  
CAGCGGGGCCACTGCAGCCTCAGAGACACTGTGAGGCCATGGGCCACTGGCCAGCCTTTGACACTGCAAGTCTT  
AGTGGCTGGCAACCCCCAGGACACAGCCTCCGATACAGCTTCTTCGTGCCCGGGCCGACCCCTTCAACGCCACG  
CCCCACTCCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCGGCGGCGCCCCCTGGGCGGGCAG  
GAAATAACTCACTATCCCGGCTGCCCTTTCTGGGCACCGGGGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTT  
CTGTGCTGCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCGTGAGACCTGCCCCCTCCTCTCTGCCCTAAT  
GCGCAGGCTGGCCCTGCCCTGGTTTCTGCCCTGGGAGGCGATGATGGGTAGTGGATGGAAGGGGCTGACAGAC  
AGCCCTCCATCTAAACTGCCCCCTCTGCCCTGCGGGTACAGGAGGGAGGGGGAAGGCAGGGAGGGCCTGGGCC  
CAGTTGATATTTATTTAGTATTTATTTCACTTTTATTTAGCACAGGGAAGGGGACAAGGACTAGGGTCTGGGGAA  
CCTGACCCCTGACCCCTCATAGCCCTCACCCTGGGGCTAGGAAATCCAGGGTGGTGGTATAGGTATAAGTGGTG  
TGTGTATGCGTGTGTGTGTGTGTGTGAAAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTTCTC  
TTCTGAATTTTATTTTGGGAAAAGAAAGTCAAGGGTAGGGTGGCCCTTCAGGGAGTGAGGATATCTTTT  
TTTTTTTTCTTTCTTTCTTTCTTTTCTTTTGGAGACAGAATCTCGCTCTGTGCCCCAGGCTGGAGTGCAATG  
GCACAATCTCGGCTCACTGCATCCTCCGCCTCCCGGGTCAAGTGATTCTCATGCCTCAGCCTCCTGAGTAGCTG  
GGATTACAGGCTCCTGCCACACGCCCAGCTAATTTTGTGTTTGTGTTTGGAGACAGAGTCTCGCTATTGTC  
ACCAGGGCTGGAATGATTTCACTCACTGCAACCTTCGCCACCTGGGTCCAGCAATTCTCCTGCCTCAGCCTCC  
CGAGTAGCTGAGATTATAGGCACCTACCACACGCCCCGCTAATTTTGTATTTTGTAGTAGAGACGGGGTTTTCAC  
CATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTTAGTGATCCACTCGCCTCATCTCCAAAGTGCTGGGATT  
ACAGGCGTGAGCCACCGTGCTGGCCACGCCCCAATAATTTTGTATTTTGTAGTAGAGACAGGGTTTCAACATG  
TGCCAGGCTGCTCTTGAACCTCTGACCTCAGGTAATCGACCTGCCTCGGCCTCCCAAGTGCTGGGATTACAGG

**FIGURE 351B**

[illegible]

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**FIGURE 352**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

&gt;&lt;subunit 1 of 1, 837 aa, 1 stop

&gt;&lt;MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLLASLLPSARLASPLPREEEIVF  
PEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYILGQAPELLGGAEPGT  
YLTGTINGDPESVASLHWDGGALLGVLYRGAEHLQPLEGGTPNSAGGPGAHLRRKSPASG  
QGPMCNVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAAAKA  
FKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHFDTAIL  
FTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHDNSKPCI  
SLNGPLSTSRHVMAFVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHLPVTFPGK  
DYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGG  
RCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRPVPRNGGKYCEGRTRFR  
SCNTEDCPTGSALTFREEQCAAYNHRDLEFKSFPGPMDWVPRYTGVAPODQCKLTCQARALGY  
YYVLEPRVVDGTPCSPDSSSVQVQGRCIHAGCDRIIGSKKKFDKCMVCGGDGSGCSKQSGSFR  
KFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTLMPSPTDVVLPGA  
VSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPTPSTPRPTPQDWLH  
RRAQILEILRRRPWAGRK

**Important features of the protein:****Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-  
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-  
582, 679-684, 682-687, 763-768**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 358-367

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**FIGURE 353**

GC GGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCCC  
GGCTGGCCTAGGCAGGCAGCCGCACC**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCTGC  
TCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGACAG  
CGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAGTGTG  
TGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCCCCAAG  
ACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCTGCGCCT  
GCGCCGTCATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACCACCTTTG  
CCATCCTCGGCGGCACCCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGTCTCCTGGA  
CCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGAAGTTTGAGA  
TTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGTGGCACCCCTGC  
TTTGCCTGTCTTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCCAGGGCCACCA  
CGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAGACAATCGGGCCC  
CCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG**TGA**GTCCCCACAG  
CCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGGG  
TTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATAATGTGAATGCGAGGA  
AATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAAAGCTCTCTATACCAAA  
GACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATATTTATGTGGGTGATTTGA  
TAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGTTGGTTTGTGATCCAGGAA  
TAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA



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## **FIGURE 354**

MASTAVQLLGFLLSFLGMVGTLLITLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQ  
CQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTLFI  
LAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSLSLIGGTLLCLSCQDEA  
PYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

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**FIGURE 355**

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGC  
AGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCTCC  
TGTCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCAGCCAGG  
ACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGA  
GGCAGAGTTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGCCATGC  
TGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCCTGGTAT  
CCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCCAACATGA  
CACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTGTCTGTGT  
TTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTG  
GGATGGTGCAGACTGTTTACAGACCAGGTACACATTTGGTGCAGGCTCTGTTTCGTGGGCTGGGTG  
CTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTCATCGCCTGCCGGGGCCTGGCACCAG  
AAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTGCCTACAAGCCTG  
GAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAGATATACGATGGAG  
GTGCCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCAGCACTATGTG**TAA**TGCTCTA  
AGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAAACAAGGAGATCCCA  
TCTAGATTTCTTCTTGCTTTTGAATCACAGCTGGAAGTTAGAAAAGCCTCGATTTTCTCTTTG  
GAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACAGCTGAG  
TTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTCTCTCACATTTTGATGATTTAGACAG  
CTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAG  
ACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCCAAG  
AAAACTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTTGTCTC  
CCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATT  
TGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTGTGATCTTAAAGTTACCAAACCA  
AAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTGCTGTTGACATCTTCTTATTACAGC  
AACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCCTCTTCTGTGCGGGTGCAGAAA  
TTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAATTTAAGTCCTAAATATAGTTAAATAA  
ATAATGTTTTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAG  
AAGGAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAA  
GTACAAATTCCATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGG  
ATCACTTGAGCCCAGAAGTTCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAA  
ATACAGAGAGAAAAAATCAGCCAGTCATGGTGGCATACACCTGTAGTCCCAGCATTCGGGGAG  
GCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGTTGGGGCTGCAGTGAGCCATGATCACACC  
ACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAAATAAAAAATAAATAATGGA  
ACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTTAA

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**FIGURE 356**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

&gt;&lt;subunit 1 of 1, 261 aa, 1 stop

&gt;&lt;MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTEC  
RPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFI  
VSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGG  
VMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQ  
SYPSKHDYV

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

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**FIGURE 357**

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGG  
AGTCCAGCTGGCTAAAACTCATCCAGAGGATAATGCAACCCATGCCTTAGAAATCGCTGGG  
CTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGA  
GTGTCGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTGGATG  
AATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTT  
TCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTCCGTGATGTCCTTCTTGGCT  
TTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAG  
GCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGCTCATCCCT  
GTGAGCTGGGTGCGCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAATGTTGCCCAA  
AAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTTGGA  
GGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATA  
CCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCGTCTACTCC  
AGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATGACA  
AAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTACTGTTCTTAACTGC  
CTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTTCAGCAGAA  
TGAGATATTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGG  
TTCAAGCATCTACTCTTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTT  
ACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAGTGTAACATTTATATCTCA  
CATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAAT  
AGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAGAAGGTTACTATTAATTG  
TTTAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGAAGATTAATAAAGGCTTTTAA  
TCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAGAA  
ATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTTCTTGTGTATTAAATTAACATT  
TTTAAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCAAACCTGCTTTTCCAGGGCTATACTC  
AGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTGAAAATATTTTT  
GTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGATATATTT  
TAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATAT  
GTCTTGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTC  
ACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTTGTTCTGTGAAAAATAAATTC  
CTTCTTGTAACCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTATT  
CCAAATTTGATGAAACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCTAGCTTAAAT  
GAATGTGTTCTATTTGCTTTATACATTTATATTAATAAATTGTACATTTTTCTAATT

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**FIGURE 358**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

&gt;&lt;subunit 1 of 1, 225 aa, 1 stop

&gt;&lt;MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRMQ  
CKIYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIF  
IITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCN  
EKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

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**FIGURE 359**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCCC  
GCCGCC**ATG**GCTGCCTCCCCGCGCGGCCTGCTGTCTGGCCCTGACCGGGCTGGCGCTGCTC  
CTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAAAAA  
CGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGAATTC  
CTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGCAGCAG  
TGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATCACCTAT  
TGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCACATATGAT  
GAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCGTCAACTAC  
GATGACTAC**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCTCTTCATGT  
ATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGATCTTTTCTACC  
TACTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTTTGATATTTTCAT  
GGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

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**FIGURE 360**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

&gt;&lt;subunit 1 of 1, 148 aa, 1 stop

&gt;&lt;MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLLMLQKREAPVPTKTKVAVDENKAKEFLG

SLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDYYQRHYDED

SAIGPRSPYGFRHGASVNYDDY

**Signal peptide:**

amino acids 1-30

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FIGURE 361

[illegible]



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**FIGURE 362**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

&gt;&lt;subunit 1 of 1, 148 aa, 1 stop

&gt;&lt;MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCIAFVESKFNISKIN  
ENADGSFDYGLFQINSHYWCNDYKSYSENLC HVDCQDLLNP NLLAGIHCAKRIVSGARGMNNW  
VEWRLHCSGRPLSYWLTGCRLR**Signal peptide:**

amino acids 1-18

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**FIGURE 363**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCAC  
CAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAGCA  
GAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTCAAT  
TTGAAGTCCCTGTGAATGGGCTTTTCTGATTGTAAGTGAAGCAGGTCTTGCACACGCTGTTG  
GGTGAACTTGGGTCTGTGGTTTTCTGATTGTAAGTGAAGCAGGTCTTGCACACGCTGTTG  
GCAAATGTCAGGACCAGGTAAAGTGAAGTGGCAGAAAACTTCCAGGTGGAACAAGCAACCCAT  
GTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGACCTGTTGC  
ATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATGCAGACTCC  
AGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGTTGCACCCTC  
CCCACCACACCCTGCACCAGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCTGAAGCCAGGT  
ACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGAGGGTGAAGAGT  
ACAGCCCTCTGGAGGGCCTGCCACCTTTATCTCACTGCGGGAGGATCAGCTGCTGGTGGCCG  
TGGCCTTACCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGGAGCTACCGCCTCA  
TCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGGGGCTGATGAGGACG  
GGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTTCAAGCCTGGACCCACGTGGCCTCCAGGAGG  
CACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGGCACCCACTGTGTCTGC  
AGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTGTTTCCATGATGAGGCCT  
GGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGCCCAAGGGCCTTCCCTGAAGG  
AGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAGTCTGCTCTCAGCGAATATG  
TGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAGGCTGGGTGCCATCAGGGCCC  
GGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCTTCAATGGATGCCCACTGCGAGT  
GCCACCCAGGCTGGCTGGAGCCCCCTCCTCAGCAGAATAGCTGGTGACAGGAGCCGAGTGGTAT  
CTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTATTACCCCTCAAAGGACCTGCAGC  
GTGGGTGTTGACTGGAAGCTGGATTTCCACTGGGAACCTTTGCCAGAGCATGTGAGGAAGG  
CCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTGGTGCCCGGAGAGGTGGTGGCCATGG  
ACAGACATTACTTCCAAAACACTGGAGCGTATGACTCTCTTATGTGCTGCGAGGTGGTGAAA  
ACCTCGAAGTGTCTTTCAAGGCCTGGCTCTGTGGTGGCTCTGTTGAAATCCTTCCCTGCTCTC  
GGGTAGGACACATCTACCAAATCAGGATTCCCATTTCCCCCTCGACCAGGAGGCCACCCTGA  
GGAACAGGGTTTCGCATTGCTGAGACCTGGCTGGGGTCATTCAAAGAAACCTTCTACAAGCATA  
GCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGAAGCCAGACTGCATGGAACGCTTGCAGCTGC  
AAAGGAGACTGGGTGTGTCGGACATTCCACTGGTTTTCTGGCTAATGTCTACCCTGAGCTGTACC  
CATCTGAACCCAGGCCAGTTTCTCTGGAAAGCTCCACAACACTGGACTTGGGCTCTGTGCAG  
ACTGCCAGGCAGAAGGGGACATCCTGGGCTGTCCCATGGTGTGGCTCCTTGCAGTGACAGCC  
GGCAGCAACAGTACCTGCAGCACACCAGCAGGAAGGAGATTCACTTTGGCAGCCCACAGCACC  
TGTGCTTTGCTGTGAGGCAGGAGCAGGTGATTCTTCAGAAGTGCACGGAGGAAGGCCTGGCCA  
TCCACCAGCAGCACTGGGACTTCCAGGAGAATGGGATGATTGTCCACATTCTTTCTGGGAAAT  
GCATGGAAGCTGTGGTGCAAGAAAACAATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAG  
CCCGCCAGCAGTGGCGATTTGACCAGATAAATGCTGTGGATGAACGATGAATGTCAATGTCAG  
AAGGAAAAGAGAATTTTGGCCATCAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATT  
TCATGAAGCTGATCCTTTTGTGTGTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAA  
GAATATAGGAAGTTTCTCCTTTTTCACACCTTATTTCAATTGACTGCTGGCTGCTTA

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**FIGURE 364**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

&gt;&lt;subunit 1 of 1, 639 aa, 1 stop

&gt;&lt;MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFGE  
SQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPRRQ  
DKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHPQDS  
LPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVARLEGV  
KLLRSNKRLGAIRARMLGATRATGDVLFVMDAHCECHPGWLEPLLSRIAGDRSRVVSVIDVI  
DWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMDRHYFQN  
TGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIYQNQDSHSPLDQEATLRNRVRIA  
ETWLGSFKETFYKHSPEAFSLSKAEPDCMERLQLQRRLGCRTFHWFLANVYPELYPSEPRPS  
FSGKLHNTGLGLCADCQAEGLGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSPQHLCFVRQ  
EQVILQNCTEEGLAIHQHWFQENGMIVHILSGKCMEAVVQENNKDLYLRPCDGKARQQWRF  
DQINAVDER

**Signal peptide:**

amino acids 1-28

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**FIGURE 365**

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGG  
AGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGC  
AGCCGGGAGCCATGCGACCCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGC  
TGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAA  
AGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAG  
CAGGAGTGCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCC  
CAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCT  
GGACACCCAATACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAA  
TTGCGGAGTGCTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCACTGGCT  
CACTTCGGCTAAAATGCAGAAATGCATGCTGTGAGCGTTGGTATTTACATTCAATGGAGCTG  
AATGTTTCAGGACCTCTTCCCATTTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGA  
ATTCAACAATTAATATTCATCGCACCTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTG  
GATTAGTGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTA  
CTGGATGGAATTCAGTTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTT  
CATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCCTTAAATGACATTTTAAATAAG  
TTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGATTTCA  
CACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGTGGTTTCAATATTTTTTT  
TAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTG  
TGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATATAAAAGCTACCAATCTTTG  
TACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAATAAAAATTATTTCCAACA

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**FIGURE 366**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

&gt;&lt;subunit 1 of 1, 243 aa, 1 stop

&gt;&lt;MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVP  
GRDGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAEC  
TFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMNSTI  
NIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

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**FIGURE 367**

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGGC  
ATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTGCT  
CACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCCGTC  
GGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCCCAGC  
CCCCACCGTCGCGCCAGGACCCGAGGACAGCACC CGCAGGAGCGGCTGGACCAGGGCGGCGG  
GTCGCTGGGGCCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTGCGTGGT  
GCTGGCGCTCGTGGTCTGTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAAGGGGCCG  
CGCCCGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAAA

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**FIGURE 368**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398

&gt;&lt;subunit 1 of 1, 121 aa, 1 stop

&gt;&lt;MW: 12073, pI: 4.11, NX(S/T): 0

MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDGTP  
PAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

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**FIGURE 369**

GGCCGTTGGTTGGTGC GCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGGC  
GGGCCGGGACGGGC**ATG**GCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCACG  
GCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGAACT  
TCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTGAGGGGCGCTGCTCACCGACTGGAGCGACG  
ACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGACCAAG  
TGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCCCCGGGT  
ATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAACGCCATCA  
TCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGGACCCAGCC  
TAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC**TAA**GTAGCCCCCAGAGGCG  
CTGGGAGTGTGGCACCGCCCTCCCCGAAGTTTGCTCCATCTCACGCTGGGGGTCAACCTGG  
GGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCATCGACTGTCAGC  
ACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACGACAGACTCGCACGTGCG  
CCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGTGCCAGGGCCCTAC  
TGTCCCTGGGGTCCCAGGCTCTCCTTGAGGGGGCTCCCCGCCTTCCACCTGGCTGTCATCGG  
GTAGGGCGGGGCCGTGGGTTCAGGGGCGCACCACTTCCAAGCCTGTGTCCCACAGGTCCTCGG  
CGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACACATAAATAACTGGCACAAGTAAGTCC  
CCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTGGGTGAGTATGTGTGGGG  
CACAGGCTGGCTCCCTCAGCTCCCACGTCTAGAGGGGCTCCCGAGGAGGTGGAACCTCAACC  
CAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAGGTCTCCGACCCCTCAGCTGG  
AGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCCACCCCATCCCAGGTCTGTGG  
TCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCCATGGAGGGGCTGACTGCCCCA  
CATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGCCCTGACCTGGACTTCAGGGGGA  
GGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCTAGATCAGTGGGGGCACTGCAGGT  
GGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCACCTCTGCAACCACACCCATGTGGTG  
GTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGGCCTGGGACACACAGAGCCACCCCGG  
CCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGAAGGGGTGCTCGTAAGCCAACACCAGC  
GTGCCGCGGCCTGCACACCCCTTCGGACATCCCAGGCACGAGGGTGTCTGTGGATGTGGCCACAC  
ATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCTGGGGCCCCCAGGGAGGGAGGCAGGGGGT  
GGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCCCCGCAGCCTGGTATCGCCAGCCTTAAGGT  
GTCTGGAGCCCCCACACTTGGCCAACCTGACCTTGGAAGATGCTGCTGAGTGTCTCAAGCAGC  
ACTGACAGCAGCTGGGCCTGCCCCAGGGCAACGTGGGGGCGGAGACTCAGCTGGACAGCCCT  
GCCTGTCACTCTGGAGCTGGGCTGCTGCTGCCTCAGGACCCCTCTCCGACCCCGGACAGAGC  
TGAGCTGGCCAGGGCCAGGAGGGCGGGAGGGAGGGAATGGGGGTGGGCTGTGCGCAGCATCAG  
CGCCTGGGCAGGTCCGCAGAGCTGCGGGATGTGATTAAAGTCCCTGATGTTTCTC



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**FIGURE 370**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

&gt;&lt;subunit 1 of 1, 157 aa, 1 stop

&gt;&lt;MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMKE  
LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIERHL  
APGSWGGGQLSREGPSLAPEGSMPSPRGDL P

**Signal peptide:**

amino acids 1-15

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**FIGURE 371**

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTCAGCAGTGACTGCCCCGGGCTGCCGCCC  
CCGGGGGCTTGCCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCCTC  
TCGGCCACGGCTGGGTGCGGGGCCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGCTGG  
CAGGTGGGCTGAGGGGCGCGCCCCGGCGCAGTCCCCCGCGGCCCCGACCCTGAGGCGTCGC  
CTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGCGCCGC  
CCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGATCAAGG  
ATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTCTGGTCAG  
AAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGTTATGCGAA  
TTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAGCAGGGAAAC  
TGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCAGAAAAAGAATATGAAGGTG  
AAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAATTCGTCATTATGAAA  
AGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGATGAAAGAGAATG  
TTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTTACTAAATTTAAAA  
CAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAAAAAGAATGATTTTG  
AACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAATCCCTAAGATTATTTA  
AAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCAACTTTTGGCTATACCC  
TACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGACTATATGCAGAAAATAT  
TCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGCCAGTGATTTACAATAGAG  
CAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATCTTAACACTATTTTATTAAT  
TAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGCCACATTTTGGGAGCTTTTCT  
ACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAAACATGTTTATAAAGTAAAAAA

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**FIGURE 372**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

&gt;&lt;subunit 1 of 1, 373 aa, 1 stop

&gt;&lt;MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRGA  
APAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGAPG  
IVVGVSVDGKEVWSEGLGYADVENRVPCPETVMRIASISKSLTMVALAKLWEAGKLDLDIPV  
QHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAFEQEK  
EGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKNDPLFF  
KPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRAR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

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**FIGURE 373**

GACTACGGGGAGAGAGAGAGAGACCAGGACAGCTGCTGAGACCTCTAAGAAGTCCAGATACTAA  
GAGCAAAGATGTTTCAAACCTGGGGGCCTCATTGTCTTCTACGGGCTGTTAGCCCAGACCATGG  
CCCAGTTTGGAGGCCTGCCCCTGCCCTGGACCAGACCCTGCCCTTGAATGTGAATCCAGCCCTG  
CCCTTGAGTCCCACAGGTCTTGCAGGAAGCTTGACAAATGCCCTCAGCAATGGCCTGCTGTCT  
GGGGGCCTGTTGGGCATTCTGGAAAACCTTCCGCTCCTGGACATCCTGAAGCCTGGAGGAGGT  
ACTTCTGGTGGCCTCCTTGGGGGACTGCTTGGAAAAGTGACGTCAGTGATTCCTGGCCTGAAC  
AACATCATTGACATAAAGGTCACCTGACCCCCAGCTGCTGGAACTTGGCCTTGTGCAGAGCCCT  
GATGGCCACCGTCTCTATGTCACCATCCCTCTCGGCATAAAGCTCCAAGTGAATACGCCCCTG  
GTCGGTGCAAGTCTGTTGAGGCTGGCTGTGAAGCTGGACATCACTGCAGAAATCTTAGCTGTG  
AGAGATAAGCAGGAGAGGATCCACCTGGTCCTTGGTGACTGCACCCATTCCCCTGGAAGCCTG  
CAAATTTCTCTGCTTGATGGACTTGGCCCCCTCCCCATTCAAGGTCTTCTGGACAGCCTCACA  
GGGATCTTGAATAAAGTCCTGCCTGAGTTGGTTCAAGGCAACGTGTGCCCTCTGGTCAATGAG  
GTTCTCAGAGGCTTGGACATCACCTGGTGCATGACATTGTTAACATGCTGATCCACGGACTA  
CAGTTTGTCAATCAAGGTCTTAAGCCTTCCAGGAAGGGGCTGGCCTCTGCTGAGCTGCTTCCCAG  
TGCTCACAGATGGCTGGCCCATGTGCTGGAAGATGACACAGTTGCCTTCTCTCCGAGGAACCT  
GCCCCCTCTCCTTTCCCACCAGGCGTGTGTAACATCCCATGTGCCTCACCTAATAAAATGGCT  
CTTCTTATGCA

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**FIGURE 374**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76533
><subunit 1 of 1, 256 aa, 1 stop
><MW: 26713, pI: 5.62, NX(S/T): 0
MFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNVNPALPLSPTGLAGSLTNALSNGLL
SGLLLGILENLPLLDILKPGGGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGL
VQSPDGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRDKQERIHLVLGDC
THSPGSLQISLLDGLGPLPIQGLLDSLTGILNKVLPPELVQGNVCPLVNEVLRGLDITLVH
DIVNMLIHGLQFVIKV
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-19

**Transmembrane domain:**

Amino acids 79-97

**N-myristoylation sites:**

Amino acids 46-52;49-55;58-64;62-68;66-72;80-86;81-87;  
82-88;85-91;86-92;89-95;202-208;233-239

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**FIGURE 375**

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTTT  
AAATATGTCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTGTG  
TTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGTAAA  
TTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGGTGGC  
AGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGAATTGA  
TTCTCACAGGCGCACCATGGCAGTTTTTGCTGTTGGAGACTTGGACTCTATTTATGGGACAGA  
AGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTATATCCTGT  
TCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTAAAAACAAC  
CTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCAAAACATCAA  
ATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATAGTCTGAGGAA  
GGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATGTTTAAATAGTA  
AAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACACAACCAAATTAAT  
GCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTTTCCATCACATTTA  
GGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTCCTAGCATGGGGTCC  
ATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACATGTCCAGAACCAGAAC  
CAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAAGAAAAGTTTGGAGTTG  
AAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCTCAGCAAAAACAAGAGGT  
TTTATGCCCCAACCTGAAGAGGAAGAAATGTAGATAGAAGGTGAAGGAGATTGCTGAAGATA  
TAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCCCTTTTACAGTAATGAATGT  
GGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTGGCATTATTTGCAGCATCATG  
CTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGCAGAAGTAGCAATGAGACATCT  
TCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGACAAAACATCCATCACAGATGA  
CATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAATAAACATCAATAGATATCTAAAAA

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**FIGURE 376**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

&gt;&lt;subunit 1 of 1, 146 aa, 1 stop

&gt;&lt;MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVAA  
LLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYPVP  
APCFGPLGSPPPYEEIVKTT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

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**FIGURE 377**

CGCGGATCGGACCCAAGCAGGTCGGCGGGCGGCGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCG  
ACCCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCC**ATG**GCCAGGCCCGGC  
ATGGAGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCGCTCGGGGGGCATCGGCGCGGCC  
GTGGCCCGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAAC  
ATCGAGGAGCTGGCTGCTGAATGTAAGAGTGACAGGCTACCCCGGGACTTTGATCCCCTACAGA  
TGTGACCTATCAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGC  
GGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCCGGCCTGACACCCTGCTCTCAGGCAGC  
ACCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAA  
GCCTACCAGTCCATGAAGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATG  
TCTGGCCACCGAGTGTTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTC  
ACTGCGCTGACAGAGGGACTGAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACG  
TGCATCTCTCCAGGTGTGGTGGAGACACAATTCGCCTTCAAACCTCCACGACAAGGACCCTGAG  
AAGGCAGCTGCCACCTATGAGCAAATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTT  
ATCTACGTCCTCAGCACCCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACGGAG  
CAGGTGACCT**TAG**TGACTGTGGGAGCTCCTCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTG  
CCTCTGGATTTTAGGTGTTGATTTCTGGATCACGGGATACCACTTCCTGTCCACACCCCGACC  
AGGGGCTAGAAAATTTGTTTGAGATTTTATATCATCTTGTCAAATTGCTTCAGTTGTAAATG  
TGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCCTAATTGTTTTACTTGTTAACTTGTTCTTG  
TGCCCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTT  
GTGGCCAAAATCCCCATCTTCTTGCACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGG  
GAGGCCTTCACCTTATATCTGTGTTGTTATCCAGGGCTCCAGACTTCCTCCTCTGCCTGCCCC  
ACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAGCCCAGTCTTGGCTTCTTGT  
CCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCCTGGC  
CCAGTGGATTTTCATGGTGATCATTAAGAAAGAAAAATCGCAACCAAAAAAAAAAAAA



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**FIGURE 378**

MARPGMERWRDRLALVTGASGGIGAAVARALVQQGLKVVGCA<sub>1</sub>RTVGNIEELAAECKSAGYPGT  
LIPYRC<sub>2</sub>DL<sub>3</sub>SNEEDILSMFSAIR<sub>4</sub>SOHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNVLALS  
ICTREAYQSMKERNVDDGHIININSMGHRVLP<sub>5</sub>LSVTHFY<sub>6</sub>SATKYAVTALTEGLRQELREAQT  
HIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQ  
MRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

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**FIGURE 379**

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGTT  
TCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCCGCTTATTAGC  
TCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGGCGGCGACCGTGACGAGAAGCCCACG  
GCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCCTTTTAAACTCCCT  
CTTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAGATGAA  
GAATATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGTCTTGATTGTGGCTTACCT  
CAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTTTGCTTCTTCAGAAATGTTTTTACAATCTC  
AAGAAAAAATATGTCCCAGAAATTGAGTTTACTGTTGCTTGTATTGGACTCATTGGGGATT  
GATGTTACTGCACTATTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTTACGTGAGCA  
AATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGAACACAGTGGA  
TGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATTGCTGTCTTCT  
GGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATATTGTTGTGAATGG  
CTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAACCACAAATAAAAG  
AACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGCTGCTCCATCCACTG  
TGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGACAGAGCAATACTTTAC  
AATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTGATGGAATCTAATTCTGTACATA  
AAAATTTTAAAGTTATTTGTTTGCTTTGAGGCAAGTCTGTTCAATGCTGTACTATGTCTTAA  
AGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGTTTTGTATAAATCTTTGT  
GTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTGATTCTATTAACACATTTAT  
TTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTAATCATTCTGTATTTGTTCTC  
AATAGATGTAAGTGTAGACTACGGCTATTTGAAAAAATGTGCTTATTGTACTATATTTTGT  
ATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAATAATGTTTTGAAATCATGACCC  
AAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGAAGGTTAATTATTGTATATTTTTA  
AAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAGCAGCCACTGTCCATTACCTATCGT  
AAACATTGGGGCAATTTAATAACAGCATTAAAATAGTTGTAACTCTAATCTTATACCTTATTG  
AAGAATAAAAGATATTTTTATGATGAGAGTAACAATAAAGTATTCATGATTTTTACATACAT  
GAATGTTCAATTTAAAAGTTAATCCTTTGAGTGTCTATGCTATCAGGAAAGCACATTATTTCC  
ATATTTGGGTAAATTTTGCTTTTATTATATTTGGTCTAGGAGGAAGGGACTTTGGAGAATGGAA  
CTCTTGAGGACTTTAGCCAGGTGTATATAATAAAGGTACTTTTGTGCTGCATTAAATTGCTTG  
GAAAGTGTTAACATTATATTATATAAGAGTATCCTTTATGAAATTTGAATTTGTATAACAGA  
TGCATTAGATATTCATTTTATATAATGGCCACTTAAAATAAGAACATTTAAAATATAAACTAT  
GAAGATTGACTATCTTTTCAGGAAAAAGCTGTATATAGCACAGGGAACCCTAATCTTGGGTA  
ATTCTAGTATAAAACAAATTATACTTTTATTTAAATTTCCCTTGTAGCAAATCTAATTGCCAC  
ATGGTGCCCTATATTTCATAGTATTTATTCTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCT  
AGATTTAGACTATATAGAATTTAGATATTGTATTGTTCTGTCATTATAATATGCTACCACATGT  
AGCAATAATTACAATATTTTATTAAATAAATATGTGAAATATTGTTTCATGAAAGACAGATT  
TCCAAATCTCTCTTCTCTCTGTACTGTCTACCTTTATGTGAAGAAATTAATTATATGCCA  
TTGCCAGGT

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**FIGURE 380**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

&gt;&lt;subunit 1 of 1, 140 aa, 1 stop

&gt;&lt;MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE

NKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNLVP

VTTNKRTNVSGSIR

**Important features of the protein:****Signal peptide:**

amino acids 1-26

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**FIGURE 381**

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACC  
ATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCCGG  
GAGCACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCCAGTTCTGGTT  
TCATGCCAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTT  
TTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTTCATTTTCAGTAGCCACCAG  
CCACCTGTGGCCGTTGAGTGCTTGAAATTGAGGAACTGAGAAAATTAATTTCTCATGTATTTTT  
CTCATTTATTTATTAATTTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGG  
ATACATGTATACAATATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACAT  
TTATTTTTTATTCTTTTTTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCC  
ATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAA  
GTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTTGTATTTTTTAGTAGAGACG  
GGGTTTTGCCATGTTGCCCAGGCTGGCCTTGAACCTCCTGGCCTCAAACAATCCACTTGCCTCG  
GCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTT  
CTTTGTGTTGGGAACCTTTGAAATTATACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTG  
CTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAACCAACCGT  
ACTTCATCCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCATTCTACTCTCTACCTC  
CATGAGATCCACTTTTTTAGCTCCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTG  
CCTGGCTTATTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAAATGACAGGA  
TTTCGTTCTTAATTTCAATTAAAATAACCACACATGGCAAAAA

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**FIGURE 382**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRI PVLVSCQ  
PVKGHGTLGESPMPEFKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

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**FIGURE 383**

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAG  
CCTGGAGCATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTCAAGTAGCACCTCTATCAG  
TTATGGCTAAATCCTGTCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATC  
GCTTTCTGACATCCATTCCAACAGGAATACCAGAGGATGCTACAACCTCTTACCTTCAGAACA  
ACCAAATAAATAATGCTGGGATTCCCTCAGATTTGAAAACTTGCTGAAAGTAGAAAGAATAT  
ACCTATACCACAACAGTTTAGATGAATTTCCCTACCAACCTCCCAAAGTATGTAAAAGAGTTAC  
ATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAAAAATTCCCTATCTGG  
AAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCATTCCGAG  
ACAGCAACTATCTCCGACTGCTTTTCCCTGTCCCGTAATCACCTTAGCACAAATCCCTGGGGTT  
TGCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCAT  
CTCTTCAAGGTCTCACTAGTCTAAAACGCTGGTTCTAGATGGAAACCTGTTGAACAATCATG  
GTTTAGGTGACAAAGTTTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATT  
CCCTGACTGCTGCACCAGTAAACCTTCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATA  
ACCACATCAATCGGGTGCCCCAAATGCTTTTTCTTATCTAAGGCAGCTCTATCGACTGGATA  
TGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTTGATGATTTGGACAATATAACAC  
AACTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATGGGTACGTGACTGGT  
TACAATCACTACCTGTGAAGGTCAACGTGCGTGCGGCTCATGTGCCAAGCCCCAGAAAAGGTTT  
GTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAA  
GCACCATTGAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCCAAGGACAGTGGCCAG  
TGCCAGTGACCAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAG  
GGAGTCCCTCAAGAAAAACAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCATA  
TCTCTTGGAACCTTGCTCTACCTATGACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATA  
GCCCCGCATTTGGATCTATAACAGAAACAATTGTAAACAGGGGAACGCAGTGAGTACTTGGTCA  
CAGCCCTGGAGCCTGATTACCCCTATAAAGTATGCATGGTTCCCATGGAAACCAGCAACCTCT  
ACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTTCGAATGTACAACC  
CTACAACCACCCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACCTTTGG  
CTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTGGT  
ATGTTTCATAGGAATGGATCGCTCTTCTCAAGGAAGTGTGCATATAGCAAAGGGAGGAGAAGAA  
AGGATGACTATGCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAACTT  
CTTTTCAGATGTTACCAATAAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAAATACACACCA  
TATTTCTCCTAATGGAATGAATCTGTACAAAAACAATCACAGTGAAAGCAGTAGTAACCGAA  
GCTACAGAGACAGTGGTATTCCAGACTCAGATCACTCACACTCATGATGCTGAAGGACTCACA  
GCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATGGT

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**FIGURE 384**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCND RFLTSIPTGIPEDATTL  
YLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNI RTITYDSLK  
IPYLEELHLDDNSVSAVSIEEGA FRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRIST  
ISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAA PVNLPGTNLRKL  
YLQDNHINRVPPNAFSYL RQLYRLDMSNNNLSNLPQGIFDDL DNITQLILRNNPWYCGCKMKW  
VRDWLQSLPVKVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQ  
GQWPAPVTKQPDIKNP KLT KDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWL  
KLGHSPA FGSITETIVTGERSEYLVTALEPDS PYKVCMPMETSNLYL FDETPVCIETETAPL  
RMYNPTTTTLNREQEKEPYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSK  
GRRRKDDYAEAGTKKDNSILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNL YKNNHSES  
SSNRSYRDSGIPDS DSHS

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 531-552

**N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

**Tyrosine kinase phosphorylation site.**

amino acids 515-522

**N-myristoylation sites.**amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
640-645**Amidation site.**

amino acids 567-570

**Leucine zipper pattern.**

amino acids 159-180

**Phospholipase A2 aspartic acid active site.**

amino acids 34-44

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**FIGURE 385**

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCCAGGCCACCCAGGCTTCTTGG  
CAGCCCTGCCGGGCCACTTGTCTTC**ATGT**CTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAG  
GGCGTGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGA  
GCAGAGGCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACC  
GCTGTGGTCCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCT  
GATCCTGTCTGCGCTGGAGAGAGCCACCGTCTTCCTAGAACAGAGGCTGCCTGAAATCAACCT  
GGATGGCATGGTGGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCGGGGAGAAGTGGGC  
CCAGGAGCCCCTGCTGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGC  
TGCCATCCAGAGATCCCTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCA  
GCTGACCCTCCAGCCCGGGTTTTGGAAGCTCCCACATGCCTGGATCCACACTGATGCCTCCTT  
GGTGTAACCCACGTTCCGGGCCCCAGGACTCATTTCTCAGAGGAGAGAAGTGACGTGTGCCTGGT  
GCAGCTGCTGGGAACCGGGACGGACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAG  
CCTCATGACCAAGCCCGGCTGCTCAGGCTACTGCCTGTCCCACTGCTCTTCTTCTCCTCTG  
GGCCAGAATGAGGGGATGCACACAGGGACCACTCCAACAGAGCCAGGACTATATCAACCTCTT  
CTGCGCCAACATGATGGACTTGAACCGCAGAGCTGAGGCCATCGGATACGCCTACCCTACCCG  
GGACATCTTCATGGAAAACATCATGTTCTGTGGAATGGGCGGCTTCTCCGACTTCTACAAGCT  
CCGGTGGCTGGAGGCCATTCTCAGCTGGCAGAAACAGCAGGAAGGATGCTTCGGGGAGCCTGA  
TGCTGAAGATGAAGAATTATCTAAAGCTATTCAATATCAGCAGCATTTTTTCGAGGAGAGTGAA  
GAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGTTGCTCAGGCTGGAGTACAGTGGCGCAA  
TCTCGGCTCACTGCAACCTTTCCTCCTGGGTTCAAGCAATTCTCTTGCCTCATCCTCCCGAG  
TAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAATTTTTATATTTTTTTAGTAGAGAC  
AGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGATCTCAAGAGATCCGCCCACCTC  
AGGCTCCCAAAGTGTTGGGATT**TAGGT**GTGAGCCACCGTGCTGGCTGAAAAGCACTTTCAAA  
GAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTCATGGGGGCTCTCTCCCC  
TAGATGGCTGCTCCTCCCACAACACAGCCACAGCAGTGGCAGCCCTGGGTGGCTTCTTATACA  
TCCTGGCAGAATAACCCCCAGCAAACAGAGAGCCACACCCATCCACACCGCCACCACCAAGCA  
GCGGCTGAGACGGACGGTTCATGCCAGCTGCCTGGAGGAGGAACAGACCCCTTTAGTCCTCA  
TCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGGATAAGCAAA  
GCCACCCCGACACCCAATCTTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGGGGCCGGG  
AGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA



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**FIGURE 386**

MSARGRWEGGRRACRGSLGLARAQGAERVTSSSEQRPAMASLGLLLLLLLLTALPPLWSSSLPG  
LDTAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPL  
SLRVGMLGEKLEAAIQRSYLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQ  
DSFSEERSDVCLVQLLGTGTDSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQ  
GPLQQSQDYINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILS  
WQKQQEGCFGEPADEDEELSKAIQYQQHFSSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLP  
PGFKQFSLILPSSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRPPTSGSQSVGL

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

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**FIGURE 387**

GGTCTGAGTGCAGAGCTGCTGTC**ATG**GCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGC  
TGCTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGG  
GAGGGAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGG  
TGAAGCCTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTT  
TCCTTAAGACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAG  
TTGTATCTCCAGCTTACAGATTTGATCCCGTTTCGAGTGGATATCACTTCGAAAGGAAAAATGA  
GAGCAAGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAA  
TGAAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTC  
TAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAG  
TGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATT  
CCAACCATGAGTTGCCTGATGTTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTG  
GCAAACTCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAAGGAGG**TAG**TCAG  
GCCGTCCAGAGCTGGCATTTCACAAAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAAA  
CCGTGTGAAGCAACTACTATAAACTTGAGTCATCCCGACGTTGATCTCTTACAACGTGTGTATGTT  
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGT  
ATGAGGTCAATATTGATGTCAGTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAA  
TTATATGAACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

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**FIGURE 388**

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQDWIS  
AARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVVRVDITSKGKMRARYVNYI  
KTSEVVRLLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMLVPLLI FVLLPKVVNTSDPD  
MRREMEQSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

**Important features of the protein:****Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

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**FIGURE 389**

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCC**ATGG**CGTGGAGCCTTGGGAG  
CTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAATGTCAG  
AATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGGGAA  
CCTGACTTTTACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATACTAC  
CTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTCAGGGC  
TGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCCTGTGGATGACACCAT  
TATTGGACCCCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTTTCTTAGC  
CCCTAAAATTGAGAATGAATACGAACTTGGACTATGAAGAATGTGTATAACTCATGGACTTA  
TAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCAGTATGACTT  
TGAGGTCCTCAGAAACCTGGAGCCATGGACAACCTTATTGTGTTCAAGTTCGAGGGTTTCTTCC  
TGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACCCATGACGAAAC  
GGTCCCCTCCTGGATGGTGGCCGTATCCTCATGGCCTCGGTCTTCATGGTCTGCCTGGCACT  
CCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTTACAAGAAGACAAAGTACGCCTTCTCCCCTAG  
GAATTCTCTTCCACAGCACCTGAAAGAGTTTTTTGGGCCATCCTCATCATAACACACTTCTGTT  
TTTCTCCTTTCCATTGTGCGGATGAGAATGATGTTTTTTGACAAGCTAAGTGTGATTGCAGAAGA  
CTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGACCCCGCCTGGGCAGGG  
GCCCCAAAGCT**TAGG**CTCTGAGAAGGAAACACACTCGGCTGGGCACAGTGACGTACTCCATCTC  
ACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGACCATCTGAGCCAGCCCCA  
CATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACATTTTAAAGGCTGTCTTGGA  
AAAATACTCCATTTGGGAACCTACTGCCTTATAAAGGCTTTTCATGATGTTTTTCAGAAGTTGGC  
CACTGAGAGTGTAATTTTTCAGCCTTTTATATCACTAAAATAAGATCATGTTTTTAATTGTGAGA  
AACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCACCTTAGAGGTCGAGGCAGGCGG  
ATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAATATGGTGAAACCCAGTCTCTACTAA  
AAATACAAAATTAGCTAGGCATGATGGCGCATGCCTATAATCCCAGCTACTCGAGTGCCTGA  
GGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGAGGTTGCAGTGAGCCGAGATAGCGGC  
ACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAATTGTG  
AGAAACAGAAATACTTAAAATGAGGAATAAGAATGGAGATGTTACATCTGGTAGATGTAACAT  
TCTACCAGATTATGGATGGACTGATCTGAAAATCGACCTCAACTCAAGGGTGGTCAGCTCAAT  
GCTACACAGAGCACGGACTTTTGGATTCTTTGCAGTACTTTGAATTTATTTTTCTACCTATAT  
ATGTTTTATATGCTGCTGGTGTCTCCATTAAAGTTTTACTCTGTGTTGC

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**FIGURE 390**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551  
><subunit 1 of 1, 325 aa, 1 stop  
><MW: 37011, pI: 5.09, NX(S/T): 4  
MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIFQ  
DKCMNTTLTECDFSSLSKYGDHTLRVRAEFADSHSDWVNITFCPVDDTIIGPPGMQVEVLADS  
LHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTTYCV  
QVRGFLPDRNKAGEWSEPVCEQTTHDETVPSWMVAVILMASVFMVCLALLGCFSLWCVYKKT  
KYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNPBGDSCSL  
GTPPGQGPQS

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 222-245

**N-glycosylation sites.**

amino acids 49-53, 68-72, 102-106, 161-165

**N-myristoylation sites.**

amino acids 6-12, 316-322

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**FIGURE 391**

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCG**ATG**AGGA  
AGCACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGG  
TCCAGACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCAGCACTGCCC  
AGATCACTGAGGGCCCAGGTGGCTGAGAACCGCCCGGAGCCTTCATCAAGCAAGGCCGCAAGC  
TCGACATTGACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCG  
ATGGCATCCACTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCT  
GCATCAATGCCACCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACC  
AGCAGGTGCTCTGGCGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGG  
AGAGGGGCGCAGGACTTCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGA  
TCTGGCTCATGGTGAAA**TA**AGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAA  
TCCTGGCAAGTGACCCAGCTCTTCTCCCCAAACCCACGCGTGTTCTGAAGGTGCCAGGAGC  
GGCGATGCACTCGCACTGCAAATGCCGCTCCACGTATGCGCCCTGGTATGTGCCTGCGTTCT  
GATAGATGGGGGACTGTGGCTTCTCCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCA  
CACTAGATTAGTAGTAAATGCTTGATGAGAAGAACACATCAGGCACTGCGCCACCTGCTTCAC  
AGTACTTCCCAACAACCTCTTAGAGGTAGGTGTATTCCCGTTTTACAGATAAGGAAACTGAGGC  
CCAGAGAGCTGAAGTACTGCACCCAGCATCACCAGCTAGAAAGTGGCAGAGCCAGGATTCAAC  
CCTGGCTTGTCTAACCCAGGTTTTCTGCTCTGTCCAATTCCAGAGCTGTCTGGTGATCACTT  
TATGTCTCACAGGGACCCACATCCAAACATGTATCTCTAATGAAATTGTGAAAGCTCCATGTT  
TAGAAATAAATGAAAACACCTGA

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## **FIGURE 392**

MRKHLSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQG  
RKLDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNK  
LHQQVLWRLVQELCSLKHCFWLERGAGLRVTMHQPVLLCLLALIWLMMVK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 157-171

**N-glycosylation sites.**

amino acids 98-102, 110-114

**Tyrosine kinase phosphorylation site.**

amino acids 76-83

**N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

**Amidation site.**

amino acids 62-66

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**FIGURE 393**

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAA  
TGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCCCT  
CAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGCCAA  
TTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTGAGAG  
**ATGA**ATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTCCTTTG  
CTGGCGACAGCCTCTCAAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTGCTTCTC  
TGGAGCCAGGTATCAGGGGCCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGTGAAGGGG  
GTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGAT  
AACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGATGCTGAGAGC  
TGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAACCTGTTTTCAAAAACCACCACAAT  
AGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAACCTTTGTTCTCATC  
GTGTCACAACTGCAACCCAGTCAAGAAAAATGAGATGTTTTCCATCAGAGACAGTGCACACAGG  
CGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTCTGACCAAAGCC  
CTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGCTCT**TGA**ATGTCTAGA  
CCAGGACCTCCCTCCCCCTGGCACTGGTTTTGTTCCCTGTGTCAATTTCAAACAGTCTCCCTTCC  
TATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCTTGGCCCAGGATTATT  
GTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAGGTGCCTCTGGATGCTGT  
GAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACCTCTATTTAATTAATGTCAGTATTTT  
AACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGGCAGCAGAATATTGTGCCCC  
ATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAGTGGATGGGTGCTTAGTAAGT  
ACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATTGTTAAAAAACAGAGAGGGATG  
CTTGGATGTAAACTGAACTTCAGAGCATGAAAATCACACTGTCTTCTGATATCTGCAGGGAC  
AGAGCATTGGGGTGGGGGTAAAGGTGCATCTGTTTGAAAAGTAAACGATAAAATGTGGATTAAA  
GTGCCCAGCACAAAGCAGATCCTCAATAAACATTTCAATTTCCCACCCACACTCGCCAGCTCAC  
CCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTTATCCTAGTCATTCTTCCCTAATCT  
TCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGACATTGCACCTGGATGTACTATCCAATC  
TGTGATGACATTCCCTGCTAATAAAAGACAACATAACTCCAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAA



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**FIGURE 394**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

&gt;&lt;subunit 1 of 1, 206 aa, 1 stop

&gt;&lt;MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPLLATASQMOMVVLPCLGFTLLLSQVSGAQGQEFHFGPCQVKG  
VVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLYKTVFKNHHN  
RTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRREFLLFRRAFKQLDVEAALTKA  
LGEVDILLTWMQKFYKL

**Signal sequence:**

amino acids 1-42

**N-glycosylation sites.**

amino acids 85-89, 99-103, 126-130

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**FIGURE 395**

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCAT  
TTCCTGATGATTTATAGACTCAAAGAAAAC**TCATG**TTCAGAAGCTCTCTTCTCTTCTGGCCTC  
CTCTCTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCA  
AGCTGGAAATCTTTCATTTTGCTTGTGAGTGGGGTAGGTCAGTCTTAGTTTTTATTTTT  
TGAAATTTCAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCAT  
**GAT**GCTGAGGTTTGGGGT

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**FIGURE 396**

MFRSSLLFWPPLCLLSLFLILISSIYSECKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGT  
CEGLFYEYIA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-myristoylation site.**

amino acids 62-68

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**FIGURE 397**

**CATG**CCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTG  
TGTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT  
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT  
CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG  
TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG  
GGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAAACACAAAT  
TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC  
AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCT  
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA  
CCACACGCTGGTGTCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTT  
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA  
TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT  
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA  
CCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA  
AAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA  
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA  
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA  
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCAGCCAGCAAGAGTCCCTCAG  
CAGAACAATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT  
TTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATT  
ATTGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCGCAAACGTTACAGTACTCATACACCCC  
TCAGCTCCAAGACTTAGACCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCGGAGGA  
AGAGCCATCGACGACCCTGGTCGACTGGGATCCCCAACTGGCAGGCTGTGTATTCTTTCGCT  
GTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA  
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC  
CTATCTCATGCAATTCATGGAGGAATGGGGTTATATGTGCAGATGGAAAAC**TGA**TGCCAACA  
CTTCCTTTTGCCTTTTGTTCCTGTGCAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA  
GTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGTCTGTGAGAA

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**FIGURE 398**

MPLPPLLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYF  
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPFLETQI  
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN  
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV  
FLFSVMGYSIYRYIHVGKEKHANLILYGNFDRFFVPAEKIVINFITLNISSDDSKISHQD  
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSLTQQESLS  
RTIPDPKTVIEYEDVRTTDICAGPEEQELSLQEEVSTQGTLLSQALAVLGPQTLQYSYTP  
QLQDLPLAQEHTDSEEGPEEPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDLGEE  
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 240-260

**N-glycosylation sites.**amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,  
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

**N-myristoylation sites.**

amino acids 53-58, 106-111, 368-373, 492-497

**Tissue factor**

amino acids 1-278

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**FIGURE 399**

CCGGCG**ATG**TCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAG  
CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTA  
ATCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTTGCAACAGGGGAC  
TATTCAATTTTGTAGTAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAG  
GCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAAT  
TACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACATC  
GGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCATAATATTCCTAATGCAAAT  
ATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATA  
ATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGT  
AAGAAGAATGAGGAGACAGTAGAAGTGAACCTCACAACCACTCCCCTGGGAAACAGATACATG  
GCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAA  
CAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTG  
ACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGC  
CCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCT  
CTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGG  
AGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCATTAAGGTT  
CTTGTTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTT  
CAAAACCATTCAGAAAGTGAGGTCACTCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATG  
GGTCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCC  
AATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAAC  
TCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCAT  
CTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTC  
AGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCAT  
GTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTG  
**TAG**

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**FIGURE 400**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLI PGDLRLRVEFVTTSVATGDYS  
ILMNVS WVL RADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTF SYIGF  
PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKK  
NEETVEVNFTTTPLGNRYMALIQHSTIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTP  
YFPTCGSDCIRHKGTVVLC PQTGVFPFLDNNKSKPGGWL PLLLLSLLVATWVLVAGIYLMWRH  
ERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGP  
VQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLH  
KYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHV KQQVSAGKRSQACHDGCCSL

**Important features of the protein:****Signal peptide:**

amino acids 1-14

**Transmembrane domain:**

amino acids 290-309

**N-glycosylation sites.**amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201  
and 283 - 287**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

**Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

**N-myristoylation site.**

amino acids 116-122

**Amidation site.**

amino acids 488-452

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**FIGURE 401**

GGGAACAGGGAACTATCAGCCCCGTCGGCCTCCGGGCCCTGCATTCTCTAGCC**ATGG**ACCG  
GGACCTTTTGCGGCAGTCGCTAAATTGCCACGGGTCGTCTTTGCTCTCTCTACTTCGGAG  
CGAACAGCAGGACAATCCACACTTCCGTAGCCTCCTGGGGTCCGCCGCCGAGCCAGCCCCG  
GGGCCCCGCCGCCCCAGCACCCGTTGCAGGGCAGAAAAGAGAAGAGAGTTGACAACATCGA  
GATACAGAAATTCTCTCCAAAAAGCGGATCTGCTTTTTGCACTTTCCTGGAAATCAGA  
TGCACCTGCAACTTCTGAAATTAATGAAGACAGTGAAGATCATTATGCAATCATGCCACC  
TTTAGAGCAATTCTGGAGATACCTAGTATGGATCGGAGAGAGCTGTTTTTCCGAGATAT  
TGAGCGTGGTGATATAGTGATTGGAAGAATTAGTTCTATTTCGGGAATTCGGTTTTTTCAT  
GGTGTGATCTGTTTAGGAAGTGGTATCATGAGAGATATAGCCCACTTAGAAATCACAGC  
TCTTTGTCCCTTAAGAGATGTGCCTTCTCACAGTAACCATGGGGATCCTTTATCATATTA  
CCAAACTGGTGACATCATTCGAGCTGGAATCAAGGATATTGACAGATACCATGAAAAGCT  
AGCAGTATCTCTGTATAGCTCTTCTCTTCCACCACACCTATCTGGTATTAAATTAGGTGT  
AATTAGCTCTGAAGAGCTTCCTTTATACTACAGGAGAAGTGTTGAGCTAAATAGCAATTC  
TTTGGAGTCCTATGAAAATGTCATGCAGAGTTCCTTGGGATTTGTTAATCCAGGAGTAGT  
TGAATTCCTTCTAGAAAACTAGGAATAGATGAATCTAATCCACCATCTTTAATGAGAGG  
CCTACAAAGCAAAAATTTCTCTGAAGATGATTTTGCTTCTGCATTGAGAAAAACAATC  
CGCATCTTGGGCTTTAAAATGTGTGAAGATCGGAGTTGACTATTTTAAAGTTGGACGCCA  
TGTGGATGCTATGAATGAATACAATAAAGCTTTGGAAATAGACAAACAAAACGTGGAAGC  
TTTGGTAGCTCGTGGAGCATTATATGCGACAAAAGGAAGTTTGAACAAAGCAATAGAAGA  
TTTTGAGCTTGCAATTAGAAAAGTGTCCAACCTCACAGAAATGCAAGAAAATACCTCTGCCA  
GACACTTGTAGAGAGAGGAGGACAGTTAGAAGAAGAAGAAAAGTTTTTAAATGCTGAAAG  
TTACTATAAGAAAGCCTTGGCTTTGGATGAGACTTTTAAAGATGCAGAGGATGCTTTGCA  
GAAACTTCATAAATATATGCAGAAATCTTTGGAATTAAGAGAAAACAAGCTGAAAAGGA  
AGAAAAGCAGAAAACAAAGAAAATAGAAACAAGTGCAGAAAAGTTGCGTAAGCTCTTAAA  
AGAAGAGAAGAGGCTAAAGAAGAAAAGAAGAAAATCAACTTCTTCTTCAAGTGTTTCTTC  
TGCTGATGAATCAGTGTCTTCATCATCATCCTCTTCTTCTTGGTCCAAAAGGCATAA  
GAAACATAAGAGGAACCGTTCAGAGTCTTCTCGCAGTTCCAGAAGGCATTCTCTAGGGC  
ATCCTCAAATCAGATAGATCAGAATAGGAAAGATGAGTGCTACCCAGTTCAGCTAATAC  
TTCAGCATCTTTTCTTAACCATAAACAAGAAGTGGAGAACTACTGGGGAAGCAGGATAG  
GTTACAGTATGAAAAGACACAGATAAAAGAGAAAGATAGATGCCCTCTCTCTTCATCTTC  
ACTTGAAATACCGGATGATTTTGGAGTGTACTCCTATTTATTTAAAAAGTTAACTATAAA  
ACAGCCTCAGGCAGGTCCTTCAGGAGATATTCCAGAAGAGGGCATTGTTATCATAGATGA  
CAGCTCCATTCATGTTACTGACCCTGAAGACCTTCAAGTGGGACAAGATATGGAGGTGGA  
AGACAGTGGTATTGATGATCCTGACCACGGG**TAGG**CTTAGGTTTATGTGTGTGTATGTGT  
CTTAGTTTTTAACAAAAAAATTAAGTAAAAAACTAAAAATAGAAAAATGCTTAGAG  
AATAAGGATATAAAGAATATTTTTGTGCAGTTGAACAATGAGTGCTTAAGCTAAATGTCA  
TCACAAAAGAGTAAAAAAATTTTACAAAATTAAGTGTAAAGTTAAAAAGCTCTAGG  
AAGCTAAGGTCAATTTATTATTGGAGAAATAAATATTTTTATGAATTTACTGT



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**FIGURE 402**

MDRDLLRQSLNCHGSSLLSLRSEQQDNPHFRSLLGSAAEPARGPPPQHPLQGRKEKRV  
NIEIQKFISKKADLLFALSWKSDAPATSEINEDSEDHYAIMPPLEQFMEIPSMRRELFF  
RDIERGDIVIGRISSIREFGFFMVLICLGSGIMRDIAHLEITALCPLRDVPSHSNHGDPL  
SYYQTGDIIRAGIKDIDRYHEKLAVSLYSSSLPPHLSGIKLGVISSEELPLYRRSVELN  
SNSLESYENVMQSSLGFVNPGVVEFLEKLGIDESNPPSLMRGLQSKNFSEDDFASALRK  
KQSASWALKCVKIGVDYFKVGRHVDAMNEYNKALEIDKQNVREALVARGALYATKGSLNKA  
IEDFELALENCPTHNRNARKYLCQTLVERGGQLEEEEEKFLNAESYKKALALDETFKDAED  
ALQKLHKYMQKSLELREKQAEKEEKQKTKKIETSAEKLRLKLLKEEKRLKKRRRKSTSSSS  
VSSADESVSSSSSSSSSGHKKRHHKRNRSSESSRRHSSRASSNQIDQNRKDECYPVP  
ANTSASFNLHKQEVKLLGKQDRLOYEKTKQIKEDRCPLSSSSLEIPDDFGVYSYLFKKL  
TIKQPQAGPSGDIPEEGIVIIDDSSIHVTDPEDLQVGQDMEVEDSGIDDPDHG

**Important features of the protein:****Signal peptide:**

Amino acids 1-23

**Transmembrane domain:**

Amino acids 138-155

**N-glycosylation sites:**

Amino acids 288-292;508-512;542-546

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 300-304;472-476;473-477;517-521;598-602

**N-myristoylation sites:**

Amino acids 218-224;222-228;271-277;348-354

**Amidation site:**

Amino acids 52-56

**Cell attachment sequence:**

Amino acids 125-128

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**FIGURE 403**

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTC  
CAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAC TGCCAGCTCAGAATA  
GGAAAATAACTTGGGATTTTATATTGGAAGAC **ATG**GATCTTGCTGCCAACGAGATCAGCATTT  
ATGACAAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAG  
AGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCC  
CGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCA  
CTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCTGGAGCTC  
ACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAAGAAGTACA  
TGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCCTTTCAGACTTTG  
ACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCCAACTGCACTG  
GCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAAATTTGAGAGGC  
TCCATCCACTGGTGATCAAGACGGGAAAGCCCCGTGTTGGAGGAAGAGATT CAGCATTTTTTGT  
GCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAGTGGTGGCGCTGCT  
TTCCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAACAGATCACAAATGT  
TACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATGCCTCTTTAAACAAGT  
GCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAGATGCCTGACCTATTTA  
TCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCAGTGCCGAAGACATTGTC  
AGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCGACACCACCCACTGGAAGG  
TCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGATGGAACCGCTTTCTCAGAAC  
TG **TAG**GAAATAGAACTGTGCACAGGAACAGCTTCAGAGCCGAAAACCAGGTTGAAAGGGGAA  
AAATAAAAACAAAAACGATGAAACTGCAAAAA

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**FIGURE 404**

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPQYPLLIVVYK  
VLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSIIHHIRLMSLPIAKKYMSENKGVPLHG  
GDEDRPFDPDFDPWWTNDCEQNESEPI PANCTGCAQKHLKVMILLEDAPRKFERLHPLVIKTGKP  
LLEEEIQHFLLCQYPEATEGFSEGFFAKWWRCFPERWFFPYPWRRPLNRSQMLRELFVVFTHL  
PFPKASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQRRHCQSVAMPIEPGD  
IGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

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**FIGURE 405**

TGCCGGGCTGCGGGGCGCCTTGACTCTCCCTCCACCCTGCCTCCTCGGGCTCCACTCGTCTGCCCCCTGGACTCCC  
GTCTCCTCCTGTCCCTCCGGCTTCCCAGAGCTCCCTCCTTATGGCAGCAGCTTCCCGCGTCTCCGGCGCAGCTTCT  
CAGCGGACGACCCCTCTCGCTCCGGGGCTGAGCCAGTCCCTGGATGTTGCTGAAACTCTCGAGATCATGCGCGGG  
TTTGGCTGCTGCTTCCCCGCCGGGTGCCACTGCCACCGCCGCCCTCTGCTGCCGCCGTCCGCGGGATGCTCAG  
TAGCCCCGTGCCCGCCCCCGCGATCCTGTGTTCTCGGAAGCCGTTTGCTGCTGCAGAGTTGCACGAACTAGTC  
ATGGTGCTGTGGGAGTCCCCGCGGCAGTGCAGCAGCTGGACACTTTGCGAGGGCTTTTGCTGGCTGCTGCTGCTG  
CCCGTCATGCTACTCATCGTAGCCCGCCGGTGAAGCTCGCTGCTTCCCTACCTCCTTAAGTGACTGCCAAACG  
CCCACCGGCTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTTCTCTGTGACACCAACACCTGTAAA  
TTTGATGGGGAAATGTTTAAGAATTGGAGACACTGTGACTTGCGTCTGTTCAGTTCAAGTGCAACAATGACTATGTG  
CCTGTGTGTGGCTCCAATGGGGAGAGCTACCAGAATGAGTGTACCTGCGACAGGCTGCATGCAACAGCAGAGT  
GAGATACTTGTGGTGTGAGAAGGATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGGC  
TCTGGAGAACTAGTCAAAAGGAGACATCCACCTGTGATATTTGCCAGTTTGGTGCAGAATGTGACGAAGATGCC  
GAGGATGTCTGGTGTGTGTGTAATATTGACTGTTCTCAAACCAACTTCAATCCCCCTCTGCGCTTCTGATGGGAAA  
TCTTATGATAATGCATGCCAAATCAAAGAAGCATCGTGTGAGAAACAGGAGAAAATTGAAGTCATGTCTTTGGGT  
CGATGTCAAGATAACACAACCTACAACCTAAGTCTGAAGATGGGCATTATGCAAGAACAGATTATGCAGAGAAT  
GCTAACAAATTAGAAGAAAGTGCCAGAGAACACCACATACCTTGTCCGGAACATTACAATGGCTTCTGCATGCAT  
GGGAAGTGTGAGCATTCTATCAATATGCAGGAGCCATCTTGACAGGTGTGATGCTGGTTATACTGGACAACACTGT  
GAAAAAAAGGACTACAGTGTTCTATACGTTGTTCCCGGTCTGTACGATTTAGTATGTCTTAATCGCAGCTGTG  
ATTGGAACAATTGAGATTGCTGTCATCTGTGTGGTGGTCTCTGCATCACAAGGAAATGCCCCAGAAGCAACAGA  
ATTCACAGACAGAAGCAAAATACAGGGCACTACAGTTGAGACAATACAACAAGAGCGTCCACGAGGTTAATCTAA  
AGGGAGCATGTTTACAGTGGCTGGACTACCGAGAGCTTGGACTACACAATACAGTATTATAGACAAAAGAATAA  
GACAAGAGATCTACACATGTTGCCTTGCATTTGTGGTAATCTACACCAATGAAAACATGTACTACAGCTATATTT  
GATTATGTATGGATATATTTGAAATAGTATACATTGTCTTGATGTTTTTCTGTAATGTAAATAAACTATTTATA  
TCACACAATATAGTTTTTTCTTTCCCATGTATTTGTATATATAATAAATACTCAGTGATGAG

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**FIGURE 406**

MVLWESPRQCSSWTLCEGFCWLLLLPVMLLIVARPVKLAFFPTSLSDCQTPTGWNC SGY  
DDRENDLFLCDTNTCKFDGECLRIGDTVTCVCQFKCNNDYVPVCGSNGESYQNECYLRQ  
AACKQQSEILVVSEGSCATDAGSGSGDGVHEGSGETSQKETSTCDICQFGAECDEDAED  
VWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLGRCQDNTTTTTK  
SEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSCRC DAGY  
TGQHCEKKDYSVLYVVP GPVRFQYVLIAAVIGTIQIAVICVVVLCITRK CPRSNRIHRQ  
KQNTGHYSSDNTTRASTRLI

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**FIGURE 407**

CTCGCAGCCGAGCGCGGCCGGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCAG  
ACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCTGT  
GTCCAGACTGAGGCCCCATTTGCATTGTTTAAACATACTTAGAAAATGAAGTGTTCAATTTTAA  
CATTCTCTCTCCAATTGGTTTAAATGCTGAATTACTGAAGAGGGCTAAGCAAAACCAGGTGCTT  
GCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCGCGCTCTCCCCGTGTCTCTCCACGACT  
CGCTCGGCCCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCCAGAGGAGGCCGACGTGCC  
CGAGCTCTCTCGGGGGTCCCGCCCCGCGAGCTTTCTTCTCGCCTTCGCATCTCTCTCTCGCGCG  
TCTTGACATGCCAGGAATAAAAAGGATACTCACTGTTACCATTCTGGCTCTCTGTCTTCCAA  
GCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGT  
GTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTTA  
ACCAAAATGGCGGGTATTTATGCATTCCCCGACAAACCCTGTGTATCGAGGGCCCTACTCGA  
ACCCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAA  
ACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGATGAAAGCAACC  
AATGTGTGGATGTGGACGAGTGTGCAACAGATTTCCACCAGTGCAACCCACCCAGATCTGCA  
TCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCAGT  
GCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCTCTGGAT  
CCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTGCCAAGATG  
TGAACGAGTGTGCCACCGAGAACCCTGCGTGCAAACCTGCGTCAACACCTACGGCTCTCTCA  
TCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTTCAATTGCAGTGATATGGACG  
AGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACCAGCCCGGCACATACTTCT  
GCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAAT  
GTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGCTACAATTTACAAGGGGGGCTTCA  
AATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGT  
GTCTGTCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTACCATCTTGTACCGGGACATGGACG  
TGGTGTCTAGGACGCTCCGTTCCCGCTGACATCTTCCAAATGCAAGCCACGACCCGCTACCCCTG  
GGGCTATTACATTTTCCAGATCAAATCTGGGAATGAGGGCAGAGAATTTTACATGCGGCAAA  
CGGGCCCCATCAGTGCCACCCTGGTGATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGC  
TGGACTTGGAATGATCACTGTCAACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGAC  
TGCGGATATATGTGTGCGAGTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTGCCTCT  
CATTGGCACCAAGGGACAGGAGAAGAGAGGAAATAACAGAGAGAATGAGAGCGACACAGACGT  
TAGGCATTTCTGTGCTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCTGACTCTCACCTGTA  
CTATTGCAGACCTGTCACCCTGCAGGACTTGCCACCCCCAGTTCCTATGACACAGTTATCAAA  
AAGTATTATCATTGCTCCCCTGATAGAAGATTGTTGGTGAATTTTCAAGGCCTTCAGTTTATT  
TCCACTATTTTCAAAGAAAATAGATTAGGTTTGGGGGGTCTGAGTCTATGTTCAAAGACTGT  
GAACAGCTTGCTGCTCACTTCTTCACTCTTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCA  
AAGACCCGGGAGCTGGCGGGGAACCTGGGAGTAGCTAGTTTGCTTTTTGCGTACACAGAGAA  
GGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTTAGAGAATGTGTTTCAAACCATGC  
CTGGTATTTTCAACCATAAAAGAAGTTTCAGTTGTCCTTAAATTTGTATAACGGTTTAAATCT  
GTCTTGTTCAATTTGAGTATTTTAAAAAATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGA  
CACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCTCTCCATTTTAGCCAGTGTTTTCTTT  
GAGGACCCCTTAATCTTGCTTTCTTTAGAAATTTTACCCAATTGGATTGGAATGCAGAGGTCT  
CCAAACTGATTAAATATTTGAAGAGA

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**FIGURE 408**

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSLICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 283-287, 296-300

**N-myristoylation sites.**

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248, 267-273, 310-316

**Aspartic acid and asparagine hydroxylation sites.**

amino acids 144-156, 181-193, 262-274

**Cell attachment sequence.**

amino acids 54-57

**Calcium-binding EGF-like.**

amino acids 131-166, 172-205, 211-245, 251-286

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**FIGURE 409**

CCCACGCGTCCGCGGACGCGTGGGTCTAGATTCTAGATCGCGAGCGGCCGCCGCGGGCTCA  
GGGAGGAGCACCGACTGCGCCGCACCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTGTT  
TCGCTGGTCTTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGTGTT  
TCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCTTACATTGAAGCTGGG  
AAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTGAACATGAAGAGT  
TATGCCGGCTTCCTCACCCTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTCTTCCCA  
GCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGGAGGTTCA  
TCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGACCTTGCGT  
GACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCAGTGGGCACA  
GGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGTAGCACGGGAT  
TTATACAGTGCACCTAATTCAGTTTTTCCAGATATTTCTGAATATAAAAATAATGACTTTTAT  
GTCAGTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTCATCCATTCCCTC  
AACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGATGGATATTCTGAT  
CCCGAATCAATTATAGGGGGCTATGCAGAAATTCCTGTACCAAATTGGCTTGTTGGATGAGAAG  
CAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATCAGGAAGCAGAACTGG  
TTTGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAACAAGTGATCCTTCTTAC  
TTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGTGCACGGAACCTGAGGAT  
CAGCTTTACTATGTGAAATTTTGTCACTCCCAGAGGTGAGACAAGCCATCCACGTGGGGAAT  
CAGACTTTTAATGATGGAATATAGTTGAAAAGTACTTGCGAGAAGATACAGTACAGTCAGTT  
AAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGATCTACAATGGCCAACTGGAC  
ATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGCATGGACTGGAAAGGATCCCG  
GAATACAAGAAGGCAGAAAAAAAGTTTGGAAAGATCTTTAAATCTGACAGTGAAGTGGCTGGT  
TACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTCGAGGTGGAGGACATATTTTACCC  
TATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGATTCAATTTATGGAAAAGGATGGGAT  
CCTTATGTTGGATTAACCTACCTTCCCAAAAGAGAACATCAGAGGTTTTCATTGCTGAAAAGAA  
AATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAATTATCTTTTCATATCTGCAAGATTTT  
TTTCATCAATAAAAATTATCCTTGAAACAAGTGAGCTTTTGTGTTTTGGGGGGAGATGTTTACT  
ACAAAATTAACATGAGTACATGAGTAAGAATTACATTATTTAACTTAAAGGATGAAAGGTATG  
GATGATGTGACACTGAGACAAGATGTATAAATGAAATTTAGGGTCTTGAATAGGAAGTTTTA  
ATTTCTCTAAGAGTAAGTGAAAAGTGACAGTTGTAACAAACAAAGCTGTAACATCTTTTTCTG  
CCAATAACAGAAGTTTGGCATGCCGTGAAGGTGTTTGGAAATATTATTGGATAAGAATAGCTC  
AATTATCCCAATAAATGGATGAAGCTATAATAGTTTTGGGGAAAAGATTCTCAAATGTATAA  
AGTCTTAGAACAAAAGAATTCTTTGAAATAAAAAATATTATATATAAAAGTAAAAA



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**FIGURE 410**

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSLV  
GPFPGLNMKSYAGFLTIVNKTYSNLSFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEHGP  
YVVTSMNMTLRDRDFPWTTLTMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQFFQI  
FPEYKNNDIFYVTGESYAGKYVPAIAHLIHSNLPVREVKINLNGIAIGDGYSDPESIIGGYAEF  
LYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNVGTGCSNYY  
NFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKFWLTEIMNNY  
KVLIIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEEKVWKIFKSDSEVAGYIRQAGDFHQV  
IIRGGGHILPYDQPLRAFDMINRFIYGKWDPPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

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**FIGURE 411**

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCGGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT  
CTACATGCGGCGAGCCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCCACCC  
CCTGGCCACACTCTTCAAGATCCTGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA  
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAAGCACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA  
GCGCTTCGCGCTCTTCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT  
GGACAAGCTCCGGCAGCGGCTCACCAGAAGCGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT  
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC  
CAGCATTGCCAGCTCAGGGCCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT  
GGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA  
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA  
CGGCTGCGGGAGCTCAAACGCCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC  
AGATGTGGGCGTGCACCTGCAGAAGCTGCCATCAACAATGAGGGCACCAAGCTCATCGTCTCTCAACAGCCTCAA  
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT  
CCACAACCTGCAGGAGATTGACCTCAAGGACACAACCTCAAGACCATCGAGGAGATCATCAGCTTCAGCACCT  
GCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACC  
CCTGGAGCGCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG  
CTACCTGGACCTCAGCCACAACAACCTGACCTTCCTCCCTGCCGACATCGGCCTCCTGCAGAACCTCCAGAACCT  
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT  
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG  
CAACCGGCTGGAGTGCCTGCCTGTGGAGCTGGGCGAGTGCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA  
GGACCTGTTCAACACACTGCCACCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTGAGCGAG  
GCCGCCCCGACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCCGAGGGGCGAGGCTAGCTTCTCCAG  
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCAGGAGCCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA  
GGACAGTATCTGTGGGCTGGCCCTTTTCTCCCTCTGAGACTCACGTCCCCAGGGCAAGTGCTTGTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCGAGGGCTGAG  
CTGCCACCAGAGGTCTGGGACCTCACTTTAGTTCTTGGTATTTATTTTTCTCCATCTCCACCTCCTTCATCC  
AGATAACTTATACATTCCCAAGAAAGTTAGCCCCAGATGGAAGGTGTTAGGGAAAGGTGGGCTGCCTTTTCCCC  
TTGTCTTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCAG  
CCATGGGACGGTCAACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCTCCAGCTGGA  
AAGGCCAGGCTGGAGCTTGCTCTTCAGTTTTTGTGGCAGTTTTAGTTTTTTGTTTTTTTTTTTAAATCAAA  
AAACAATTTTTTTTAAAAAAGCTTTGAAAATGGATGGTTTGGGTATTAAAAAGAAAAAAGCTTAAAAA  
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTTCCCTTGAGCAAAGCAGCCAGACGT  
TGAAGTGTGTTTCCCTTTCCCTGGGCGCAGGGTGCAAGGTGTCTTCCGATCTGGTGTGACCTTGGTCCAGGAGTT  
CTATTTGTTCTGGGGAGGGAGGTTTTTTGTTTGTGTTTTGGGTTTTTTTGGTGTCTTGTGTTTTCTTCTCCTCC  
ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG  
ACTCGGTTGGCTAATCCCCGGATGAACGGTGCTCCATTGCGACCTCCCCTCCTCGTGCCTGCCCTGCCTCTCCA  
CGCACAGTGTAAAGGAGCCAGAGGAGCCACTTCGCCCAGACTTTGTTTCCCCACCTCCTGCGGCATGGGTGTGT  
CCAGTGCCACCGCTGGCCTCCGCTGCTTCATCAGCCCTGTGCGCACCTGGTCTTCATGAAGAGCAGACACTTA  
GAGGCTGGTGGGAATGGGGAGGTGCCCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGGTTCCCGTCCCTGGCGC  
CTGGAGTGCACACAGCCAGTGGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT  
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT  
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTCTGTGATTGGATATAATCCTCAGAAATAATGCACACTAG  
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAAGTTGTAGACTCGGTACAGTATCAAATAAA  
ATCTATAACAGAAAAA

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**FIGURE 412**

MRQTIKVIKFIILICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYIS  
LVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSKRF  
AVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSIGIPDTVFDLVELEVLLK  
ELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTDIKEIPLWIYSLK  
TLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSINNEG  
KLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQHLHRLT  
CLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLTFLPADIG  
LLQNLQNLAITANRIETLPPELFQCRKLRLALHLGNNVLQSLPSRVGELTNLTQIELRGNRLEC  
LPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

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**FIGURE 413**

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCATC  
TTCATCATTCATATGAGGAAATAAGTGGTAAATCCTTGGAAATACA**AT**GAGACTCATCAGAA  
ACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAGAA  
AAAGGGAAGTATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTGACCC  
CAGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTTCAACTCCAGAGTTCAGATTTTC  
ATTCTGTCTCCAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCACAGCTGGATCTCA  
AAACCTTTGAATTCACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTGAAGAGTG  
TAACTTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTTTGACACCA  
TGCCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGAGTGGGGCAA  
AAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATACTGTCTCTTAGGAT  
TCAGAACTCTTCCTCATTATGAAGAAGGTAGCCTGCCATCTTAAACACAACAAAATGCACA  
TTGTTTTACCAATGGACACAAATTTCTGGGTTCTTTTGCGTGATGGAATCAAGACTTCAAAAA  
TATTAGAAATGACAAATATAGATGGCAAAAGCCAAATTTGTAAGTTATGAAATGCAACGAAATC  
TTAGTTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGATTTACTCTGGGACG  
ACCTTTTCCTTATCTTACAATTTGTTTGGCATAACATCAGTGGAACTTTTCCAGATCCGAAATG  
TGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTACTCAAATACTGTAATGA  
GAACATAAAAATTTGGAGCATGTACATTTAGAGTGTTTTACATTCAACAGGATAAAAATCTATT  
TGCTTTTGACCAAAAATGACATAGAAAACCTGACAATATCAAATGCACAAATGCCACACATGC  
TTTTCCCGAATTATCCTACGAAATCCAATATTTAAATTTTGCCAATAATATCTTAACAGACG  
AGTTGTTTTAAAGAAGTATCCAAGTGCCTCACTTGAAACTCTCATTTTGAATGGCAATAAAC  
TGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACAACACACCCTTGGAACACTTGGATCTGA  
GTCAAATCTATTACAAACATAAAAATGATGAAATTTGCTCATGGCCAGAACTGTGGTCAATA  
TGAATCTGTACATAATAAATTTGTCTGATTCTGTCTTCAGGTGCTTGCCCAAAGTATTTCAA  
TACTTGACCTAAATAATAACCAATCCAAGTGTACCTAAAGAGACTATTTCATCTGATGGCCT  
TACGAGAAGTAAATATTGCATTTAATTTTCTAAGTATCTCCCTGGATGCAGTCATTTAGTA  
GACTTTTCAGTTCTGAACATTGAAATGAATTCATTCTCAGCCCATCTCTGGATTTTGTTCAGA  
GCTGCCAGGAAGTTAAACTCTAAATGCGGGAAGAAATCCATTCCGGTGATCTGTGAATTA  
AAAATTTTATTTCAGCTTGAAACATATTTCAGAGGTTCATGATGGTTGGATGGTCAGATTCATCA  
CCTGTGAATACCCCTTTAAACCTAAGGGGAAGTAAAGACGTTTATCTCCACGAATTAT  
CTTGCAACACAGCTCTGTTGATTGTACCATTTGTGGTTATTATGCTAGTTCTGGGGTTGGCTG  
TGGCCTTCTGTCTCTCCACTTTGATCTGCCCTGGTATCTCAGGATGCTAGGTCAATGCACAC  
AAACATGGCACAGGGTTAGGAAAACAACCCCAAGAACAACTCAAGAGAAATGTCGGATTCCACG  
CATTTATTTTATACAGTGAACATGATTCTCTGTGGGTGAAGAATGAATTGATCCCCAATCTAG  
AGAAGGAAGATGGTTCTATCTTGATTTGCCTTTATGAAAGCTACTTTGACCCTGGCAAAAGCA  
TTAGTGAAAATATTGTAAGCTTCATTGAGAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCA  
ACTTTGTCCAGAATGAGTGGTGGCATTATGAATTTCTACTTTGCCCACCACAATCTCTCCATG  
AAAATCTGATCATATAATTCTTATCTTACTGGAACCCATTCCATTCTATTGCAATTTCCACCA  
GGTATCATAACTGAAAGCTCTCCTGGAAAAAAGCATACTTGGAATGGCCCAAGGATAGGC  
GTAAATGTGGGCTTTTCTGGGCAACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACCA  
GAGAAATGTATGAACTGCAGACATTACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCT  
CTCTGATGAGAACAGATTGTCTA**TAA**ATCCCACAGTCCCTTGGGAAGTTGGGGACCACATACA  
CTGTTGGGATGTACATTGATACAACCTTTATGATGGCAATTTGACAATATTTATTTAAATAAAA  
AAATGGTTATTTCCCTTCATATCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACA  
CCTTCACAAGTTTATAAGGGCTTATGGAAAAAGGTGTTTCATCCCAGGATTGTTTATAATCATG  
AAAAATGTGGCCAGGTGCAGTGGCTCACTCTTGTAAATCCCAGCACTATGGGAGGCCAAGGTGG  
GTGACCCACGAGGTCAAGAGATGGAGACCATCTTGGCCAAACATGGTGAAACCTGTCTCTACT  
AAAAATACAAAATTAGCTGGGCGTGATGGTGCACGCCTGTAGTCCCAGCTACTTGGGAGGCT  
GAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTG  
CACTCCAGCCTGGTGACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAA  
ATGGAAAAACATCCTCATGGCCACAAAAAAGGTCTAATTCATAAATTATAGTACATTAATGT  
AATATAATATTACATGCCACTAAAAAGAATAAGGTAGCTGTATATTTCTGGTATGGAAAAA  
CATATTAATATGTTATAAACTATTAGGTTGGTGCAAACTAATTGTGGTTTTTGCCATTGAAA  
TGGCATTGAAATAAAGGTGTAAGAAATCTATACCAGATGTAGTAACAGTGGTTGGGCTGTG  
GAGGTTGGATTACAGGGAGCATTGATTCTATGTTGTGTATTTCTATAATGTTTGAATGTTT  
TAGAATGAATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

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**FIGURE 414**

MRLIRNIYIFCSIIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQL  
QSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDLSF  
NDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLPILN  
TTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLLLNV  
DLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFRVFYIQ  
QDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLPHLKTLI  
LNGNKLETLSLVSCFANNTPLEHLDLSQNLQHKNDENCWPETVVNMNLSYNKLSDSVFRCL  
PKSIQILDNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIEMNFILSPS  
LDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLNLRGTRLKDV  
HLHELSCNTALLIVTIVVIMLVGLAVAFCCCLHFDLPWYLRMLGQCTQTWHRVRKTTQEQLKR  
NVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSI  
FVLSPNFVQNEWCHYEFYFAHNLFHENS DHIILILLEPIPFYCIPTRYHKLKALLEKKAYLE  
WPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLMRTDCL

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**FIGURE 415**

CGGACGCGTGGGCGGACGCGTGGGCGCTGGGCAAGGGCCGGGGCGCCGGGGCCGAGCCACCTCTTCCCCCTCCCCCGC  
TTCCCTGTGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACC CGGCGGCGCTGGGGGCTGACAGT  
CGGCAAAGTTTGGCCCCAAGAGGAAGTGGTCTCAAACCCCGGCAGGTGGCGACCAGGCCAGACCAGGGGCGCTCG  
CTGCGCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGGCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG  
AGAAGAGTGGCGGGCGGACGGAGAAAACAACTCCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCCG  
CCGCGCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCCGGGCCATGGAGCCCCCTGGGGAGGCGG  
CACCAGGGAGCCTGGGCGCCCCGGGGCTCCGCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTTCCG  
GCACCTCTGGACAGCCAGGATGCTGTTGGCCACCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCCATCCAG  
ACCGGATTATTTTTCCAAATCATGCTTGTGAGGACCCCCCAGCAGTGTCTTAGAAGTGCAGGGCACCTTACAGA  
GGCCCCCTGGTCCGGGACAGCCGCACCTCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAACAGACTG  
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCCTACGCTCCCCTCTCCAGCCAC  
TGATCTCCCTGTGTGAGGCACCTCCCAGCCCTCTGCAGCTGCCCCGGGGCAACGTCACCATCACTTACAGCTATG  
CTGGGGCCAGAGCACCATGGGCCAGGGCTTCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAG  
AGTTTCAGTGCCCTGAACCACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCT  
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCGCCCTCCCTGCCCTTGCAATG  
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT  
CCTGCCATTGGCTGCTGGACCCCATGATGGCCGGCGGCTGGCCGTGCGCTTCACAGCCCTGGACTTGGGCTTTG  
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCACCTTCA  
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTTACCACACAGTTGCTTGGAGCA  
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCCTGGGACAGACCCCTGTGGCTTAGGCT  
CTGGCCTGGGAGCTGGCGAAGGCCCTAGGTGAGCGCTGTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT  
GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCCTGTGGGGCTGCTGGCACCT  
CTGGTGCCACAGCTGCTACCTGCCTGTGACCGCTGCAACTACCAGACTTCTGTGCTGATGGAGCAGATGAGA  
GACGCTGTGGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCCTGTATGAGACGTGGGTGTGCG  
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCAATTACAG  
CTGCAGTCATTGGCAGCCTAGTGTGCGGCTGCTCCTGGTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA  
TTGCGACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC  
CTTCTACGGGCAGCTCATTGCCAGGGTGCCATCCCACCTGTAGAAGACTTCTCTACAGAGAATCCTAATGATA  
ACTCAGTGTGGGCAACCTGCGTTCTCTGTCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCCAGGTG  
CCCCCGTCTGTCAGCGGGGCGCTTGATGCGACGCTGTGACGCCGTCTCCGCGGCTGGGGCTTGCTCCCTCGAA  
CCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCAGGTACACCTTCTGCTGCTCCCTTGAGGCCCTAGATG  
GTGGCACAGGTCCAGCCCGTGAAGGCGGGCAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCCACTGCCATCA  
AGGCTCCCCTCCCATCTGCTAGCACGTCTCCAGCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC  
TGCCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCCGCTGTGCCCCAGCCTGGGGCCCC  
CAGGACCAACCCGAGCCCCCTGGACCCACACAGCAGTCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG  
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG  
CTCTACTGAGGCCTCTCCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTAGAGGTGGGTGAGCCTCCCCTCC  
ACCACTTCTTCCCTGTCCCTGGATTTCAGGGACTTGGTGGGCCTCCCGTTGACCCTATGTAGCTGCTATAAAGT  
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT  
TCACCACCACCTGCTCCCCACGCCACCACCATTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA  
GGTCTGGACACTCCATCCTTGCCAAACCTTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGA  
CCCTCCAGCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGG  
CTCACA AAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA  
GGAATCATACATCTC

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**FIGURE 416**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631
<subunit 1 of 1, 713 aa, 1 stop
<MW: 76193, pI: 5.42, NX(S/T): 4
MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTLLQRPLVRDSRTSPANCTWLILG
SKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAPMG
QGFLLSYSQDWLMCLQEEFQCLNHRCVSAVQRCDGVDACGDGSDEAGCSSDPFPGLTPRPVPS
LPCNVTLEDFYGVFSSPGYTHLASVSH PQSCHWLLDPHDGRRRLAVRFTALDLGFDAVHVYDG
PGPPSSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLPWDRPC
GLGSGLGAGEGLGERCYSEAQRCDGSWD CADGTDEEDCPGCPPGHFPCGAAGTSGATACYLPA
DRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPD CADGSDEWDCSYVLPKRV
ITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSYGQLIAQGA
IPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQGRRLMRRLVRRRLRRWGLLP
RTNTPARASEARSQVTPSAAPLEALDGGTG PAREGGAVGGQDGEQAPPLPIKAPLPSASTSPA
PTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLP SLGPPGPTRSPPGPHTAVLALEDEDDVLL
VPLAEPGVWVAEAEDEPLLT
```

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 442-462

**LDL-receptor class A (LDLRA) domain proteins**

amino acids 411-431, 152-171, 331-350 and 374-393

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**FIGURE 417**

GTCGTTCTTTGCTCTCTCGCGCCAGTCCTCTCCCTGGTTCTCTCAGCCGCTGTCGGAGGAGAGCACCCGGA  
GACGCGGGCTGCAGTCGCGGCGGCTTCTCCCCGCTGGGCGGCTCGCCGCTGGGCAGGTGCTGAGCGCCCCCTAG  
AGCCTCCCTTGCCGCTCCCTCCTCTGCCCCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCCG  
GCCCCGGAGGCGGCGGTGGATGCGGCGCTGGGCAGAACGAGCCGCGATTCAGCTGCCCGCGCCCCGGCG  
CCCCTGCGAGTCCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCTGCAGCCGCATC  
GCCCCCGAGCCACAGCCACGATGATCGGGGCTCCCTTCTCTGCTTGGATTCCCTAGCACACCACAGCTCAG  
CCAGAACAGAAGGCCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT  
GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACAAGCCTGCGCGTCTGCAGCAGTTGCCCT  
GTGGGGACCTTTACCAGGCATGAGAATGGCATGAGAAATGCCATGACTGTAGTCAGCCATGCCATGGCCAATG  
ATTGAGAAATTACCTTGTGCTGCCCTTGACTGACCGAGAATGCACCTGCCACCTGGCATGTTCCAGTCTAACGCT  
ACCTGTGCCCCCATAACGGTGTGTCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG  
TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCCTTCTAGTGTGATGAAATGCAAAGCATAACAGACTGT  
CTGAGTCAGAACCTGGTGGTGTCAAGCCGGGGACCAAGGAGACAGACAACGCTGTGGGCACACTCCCGTCTTTC  
TCCAGCTCCACCTCACCTTCCCCTGGCACAGCCATCTTCCACGCCCTGAGCACATGGAACCCATGAAGTCCCT  
TCCTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAATCCAACTCTTCTGCCTCTGTTAGACCAAAGTACTG  
AGTAGCATCCAGGAAGGGACAGTCCCTGACAACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCCTC  
CCAAACCTTCAGTAGTCAACCACCAGCAAGGCCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG  
GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG  
CATTTTGCATCAATGAGCATTGCCCCGGATGATTGTGCTTTTCTGCTGCTGGTGTGTTGGTGTGTTGGTGTG  
TGCAGTATCCGGAAAAGCTCGAGGACTCTGAAAAGGGGCCCCGGCAGGATCCCAGTGCCATTGTGGAAGGCA  
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT  
ATCCTGAAGCTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG  
AGGGAGGTGTGCTTTTCTCAATGGGTACACAGCCGACCACGAGCGGGCTACGCAGCTCTGCAGCACTGGACC  
ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTGTGGAG  
AAGATTTCGTGGGTGATGGAAGACACCACAGCTGGAACCTGACAACTAGCTCTCCCGATGAGCCCCAGCCCCG  
CTTAGCCCCGAGCCCCATCCCCAGCCCCAACGCGAACTTGAGAATTCCGCTCTCCTGACGCTGGAGCCTTCCCCA  
CAGGACAAGAACAAGGGCTTCTTCGTGGATGAGTCGGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTC  
TCCGCGCTGAGCAGGAACGGTCTCTTATTACCAAAGAAAAGAGACACAGTGTGCGGCAGGTACGCTGGAC  
CCCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG  
ATTCCCCAGGCTGAGGACAACTAGACCGGCTATTGAAATTTATGGAGTCAAGAGCCAGGAAGCCAGCCAGACC  
CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAAATTACTCA  
ATTTAGTGGCAGGGTGGTTTTTAATTTTCTTCTGTTTCTGATTTTTGTGTTTGGGGTGTGTGTGTGTGTTTGT  
GT  
TCTCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTTATAAGCCTTTGCCAGGTGTAAGTGTGTGAA  
ATACCCACCACTAAAGTTTTTTAAGTTCATATTTTCTCCATTTTGCCTTCTTATGTATTTTCAAGATTATTCTG  
TGCATTTTAAATTTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC  
TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTT  
AAAAACAATATTATTACTATTTTTATTATTGTTTGTCTTTATAAATTTTCTTAAAGATTAAAGAAATTTAAGA  
CCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTCATATTCATGG  
CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTACCTGGACACCGGTGAGAATGCTTGATTACTTGTAC  
TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT  
GACAACCTGGGCCACCAAGAACTTGAACCTTACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT  
GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG  
TTTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCTGGTGGGATTCTTACCAATT  
ACTTTAATTAATAATGGCTGCACTGTAAGAACCCTTGTCTGATATATTGCAACTATGCTCCATTTACAAATG  
TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTTGTGG  
GTAGTGGTGAAGACCGATATCAGAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTTA  
AAAAAAA



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**FIGURE 418**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594  
><subunit 1 of 1, 655 aa, 1 stop  
><MW: 71845, pI: 8.22, NX(S/T): 8  
MGTSPSSSTALASCSRIARRATATMIAGSLLLLLGFLSTTTAQPEQKASNLIQTYRHVD RATGQ  
VLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCAAL  
TDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKGTTETEDVRCKQCARGTFSDVPSSVMKCKAY  
TDCLSQNLVVIKPGTKETDNVCGTLPSPSSSTSPSPGTAFPRPEHMETHEVPSSTYVPKGMN  
STESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHILKLLPS  
MEATGGEKSSTPIKGPGRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVIVVCSIRKSSRTLK  
KGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGIDILKLVA AQVGSQWKDIYQFLCNAS  
EREVAAFSNGYTADHERAY AALQHW TIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTTQL  
ETDKLALPMSPSPSPSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLLRC DSTSSGS  
SALSRNGSFITKEK KDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFE  
IIGVKSQEASQTLLDSVYSHLPDLL

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 350-370

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**FIGURE 419**

ATGGCTGGTGACGGCGGGGCGGGCAGGGGACGGGGCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA  
ATCACCGCCTGGCCCGACTCCACCATGAACGTGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG  
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCCTCTACTGCTGGCT  
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACA  
GAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTTTAC  
CAGTTCTCCTGTGGGGCTGGATTTCGAGGAACCCCTGCCCGATGGGCGTTCTCGTGGAACACCTTCAACAGC  
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG  
CAGAAGACACAGCGCTTCTACCTATCTTGCCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGA  
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTATGGAGGTGTTGAAG  
GCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTACCCTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC  
AATGTTATCCAGGTGGACCACTGCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAAGTCCCAATGAG  
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAAGTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG  
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGCCCGAGGACCAGCGGCGCGAC  
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC  
CTGTCTTTCTTGCTGTCAACATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG  
CAGGTGTGAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG  
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCCTCTATGGCACTAAGAAG  
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGCTTTGCTTTGGGGTCACTCTTC  
GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG  
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT  
GATATGATTGGTTTCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT  
GAAGATTCTTTCTTCCAAACATGTTGAATTTGTACAACCTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG  
CCTCCCAGCCGAGACCACTGGAGCATGACCCCCCAGACAGTGAATGCCCTACTACCTTCCAACCTAAGAATGAGATC  
GTCTTCCCCGCTGGCATCCTGCAGGCCCTTCTATGCCCCGAACACCCCAAGGCCCTGAACCTCGGTGGCATC  
GGTGTGGTCATGGGCCATGAGTTGACGCATGCCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG  
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACACGGCCTGCATGGAGGAACAGTACAATCAA  
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG  
GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC  
AACCACAGCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCAGAGGGG  
CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCTGCGG  
CACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA  
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAA  
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTG  
TGCTCTGCTTTGGGGGTGCCCCTGCTCCAGCAGAGCCCCACCATTCACTGTGACATCTTCCGTGTACCCCT  
GCCTGGAAGAGGTCTGGGTGGGAGGCCAGTCCCATAGGAAGGAGTCTGCC

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**FIGURE 420**

MNVALQELGAGSNVGFQKGTROQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHS  
TCLTEACIRVAGKILESIDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL  
KHLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLEKIGGWNITGPWDQDNFME  
VLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLPSRDYYLNRTANEKVLTAFLDYM  
EELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAPSMDWL  
EFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSLDRRFES  
AQEKLETLTYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDQRSKEIAEGMISEIRTA  
EEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMNLNLY  
NFSKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNHPKALNFGGI  
GVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQVNGERLNGROT  
LGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFQVWCSVRTPESSHEGL  
VTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPGLCEVW

**Type II Transmembrane domain:**  
amino acids 32-57

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**FIGURE 421**

GGCGCCGCGTAGGCCCGGGAGGCCGGGCGGGCTGCGAGCGCCTGCCCCATGCGCCGCC  
GCCTCTCCGCACG**ATG**TTCCTTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGCAG  
GTCCGGGTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGCCTG  
CCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGGCCCCG  
GGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAGCCGCC  
CCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACCCTGGCAGTGCTGGTGCCCTT  
CCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGAGCAGGAA  
GAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAACCGGGCAGC  
GCTCATCAACGTGGGCTTCTGGAGAGCAGCAACAGCACGGACTACATTGCCATGCACGACGT  
TGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGCCCTTCCACGT  
GGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGCATCCTGCTGCT  
CTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGGCTGGGGCCGCGA  
GGACGACGAGTTCTACCGGCGCATTAAAGGGAGCTGGGCTCCAGCTTTTCCGCCCTCGGGAAT  
CACAACCTGGGTACAAGACATTCGCCACCTGCATGACCCAGCCTGGCGGAAGAGGGACCAGAA  
GCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGGAGGCCTGAACACTGT  
GAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCCCCCTGCACTGTCCTCAA  
CATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTCAGCT**GA**GCTGGATGGAC  
AGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGACAAGGCCTCAGGTCGTGG  
GCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCAAGCTACGCAATTGCAGCCA  
CCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGGGTGCTGGGACGCTGCTTGC  
CATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCCTGTCCGGGACCCCCCTGCCTTCCTGC  
TCACCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGA  
CAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGGTAGTGGGGAGGG  
CTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

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**FIGURE 422**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531  
><subunit 1 of 1, 327 aa, 1 stop  
><MW: 37406, pI: 9.30, NX(S/T): 1  
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGGFFSLLWLQLSCSGDVARAVRG  
QGQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKIRH  
HIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFPFAGPFHVASPE  
LHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGITTGY  
KTRHRLHDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVLNIMLD  
CDKTATPWCTFS

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

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**FIGURE 423**

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATAACCAGATC  
TCACCAGAGAGTCGCAGACACT**ATG**CTGCCTCCCATGGCCCTGCCCAGTGTGTCTGGATGCT  
GCTTTCCTGCCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCCCTC  
TCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGTTTTT  
GTCACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAACCTGGT  
GTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCCTGGTGAGGAGCATTAGTAACAG  
CTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATGGAGATGG  
ATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCCTCCACCAT  
CTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTGGAAAGATTA  
TAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACT**TAG**GGCAGGTGGGAAGTCAG  
CAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGACTCACCTGGAA  
GAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTCATGATCCTCCTTCTTTTCTCTT  
TTTCTTCACCTTCATTTTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATCTCAGAGAATAATA  
ATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 424**

&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

&lt;subunit 1 of 1, 175 aa, 1 stop

&lt;MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWMD  
ADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSSTD  
VMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD**Important features:****Signal peptide:**

amino acids 1-26

**C-type lectin domain signature.**

amino acids 146-171

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**FIGURE 425**

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCC**ATG**GTGGCGGCGACGGTGGCAGCGGCGTGG  
CTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGGTC  
AACATCCGGGGCAAACCTGGTGTGCTGCGTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTGAAT  
GTGGCCAGCGAGTGCGGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCGAGAC  
CTGGGCCCCCACCCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGGAGCCT  
GACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCCATGTTT  
AGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCAGACTTCT  
GGGAAGGAGCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGGTGGTAGGG  
GCTTGGGACCCAACCTGTGTCAGTGGAGGAGGTGAGACCCCAGATCACAGCGCTCGTGAGGAAG  
CTCATCCTACTGAAGCGAGAAGACTTAT**TAA**CCACCGCGTCTCCTCCTCCACCACCTCATCCCG  
CCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAGAGACCCACTGA  
CTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAAAAATCTAGTAT  
TTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAGAGCTCTTGACCAG  
TGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAATAGAAGTATATCAA  
GCAATAATCTCCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTACCTCATAGGGCTGTTG  
TGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGCCAAATAGGAGGCATTC  
AATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAATAAAAACTTGCATCCAAC  
ATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTAGTTGTTGTTATTTCTCTGTATTA  
TTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAAACAATCCAAACAATACCTCACGATATA  
AAATAAAAAATGAAAGTATCCTCCTCAAAAA



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**FIGURE 426**

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVNVVASECGFTDQH  
YRALQQLQORDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTGAH  
PAFKYLAQTSKGKEPTWNFWKYLVPDGTKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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**FIGURE 427**

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGGTGGAGATTGCC  
TTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTCTT  
CTCCAGCCAGTTCCAATCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGCTTT  
GCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCTTCAT  
GATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCAAATTT  
TTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTTAGGTTT  
AAGGTTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATCTTCACTA  
TTAATTGTAACGATTAAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTTTATCCCTG  
GGTGCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAATGTTATTCT  
AATATTAGTACATTCAAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTTAAAAGTTTTG  
AGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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**FIGURE 428**

MGVEIAFASVILTCLSLAAGVSQVVLLQPVPQTQETGPKAMGDLSCGFAGHS

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**FIGURE 429**

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCTG  
CACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAA**ATGG**TGCTGACCATCTTT  
GGGATACAATCTCATGGATACGAGGTTTTTAAACATCATCAGCCCAAGCAACAATGGTGGCAAT  
GTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGCAGGA  
TCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGCTCTCC  
CGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAATCTCCAA  
TGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTGGGTCAAG  
TACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCACCCATTGAG  
AAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACATAATGTCGGT  
GCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTGTGCAGACATT  
CATGTT**TAG**GATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCCTTGGTTTACAC  
TCAAAGTCAAATTAAATTCTTTCCCAATGCCCCAACTAATTTTGAGATTCAGTCAGAAAATA  
TAAATGCTGTATTTATA

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**FIGURE 430**

><ss.DNA57834  
><subunit 1 of 1, 176 aa, 1 stop  
><MW: 19616, pI: 7.11, NX(S/T): 0  
MVLTIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTTIFDYKH  
GYIASRVLSRRACFILKMDHQNIPPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLESLIK  
DVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

**Important features:****Signal peptide:**

Amino acids 1-26

**N-myristoylation sites:**

Amino acids 48-54;153-159;156-162;167-173

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**FIGURE 431**

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCCA  
CAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTATCA  
GAGACATTGAGAGGCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTATTT  
TGA CTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAATCAT  
GACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGATGGAGA  
GTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAACTTGATCAAATAAA  
GGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGAGTGTGGG  
CAGACACTTTTTTGGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGGTCACTGTC  
CAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGATGGATAGTA  
GCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACATCGACCTCAG  
AAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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**FIGURE 432**

MSRSSKVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILTE  
QLEAEREKMLLAKGSQKS

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**FIGURE 433**

GAATTCGTGTCTCGGCACTCACTCCCGGCCGCGGACAGGGAGCTTTCGCTGGCGCGCTTGGCCGGCGACAGGA  
CAGGTTCCGGGACGTCCATCTGTCCATCCGTCGGAGAGAAATTACAGATCCGCAGCCCCGGGATGGGGCCGGCCC  
CGCTGCCGCTGCTGCTGGGCCTCTTCCTCCCCGCGCTCTGGCGTAGAGCTATCACTGAGGCAAGGGAAGAAGCCA  
AGCCTTACCCGCTATTCCCGGACCTTTTCCAGGGAGCCTGCAAACTGACCACACACCGCTGTTATCCCTTCCTC  
ACGCCAGTGGGTACCAGCCTGCCTTGATGTTTTCCCAACCCAGCCTGGAAGACCACATACAGGAAACGTAGCCATT  
CCCCAGGTGACCTCTGTGCAATCAAAGCCCCCTACCGCCTCTTGCCCTCAAACACACAGTTGGACACATAATACTT  
TCTGAACATAAAGGTGTCAAATTTAATTGCTCAATCAATGTACCTAATATATATACCAGGACACCACAATTTCTTGG  
TGGAAAGATGGGAAGGAATTGCTTGGGGGACATCATCGAATTACACAGTTTTATCCAGATGATGAAGTTACAGCA  
ATAATCGCTTCCTTCAGCATAACCAGTGTGCAGCGTTCAGACAATGGGTCTGATATCTGTAAGATGAAAATAAAC  
AATGAAGAGATCGTGTCTGATCCCATCTACATCGAAGTACAAGGACTTCCTCACTTTACTAAGCAGCCTGAGAGC  
ATGAATGTCAACAGAAACACAGCCTTCAACCTCACCTGTGAGGCTGTGGGCCCCGCTGAGCCCGTCAACATTTTC  
TGCGTTCAAACAGTAGCCGTGTTAACGAACAGCCTGAAAAATCCCCGGCGTGCTAACTGTTCCAGGCGTGACG  
GAGATGGCGGTCTTCAGTTGTGAGGCCCCACATGACAAAGGGCTGACCGTGTCCAGGGAGTGACAGATCAACATC  
AAAGCAATTCCCTCCCCACCAACTGAAGTCAGCATCCGTAACAGCACTGCACACAGCATTCTGATCTCCTGGGTT  
CCTGGTTTTGATGGTACTCCCCGTTGAGGAATTGCAGCATTCAAGTCAAGGAAGCTGATCCGCTGGGTAATGGC  
TCAGTCATGATTTTTAACACCTCTGCCTTACCACATCTGTACCAATCAAGCAGCTGCAAGCCCTGGCTAATTAC  
AGCATTGGTGTTCCTGCATGAATGAAATAGGCTGGTCTGCAGTGAGCCCTTGGATTCTAGCAAGCAGACTGAA  
GGAGCCCCATCAGTAGCACCTTTAAATGTCACTGTGTTTCTGAATGAATCTAGTGATAATGTGGACATCAGATGG  
ATGAAGCCTCCGACTAAGCAGCAGGATGGAGAAGTGGTGGGCTACCGGATATCCACGTGTGGCAGAGTGCAGGG  
ATTTCCAAAGAGCTCTTGGAGGAAGTTGGCCAGAATGGCAGCCGAGCTCGGATCTCTGTTCAAGTCCACAATGCT  
ACGTGCACAGTGAGGATTGCAGCCGTACCCAGAGGGGGAGTTGGGCCCTTCAGTGATCCAGTGAAAATATTTATC  
CCTGCACACGGTTGGGTAGATTATGCCCCCTCTTCACTCCGGCGCCTGGCAACGCAGATCCTGTGCTCATCATC  
TTTGGCTGCTTTTGTGGATTATTTTTGATTGGGTTGATTTTATACATCTCCTTGGCCATCAGAAAAAGAGTCCAG  
GAGACAAAGTTTGGGAATGCATTACAGAGGAGGATTCTGAATTAGTGGTGAATTTATATAGCAAAGAAATCCTTC  
TGTCGGCGAGCCATTGAACCTACCTTACATAGCTTGGGAGTCAGTGAGGAACACAAAATAAACTAGAAGATGTT  
GTGATTGACAGGAATCTTCTAATCTTGGAAAAATCTGGGTGAAGGAGAGTTTGGGTCTGTAATGGAAGGAAT  
CTTAAGCAGGAAGATGGGACCTCTCTGAAAGTGGCAGTGAAGACCATGAAGTTGGACAACTCTTCACATCGGGAG  
ATCGAGGAGTTTCTCAGTGAGGCAGCGTGCATGAAAGACTTCAGCCACCCAAATGTCACTCGACTTCTAGGTGTG  
TGTATAGAAATGAGCTCTCAAGGCATCCCAAAGCCCCATGGTAATTTTACCCTTCATGAAATACGGGGACCTGCAT  
ACTTACTTACTTTATTCCTGATTGGAGACAGGACCAAAGCATATTCCTCTGCAGACACTATTGAAGTTTCATGGTG  
GATATTGCCCCGGGAATGGAGTATCTGAGCAACAGGAATTTTCTTCATCGAGATTTAGCTGCTCGAACTGCATG  
TTGCGAGATGACATGACTGTCTGTGTTGCGGACTTCGGCCTCTCTAAGAAGATTTACAGTGCGCGATTATTACCGC  
CAAGGCCGATTGCTAAGATGCCGTGTTAAATGGATCGCCATAGAAAGTCTTGACAGACCGAGTCTACACAAGTAAA  
AGTGATGTGTGGGCATTTGGCGTGACCATGTGGGAAATACGTACGCGGGGAATGACTCCCTATCCTGGGGTCCAG  
AACCATGAGATGTATGACTATCTTCTCCATGGCCACAGGTTGAAGCAGCCGAAGACTGCCTGGATGAAGTGTAT  
GAAATAATGTACTCTTGCTGGAGAACCGATCCCTTAGACCGCCCCACCTTTTCACTATTGAGGCTGCAGCTAGAA  
AAACTCTTAGAAAGTTTGCTGACGTTCCGGAACCAAGCAGACGTTATTTACGTCAATACACAGTTGCTGGAGAGC  
TCTGAGGGCCTGGCCCAGGGCCCCACCTTGCTCCACTGGACTTGAACATCGACCCTGACTCTATAATTGCCTCC  
TGCACTCCCCGCGCTGCCATCAGTGTGGTCAAGCAGAAAGTTTATGACAGCAACCTCATGAAGGACGGTACATC  
CTGAATGGGGGAGTGAAGGAATGGGAAGATCTGACTTCTGCCCCCTCTGCTGCAGTCAAGAGTGAAGAAGCAGT  
GTTTTACCGGGGAGAGACTTGTTAGGAATGGGGTCTCCTGGTCCCATTTCGAGCATGCTGCCCTTGGGAAGCTCA  
TTGCCCCGATGAACTTTTGTTGCTGACGACTCCTCAGAAGGCTCAGAAGTCTGATGTGAGGAGAGGTGCGGGGA  
GACATTCAAAAATCAAGCCAATTCTTCTGCTGTAGGAGAATCCAATTGTACCTGATGTTTTTGGTATTTGTCTT  
CCTTACCAAGTGAACCTCATGGCCCCAAGCACCAGATGAATGTTGTTAAGGAAGCTGTCAATAAAAATACATAA  
TATATATTTATTTAAAGAGAAAAATATGTATATCATGAAAAAGACAAGGATATTTTAAATAAACATTACTTA  
TTTCATTTCACTTATCTTGCATATCTTAAATTAAGCTTCAGCTGCTCCTTGATATTAACCTTTGTACAGAGTTG  
AAGTTGTTTTTCAACTTCTTTTCTTTTCACTTATTAATGTAATAATATTTGTAATAATGAATGCCATATT  
TGACTTGGCTTCTGGTCTTGATGATTTGATAAGATGATTAATTTTCTGATATGGCTTCCATAATAAATTGAA  
ATAGGA



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**FIGURE 434**

MGPAPLPILLGLFLPALWRRRAITEAREEAKPYPLFPGFPGSLQTDHTPLLSLPHASGYQPALMFSPTQPGRPHT  
GNVAIPQVTSVESKPLPPLAFKHTVGHIILSEHKGVKFNCSINVPNIYQDTTISWWKDGKELGGHHRITQFYPD  
DEVTAIIASFSITSVQRSDNGSYICKMKINNEEIVSDPIYIEVQGLPHFTKQPESMNVTRNTAFNLTCQAVGPPE  
PVNIFWVQNSSRVNEQPEKSPGVLTVPGLTEMAVFSCAHNKGLTVSQGVQINIKAI P SPPTTEVSIRNSTAHSI  
LISWVPGFDGYSPFRNCISQVKEADPLGNGSVMIFNTSALPHLYQIKQLQALANYSIGVSCMNEIGWSAVSPWIL  
ASTTEGAPSVAPLNVTVFLNESSDNVDIRWMKPPTKQQDGELVGYRISHVWQSAGISKELLEEVGQNGSRARISV  
QVHNATCTVRIAAVTRGGVGPFSDFVKIFIPAHGWVDYAPSSTPAPGNADPVLIIFGCFCGFI LIGLILYISLAI  
RKRVOETKFGNAFTEEDSELVVNYIAKKSFCRRRAIELTLHSLGVSEELQNKLEDVVIDRNLILGKILGEGEFGS  
VMEGNLKQEDGTSKLVAVKTMKLDNSSHREIEEFLSEAACMKDFSHPNVIRLLGVCIEMSSQGIPKPMVILPFMK  
YGD LHTYLLYSRLETGPKHIPLQTL LKFMVDIALGMEYLSNRNFLHRDLAARNCLRDDMTVCVADFGLSKKIYS  
GDYYRQGRIAKMPVKWIAIESLADRVYTSKSDVWAFGVTMWEIRTRGMTYPYGVQNHMYDYLLHGHRLKQPEDC  
LDELYEIMYSCWRTDPLDRPTFSVLRLQLEKLLLESPLDVRNQADVIVNTQLLESSEGLAQGPTLAPLDLNIIDPD  
SIIASCTPRAAISVVTAEVHDSKPHEGRYIILNGGSEEWEDLTSAPSAAVTAEKNSVLPGERLVRNGVSWSHSSML  
PLGSSLPDELLFADDSSEGSEVLM

Signal sequence:	Amino acids 1-18
Transmembrane domain:	Amino acids 501-520
N-glycosylation sites:	Amino acids 114-118;170-174;207-211; 215-219;234-238;294-298;316-320;329-333; 336-340;354-358;389-393;395-399;442-446; 454-458;625-629
Tyrosine kinase phosphorylation sites:	Amino acids 675-683;865-873;923-930
N-myristoylation sites:	Amino acids 41-47;110-116;171-177; 269-275;275-281;440-446;507-513;535-541; 966-972
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 351-362
Tyrosine protein kinases specific active-site signature:	Amino acids 719-732

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**FIGURE 435**

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAAGTACTGGATG  
TGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAAGTGTCCGATTCTGATTCCGGCAAGGAT  
CCAAGCATGGAAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTCCCTG  
CTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTGGGGC  
CCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCCTCTACTCTCTGAGGCGCTGCCTG  
AGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGACTGCCCCA  
CCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCACCATGGC  
CAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCAAGTGCCAA  
GCCAAAGGAACAACCCTGGTTGTTGAAGTAGCACCTAAGGTCTTAGATGGTACGCGTTGCTAT  
ACAGAATCTTTGGATATGTGCATCAGTGGTTTTATGCCAAATTGTTGGCTGCGATCACCAGCTG  
GGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCACCTGCCGGCTG  
GTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACTGTGGTTGCACTT  
CCCTATGGAAGTAGACATATTCGCCTTGCTTTAAAAGGTCCTGATCACTTATATCTGGAAACC  
AAAACCCTCCAGGGGACTAAAAGGTGAAAACAGTCTCAGCTCCACAGGAACCTTTCCTTGTGGAC  
AATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGAATGGCTGGACCACTC  
ACAGCAGATTTTCAATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAGTACAGTCCAGTTCATC  
TTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTCCTTGCTCAGCAACCTGT  
GGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGGAGCAACCGTGTGGTTGCT  
GACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACCAAGCTTCAGGAGTGCAAC  
TTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGCCTTATGACCTCTACCATCCC  
CTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCCTCGTGTGGGGGGGGCATCCAG  
AGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCATGTCACTTCAGTGGAGAGTGG  
AAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCTGCAACATTTTTGACTGCCCTAAA  
TGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGTGGCCAGGGCCTCAGATAACCGTGTG  
GTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGGCTGTAGCCCCAAAACAAAGCCCCAC  
ATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATAAACCCAAAGAGAACTTCCAGTCGAG  
GCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTAGAAGAAGGAGCTGCTGTGTCAGAGGAG  
CCCTCGTTAAGTTGTAAAAGCACAGACTGTTCTATATTTGAAACTGTTTTGTTTAAAGAAAGCA  
GTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGAACTAAGTGTAATCATCTCACCAAAGCTTT  
TTGGCTCTCAAATTAAAGATTGATTAGTTTCAAAAAAAAAA

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**FIGURE 436**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847  
<subunit 1 of 1, 525 aa, 1 stop  
<MW: 58416, pI: 6.62, NX(S/T): 1  
MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCLSS  
KSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPSCLKCQAK  
GTTLVVELAPKVLDTGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCRLVR  
GQYKSQLSATKSDDTVVALPYGSRHIRLVKGPDLHLYLETCTLQGTKGENSLSSSTGTFLVDNS  
SVDFQKFDPKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCSATCGG  
GYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYDLYHPLP  
RWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNIFDCPKWL  
AQEWSPTVTTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPKKLPVEAK  
LPWFKQAQEELEGA AVSEEPS

**Important features:****Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

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**FIGURE 437**

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCCTGT  
CTTTATGTCTTTCTCCTCTTCCTATTCTGTTCATCTCCCTCACTTAAGTCTCAGGCCTGTCAGC  
AGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATGTTA  
TGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGTGATC  
TCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTTGAAATCTGGCATGAGATG  
GCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCCTCCTCCCAAGTCTGT  
TCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAGCAATCTG  
TGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGTAGCCACCT  
CCCTGTCTAGCCAGTATTAACATGTCCCCCTTCCCCCTGCCCGCCGTAGATTTCAGGACATTTCGC  
CCCTGTGTGCCACCAAACCAGGACTTTCCCCCTTGGCTTGGCATCCCTGGCTCTCTCCTGGTAC  
CCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACTATGGCGATGGC  
CATGATGTTACAATCCCACTTGCCTGAATAATCAAGTGGGAAGGGGAAGCAGAGGGAAATGGG  
GCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACCAAAGGGAAGCAACAGG  
AACTTCTGCAACTGGTTTTTATCGGAAAAGATCATCCTGCCTGCAGATGCTGTTGAAGGGGCAC  
AAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAAATAGAACAGTCTGCT  
GGGAGTCAGACCTGGAATTCTGATTCCAAACTCTTTATTACTTTGGGAAGTCACTCAGCCTCC  
CCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACA  
ATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATA  
AAACAAAATTCTCTAACACTGAAA

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**FIGURE 438**

MWLPLGLLSLCLSPILSSPSLKSQLQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGMEH  
RNHLCFCDLYDRATSPPLKCSLL

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**FIGURE 439**

GTTCCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCTT  
GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGTGTCTGAGGGGCTGG  
GGCAAAGGTGAAAGAGTTTTCAGAACAAAGCTTCTGGAACCCATGACCCATGAAGTCTTGTGCGACATTTATACCGT  
CTGAGGGTAGCAGCTCGAACTAGAAGAAGTGGAGTGTGGCCAGGGACGGCAGTATCTCTTTGTGTGACCTGGC  
GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCAATGCTGCGTGGGACGATGACGGCCTGGAGAGGAATG  
AGGCCTGAGGTCACACTGGCTTGCTCTCTCTAGCCACAGCAGGCTGCTTTGCTGACTTGAAAGAGGTCCCTCAG  
GTCACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCCGAGGACACTGTGATCTTGGGCTGCGTGGTGGAACTCCCA  
AGGATGAATGTAACCTGGCGCCTGAATGGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGCTCTCATCACC  
CACGGGACCCCTCGTCACTGACCTTAAACAACCACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCTGCG  
GGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCACGTG  
ATTGAAGTGGATGAGGGAAACACAGCAGTCATTGCCCTGCCACCTGCTGAGAGCCACCCCAAAGCCAGGTCCCG  
TACAGCGTCAACAAGAGTGGCTGGAGGCCTCCAGAGGTAACCTGATCATGCCCTCAGGGAACCTCCAGATT  
GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGACGCTACAACCCAGTGACCCAGGAAGTGAAGAAC  
TCCGGCTCCAGCGACAGGCTACGTGTGCGCGCTCCACCGCTGAGGCTGCCGCTCATCTACCCCCAGAGGCTC  
CAAACCATCATCGTCACCAAAGGCCAGAGTCTCATCTGAGTGTGTGGCCAGTGAATCCCAACCCCAAGGCTC  
ACCTGGGCAAGGATGGGTCCAGTGTACCGGCTACAACAAGACGCGCTTCTGCTGAGCAACCTCTCATCGAC  
ACCACGAGGAGGAGTACAGGCACCTACCGCTGCTGCGGACCAATGGGGTGGGCGAGCCCGGGGCGAGCGGTC  
ATCCTCTACAAATGTCCAGGTGTTTGAACCCCTGAGGTACCATGGAGCTATCCAGCTGGTCTATCCCCCTGGGG  
CAGAGTGCCAAGCTTACCTGTGAGGTGCGTGGGAACCCCCCGCCTCCGCTGCTGTGGCTGAGGAATGCTGTGCC  
CTCATCTCCAGCCAGCGCCTCCGGCTCTCCCGCAGGGCCCTGCGCTGCTCAGCATGGGCGCTGAGGACGAAGGC  
GTCTACCAAGTGCATGGCCGAGAAGGAGTGGGAGCGCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC  
ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCCTGTATCACCTCCAAACTCGGCAAC  
CCTGAGCAGATGCTGAGGGGGCAACCGGCGCTCCCCAGACCCCCAACGTCAGTGGGGCTGCTTCCCCGAAGTGT  
CCAGGAGAGAAGGGGCGAGGGGCTCCCGCGAGGCTCCCATCATCTCAGCTCGCCCCGCACTCCAAGACAGAC  
TCATATGAATGCTGTGGCGGCTCGGCATGAGGGCAGTGGCCGGGCGCAATCCTCTACTATGTGGTGAACAC  
CGCAAGCAGGTCACAAATTCCTCTGACGATTGGACCATCTCTGGCATTCCAGCCAAACGACCCGCTGACCTC  
ACCAGACTTGACCCCGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAACCTGTGCGGGAGAGGGCCAGACAGCC  
ATGGTCACCTTCCGAACCTGGACGGCGGCCCCAAACCCGAGATCATGGCCAGCAAAGAGCAGCAGATCCAGAGAGAC  
GACCTGGAGCCAGTCCCCAGAGCAGCAGCCAGCAGACCCAGCGCCCTCTCCCCCAGAAAGCTCCCCACAG  
CCCACCATCTCCAGGCTCCGAGACCTCAGTGTACGTGACCTGGATTCGCCGTGGGAATGGTGGGTTCGCAATC  
CAGTCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACCAGCGCCATCCCCCA  
TCGCGGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACTCCTACAAGTTTCGAGTCCGGGCTGTGAACATG  
CTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGCGGCTACAGCGGTGCGGTGTACGAGG  
CCCGTGGCAGGTCTTATATACCTTCACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC  
CCAGCAAGTAACAACAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTGAATGATAGT  
GACTACAGAAGGATATGGTGGAGGGGACAAGTACTGGCACTCCATCAGCCACCTGCAGCCAGAGACCTCCTAC  
GACATTAAGATGCAGTGTCTCAATGAAGGAGGGGAGAGCGAGTTTCAGCAACGTGATGATCTGTGAGACCAAGCT  
CGGAAGTCTTCTGGCCAGCCTGGTGCAGTGCACCCCCAACTCTGGCCCCACACAGCCGCCCTTCTCTGAAACC  
ATAGAGCGGCGGTGGGCACTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGCGGGTCTG  
CTGGGCTCCATCGTTCTCATCATGTCACCTTCATCCCTTCTGCTTGTGGAGGGCTGGTCTAAGCAAAAACAT  
ACAACAGACCTGGGTTTTCTCGAAGTGCCCTTCCACCTCCTGCCCCGATATCTATGTTGGTGGCATTGGGAGGACTC  
CCAGGCCACAGGCCAGTGAGCAGCCCTACCTCAGTGGCATCAGTGGACGGCCTGTGCTAATGGGATCCACATG  
AATAGGGGCTGCCCCCTCGGCTGCAGTGGGCTACCCGGGCATGAAGCCCCAGCAGCACTGCCAGGCCAGCTTCAG  
CAGCAGAGTGACACCAGCAGCCTGCTGAGGCAGACCCATCTTGGCAATGGATATGACCCCCAAAGTCACAGATC  
ACGAGGGGTCCCAAGTCTAGCCCGACGAGGGCTCTTCTTATACACACTGCCCGACGACTCCACTCACCAGCTG  
CTGCAGCCCCATCAGACTGCTGCCAACGCCAGGAGCAGCCTGCTGCTGTGGGCCAGTACGGGGTGGAGAGAGCC  
CCGACAGTCTGTCTGCTGGAAGCAGTGTGGGACCTCCATTTCACTCAGGGCCCCATGCTGCTTGGGCTTGTG  
CCAGTTGAAGAGGTGGACAGTCTGACTCCTGCCAAGTGAGTGGAGGAGACTGGTGTCCCCAGCACCCGTAAGG  
GCCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCCGGGGCCACTGGTGGTGTGTCTTTTGAACACCACT  
CTCACAATTTAGGCAGAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAGAAAAA  
AGAGACAGAGAAAATTGGTATTATTTTCTATTATAGCCATATTTATATATTATGCACTTGTAAATAAATGTA  
TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTTACCCGTTGAGGTTGGAGAGGGAAAAATAAAGAGCTGCCA  
CCTAACAGGAGTCACCCAGGAAAGCACCGCACAGGCTGGCGCGGACAGACTCCTAACCTGGGGCTCTGCAGTG  
GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTCATCAGGAGCA  
TGAGGGAACAGCAAGGGGCACGGTATCAGAGCTGGAGACCCACACAGATGGCTGGATCCGGTGCTACGGGAA  
ACATTTTCTAAGATGCCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAATAAACCTTCCAGAA  
CAATAATCCGTGGCAACATATCTCTGTAAAAACAACACTGTAACCTTAATAAATGTTAGTCTTCCCTGTAAAA

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**FIGURE 440**

MLRGTMTAWRGMRPEVTIACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEPPR  
MNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTLAN  
LQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMP SGNLQIVN  
ASQEDEGMYKCAAYNPVTQEVKTS GSSDRLRVRRSTAEAAARI IYPPEAQTIIVTKGQSLILEC  
VASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGAIVILY  
NVQVFEPPEVTMELS QLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLSRRALRV  
LSMGPEDEGVYQCMANEVGS AHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSKLGNPEQM  
LRGQPALPRPPTS VGPASPKCPGEGKGQGAPEAPIILSSPRTSKTDSYELVWRPRHEGSGRAP  
ILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGEGQTAMVTFR  
TGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASETSVYVTWIPR  
GNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRVRALNMLGESEP  
SAPSRPYVVS GYSGRVYERP VAGPYITFTDAVNETTIMLKWMIIPASNNNTPIHGFYIYYRPT  
DSDNDSYKKDMVEGD KYWHSISHLQPETSYDIKMOCFNEGGESEFSNVMICETKARKSSGQP  
GRLPPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSI VLIIVTFIPFCLWRAW  
SKQKHTTDLGFPR SALPPSCPYTMVPLGGLPGHQASGPYLSGISGRACANGIHMNRGCPSAA  
VGYPGMKPQQHCPGELQQQSDTSSLLRQTHLNGYDPQSHQITRGPKSSPDEGSFLYTL PDDS  
THQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHS GPPCCLGLVPVEEVDSPD  
SCQVSGGDWCPQHVPV GAYVGQEPGMQLSPGPLVRVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879

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**FIGURE 441**

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGGC  
TCTGGCAGGCTCCTGGCAGCATGGCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCTGG  
GCCTGGCCCAGCCAGCCTCTGCCCCGCCGGAAGCTGCTGGTGTTTCTGCTGGATGGTTTTCGCT  
CAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTCAAAGAGATTGTGAGCAGGG  
GAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTATACCC  
TAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACACATGTGGGACCCCAACCA  
CCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGGAATGGAT  
CAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTACTGGCCAG  
GCTGTGAGGTTGAGATTCTGGGTGTGAGACCCACCTACTGCCTAGAATATAAAAATGTCCCAA  
CGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGTGGCCGGGCGG  
ACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGGGCCTGCATCTC  
CGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCTGAAGTACATGACCAAGTGGATCC  
AGGAGCGGGGCTGCAGGACCGCCTGAACGTCAATTATTTCTCGGATCACGGAATGACCGACA  
TTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAATGACCTGCAGCAAG  
TGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTGGGAAACACTCTGAGATATATA  
ACAAACTGAGCACAGTGGAAACACATGACTGTCTACGAGAAAGAAGCCATCCCAAGCAGGTTCT  
ATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGATGAAGGCTGGTTCATAA  
CTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCAGGCGGGAAGGTTGGCAGC  
GTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGCATCTTCTGGCCTTCGGAC  
CTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATCAGGTCGGTGGACGTCTACAATGTCATGT  
GCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCTGGTCCAGGGTGATGTGCATGC  
TGAAGGGCCGCGCCGGCACTGCCCCGCCTGTCTGGCCAGCCACTGTGCCCTGGCACTGATTC  
TTCTCTTCTGCTTGCATAACTGATCATATTGCTTGTCTCAGAAAAAACACCATCAGCAAAG  
TGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGAATAATAGCTTCATTAACACAATCA  
AGACCATGCACATTGTAAATACATTATTCTTGGATAATTCTATACATAAAAGTTCCTACTTGT  
TAAA



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**FIGURE 442**

MAVKLGTLALLALGLAQPASARRKLLVFLLDGFRSDYISDEALES LPGFKEIVSRGVKVDYL  
TPDFPSLSYPNYYTLM TGRHCEVHQMIGNYMWDPTTNKSF DIGVNKDSL MPLWWNGSEPLWVT  
LTKAKRKVYMYYPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLA AIYH  
ERIDVEGHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRLNVIIFSDHGMDIFWMDKV  
IELNKYISLNDLQQVKDRGPVVS LWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYKKGKF  
VSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGW HGYNELMDMRGIFLAFGPDFKSNF  
RAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALILLFLLA

**Important features of the protein:****Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 100-104, 118-122, 341-345, 404-408

**N-myristoylation sites.**

amino acids 148-154, 365-371

**Amidation site.**

amino acids 343-347

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**FIGURE 443**

AGTGACTGCAGCCTTCCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAGC  
ACCA GTGTGTGAGGGGAGCAGGCAGCGGTCCCTAGCCAGTTCCTTGATCCTGCCAGACCACCCA  
GCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCATCCT  
GGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGGTTCC  
TGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTCAAAG  
CCTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAAGGAATC  
AACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGAGGAGCGT  
CCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCCTTCATCC  
CAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACCTTTATTAAGA  
CTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGTATCCCCCGAG  
AGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTCTTCCCTGTCC  
CAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGTAACATTCTTGTG  
CTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCATAGTGAATATCCC  
CAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGTCTACATTAAAAAT  
ATAATGTCTCTCTATTCTCAACAATAAAGGATTTTTGCATATGAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 444**

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKA  
LSQASTDPKESTSPKRDMDHFFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGKSS  
LGTEEQRP

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 36-45

**N-myristoylation site.**

amino acids 33-39, 59-65

**Amidation site.**

amino acids 90-94

**Leucine zipper pattern.**

amino acids 43-65

**Tachykinin family signature.**

amino acids 86-92

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**FIGURE 445**

TGGACTTCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTACAT  
CCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTA  
CCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGA  
TGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCTGTGCGCACGCCCACGCCGAGCCCCGCCCAAGATGG  
CAAAGTCTACATCAACATGCCAGGCAGGGGCTTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATC  
CTGGATGGTGTGTGGTGGCACAGGAACCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGAAACACCA

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**FIGURE 446**

MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCSLSLPLLAGLVAADAVASLLIVGAVFLCARPR  
RSPAQDGKVYINMPGRG

Signal peptide:	Amino acids 1-18
transmembrane domain:	Amino acids 51-70
Glycosaminoglycan attachment site:	Amino acids 40-44
N-myristoylation sites:	Amino acids 34-40;37-43;52-58
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 29-40

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**FIGURE 447**

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCA**ATG**ACGCTCCTCCC  
CGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGG  
GCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCAGGC  
CCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTC  
CAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCC  
GGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGGAG  
ATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTG  
CAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCT  
CCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACC  
TGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCC  
CCGTTCAGTG**TGA**CCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGCTCCCCAGAGGG  
CACCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCAACACTACCCTTGGGGTC  
TGGGCATTCGCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGT  
TGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGG  
CTGCCTGTACCTTGGCTCCCTGTCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGC  
CCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAG  
TGTACGTGTATTATTAAACTGATGAACACATCCCCAAAA

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## **FIGURE 448**

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHELLARGAKWGQALP  
VALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYYRVDTDDEDRYPQKLAF  
AECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGC  
TCVLPRSV

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 112-121

**N-myristoylation sites.**

amino acids 32-38, 55-61, 133-139

**Leucine zipper pattern.**

amino acids 3-25

**Homologous region to IL-17.**

amino acids 99-195

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**FIGURE 449**

TGCAGAGCTTGTGGAGGCC**AT**GGGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGTT  
GTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGATAA  
AATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAAATT  
TGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTCGGGGGCCGCTGGCTACCAT  
GATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTTCATCCATCCTTTAAATCTGCACAT  
GAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACTGGGGAT  
ATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGATTAAATT  
AGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTGTTAGACAA  
GTTTCATGAGGATCTACCGCTACCAGTCTCATGACTATGCCTTCAGTAGTGTCGAAAAATTACT  
TCATGCTCTAGGAGGAGATGACTTCCTTGGAATGCTTAATCGAACACTTCTTGAAACCTTGCA  
AAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATGAGGGTCAATTA  
TGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGCGGTGTCACTGTCCTGTTCTGATTCTGG  
CCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGCAGGCATCCAAAAG  
CAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACCAAGTACACAGGAAA  
TCCAACAAAGATGTATGAAGTGGTCTACCAAATTGGAAGTGAAGTTCGTTTCTAGTCTTCTATGA  
CATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTCGAATATTACTTTTCTCAACTTTGA  
TCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACAACTTTAGTTAAGGGGGA  
ATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAAATTTGGCCTTAATACAGTTTTAAC  
CACTGATAATTCAGATTTGTTTCATTAAACAGTATTGGGATTGTGCCCTCTGTGAGAGAAAAGGA  
AGATCCTGAGCCATCAACAGATGGAACATATGTTTGGAAGATCTTTTCCCAAGAACTCTTAC  
TAAAGCACAAATTTTAAAGCTCTTTCTGTCTATGATTATGCTGTGAAGAAGCCATGGCTTGC  
ATATCCTCACTATAAGCCCCGGAGAAATGCCCTCTATCATTCTCCATGATCGACTTTATTA  
CCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATGAGTGCCATTGCAGCCCACAACGC  
TGCATCCTTGCCTATCACCGCTGGAACGGGCACACAGACATGATTGATCAGGATGGCTTATA  
TGAGAACTTAAAACTGAACTAT**TGA**AGTGACACACTCCTTTTCCCCTCCTAGTTCCAAATGA  
CTATCAGTGGCAAAAAAGAACAAATCTGAGCAGAGATGATTTTGAACCAGATATTTTGCCAT  
TATCATTGTTTAATAAAAAGTAATCCCTGCTGGTCATAGGAAAAAAAAAAAAA



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**FIGURE 450**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880
<subunit 1 of 1, 505 aa, 1 stop
<MW: 56640, pI: 6.10, NX(S/T): 4
MGRVVAELVSSLLGLWLLLCSCGCPEGAELRAPD KIAIIGAGIGGTS AAYYL RQKFGKDVKI
DLFEREEVGGRLATMMVQGEYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGETL
VFEESNWFIIINVIKLVWRYGFQSLRMHMMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHALGGD
DELGMLNRTLLET LQKAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLWAVEG
GNKLVC SGLLQASKSNLISGSVMYIEEKT KTKYTGNPTKMYEVVYQIGTETRSDFYDIVLVAT
PLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFGLNTVLT TDNSDL
FINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLT KAQILKLFLSYDYAVKKPWLAYPHYKP
PEKCPSIILHDLRYYLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDGLYEKLKTEL
```

**Important features:****Signal peptide:**

amino acids 1-23

**N-glycosylation sites.**

amino acids 196-200, 323-327, 353-357

**Tyrosine kinase phosphorylation site.**

amino acids 291-298

**N-myristoylation sites.**amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,  
119-125, 260-266, 384-390, 459-465**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23, 232-243



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**FIGURE 452**

MASYLYGVLEFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLET  
PSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVPSK  
DLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGKVVD  
IIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAFGVDT  
ELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRFSISAS  
YNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTTKFIVRS  
KDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

**Signal peptide:**  
amino acids 1-20

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**FIGURE 453**

CTCCGGGTCCCCAGGGGCTGCGCCGGGCCGCTGGCAAGGGGGACGAGTCACTGGACACTCCAGGAAGAGCGGC  
CCCGCGGGGGCGATGACCGTGCGCTGACCTGACTCACTCCAGGTCCGGAGGCGGGGGCCCCGGGGCGACTCG  
GGGGCGGACCGGGCGGAGCTGCCGCCGTGAGTCCGGCCGAGCCACCTGAGCCCGAGCCGCGGGACACCGTC  
GCTCCTGCTCTCCGAATGCTGCGCACCGCGATGGGCCCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCTGCCG  
CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTGCTCCTGCTGCGAGCCGCCGCTCCGACCTGGGCGCTCAGC  
CCCCGGATCAGCCTGCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTCTGAAGCTGAACACATCTCCAACCTAC  
ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCCTGTACGTGGGTGCTCGAGAGGCCCTCTTTCAGCTCAGTAGC  
AACCTCAGCTTCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGCAGACGCAGAGAAGAAACAGCAGTGC  
AGCTTCAAGGGCAAGGACCCACAGCGGACTGTCAAACTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC  
CTGTTCACCTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAATTCACCCTGGCAAGG  
GACGAGAAGGGGAATGTCTCCTGGAAGATGGCAAGGGCCGTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC  
CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC  
CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC  
ATTCTGAGAGCCTGGGAGCTTGCAGGCGATGATGACAAGATCTACTTTTTCTTCAGCGAGACTGGCCAGGAA  
TTTGAGTTCTTTGAGAACACCATTTGTGTCCCGCATTTGCCGCTCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG  
CTACAGCAGCGCTGGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCAGGCCCCGACGATGGCTTCCCTTCAAC  
GTGCTGCAGGATGTCTTACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCTTTTCTATGGGGTCTTCACT  
TCCCAGTGGCACAGGGGAACACAGAAGGCTCTGCCGTCTGTCTTTCACAATGAAGATGTGCAGAGAGTCTTC  
AGCGCCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG  
CCTGGAGCGTGCATCACCAACAGTCCCCGGGAAGGAAGATCAACTCATCCCTGCAGCTCCAGACCGCGTGCTG  
AACTTCTCAAGGACACTTCTGATGGACGGGCGAGTCCGAAGCCGCATGCTGCTGCTGCGAGCCCAAGGCTCGC  
TACCAGCGCTGGCTGTACACCGCTCCCTGGCCTGCACACACCTACGATGTCTCTTCTGGGCATCTGGTGAC  
GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCCCGGGTGACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA  
CAGCCCGTGCAAGTCTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCGGCCCTCAGCTCGGGCGTAGTCCAG  
GTGCCCATGGCCAACTGCAGCCTGTACCGGAGCTGTGGGACTGCCTCCTCGCCCGGAGCCCTACTGTGCTTGG  
AGCGGCTCCAGCTGCAAGCACGTCAGCCTCTACCAAGCTCAGCTGGCCACCAAGGCGGTGGATCCAGGACATCGAG  
GGAGCCAGCGCCAAGGACCTTTGCAGCGCGTCTTCGGTTGTGTCCCCGTCTTTGTACCAACAGGGGAGAAGCCA  
TGTGAGCAAGTCCAGTTCCAGCCCCACACAGTGAACACTTTGGCCTGCCCGCTCCTCTCCAACCTGGCGACCCGA  
CTCTGGCTACGCAACGGGGCCCCCGTCAATGCCTCGGCCCTCTGCCACGTGCTACCCACTGGGGACCTGCTGCTG  
GTGGGCACCCAAACAGCTGGGGGAGTTCCAGTGTGCTCACTAGAGGAGGGCTTCCAGCAGCTGGTAGCCAGCTAC  
TGCCCAAGAGTGGTGGAGGACGGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCAATATCAGCACA  
TCGCGTGTGAGTGCACAGCTGGTGGCAAGGCCAGCTGGGGTGCAGACAGGTCTACTGGAAGGAGTTCTTGGTG  
ATGTGCAGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTTATTCTTGTCTACCGGCACCGGAACAGCATGAAA  
GTCTTCTGAAGCAGGGGGAATGTGCCAGCGTGACCCCAAGACCTGCCCTGTGGTGTGCCCCCTGAGACCCGC  
CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACCAGTCCCTGTGAGACAGCCCCCG  
GGGCCCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG  
TGCCCCCGCCCCGGGTCCGCCTTGGCTCGGAGATCCGTGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACGC  
TGCCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCCTCCGCTCTGCTCTTCGTGGAAC  
ACGACCGTGGTGCCCGGCCCTTGGAGCCCTTGGAGCCAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCC  
TACCACCCAGACACCCAAACAGCCGTGGCCCCAGAGGTCTTGCCCAATATGGGGGCTGCCTAGGTTGGTGGAA  
CAGTGCTCCTTATGTAACTGAGCCCTTTGTTAAAAAACAATTCCAAATGTGAACTAGAAATGAGAGGGAAGAG  
ATAGCATGGCATGCAGCACACAGGCTGCTCCAGTTTATGGCCTCCAGGGGTGCTGGGGATGCATCCAAAGTGG  
TTGTCTGAGACAGAGTTGGAAACCTCACCACTGGCCTCTTCACTTCCACATTATCCCGCTGCCACCGGCTGC  
CCTGTCTCACTGCAGATTACAGACAGCTTGGGCTGCGTGCGTTCTGCCCTTGCCAGTCAGCCGAGGATGTAGTTG  
TTGCTGCCGTGCTCCACCACCTCAGGGACAGAGGGCTAGGTTGGCACTGCGGCCCTCACCAGGTCTGGGCTC  
GGACCAACTCCTGGACCTTCCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGCGAGCTCAGGAGAGA  
TTTCGTGACAATGTACGCCTTTCCCTCAGAATTGAGGAAGAGACTGTGCGCTGCCTTCTCCGTGTGTCGTGA  
GAACCCGTGTGCCCTTCCCAACATATCCACCCTCGCTCCATCTTTGAACTCAAACACGAGGAACCTAGTGCACC  
CTGGTCTCTCCCCAGTCCCCAGTTACCCCTCCATCCCTCACCTTCTTCACTCTAAGGGATATCAACACTGCCC  
AGCACAGGGGGCCTGAATTTATGTGGTTTTTATACATTTTTTAATAAGATGCACCTTTATGTCATTTTTTAATAAA  
GTCTGAAGAATTACTGTTTAAAAA

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**FIGURE 454**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRFE
AEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKKQQCSFKGKD
PQRDCQNYIKILLPLSGSHLFTCGTAAFSMPCTYINMENFTLARDEKGNVLLEDGKGRCFPDP
NFKSTALVVDGELYTGTVSSFQGNDAISRSQSLRPTKTESSLNWLQDPAFVASAYIPESLGS
LQGDDDKIYFFFSETGQEFFEENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLCSRPD
GFPFNVLQDVFTLSPSPQDWRDTLEYGVFTSQWHRGTTEGSAVCVFTMKDVQRFVSGLYKEVN
RETQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFLKDHFLMDGQVRSRMLLLQ
PQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQPVQNLLLD
THRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQQLATRPWII
DIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPNVTNTLACPLLSNLATRLWLRNGAPVN
ASASCHVLPTGDLVLVGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQTDEGGSVPVII
STSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSMKVFLKQGECAV
HPKTCPVVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKRPLSIQDSFVEVSP
VCPRPRVRLGSEIRDSVV
```

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

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**FIGURE 455**

TAAGATGAGGGCATCCCTCACGTTACACCCCTGGTGGCATCTGCCAGCCCTGTTCTGGGGAC  
AAGGCGGGCTTTTCGTGGGAGCCATGCTCAGCCTGCCAGGAAGCCAAGCCCTACAGTGCAGAGG  
AAACAGAATTTCAACGGGAAGCTGGTTTGCTTCATACCATTGGGATCTGCTGGTAAAGCTGTT  
ATTTGGGTTTAGGGACTGATCCCTTGCACTTTACTTCTGGATCACCATGAATGGCCAAGATGG  
TGGCAGAACACGCTGTGGACCCTGAGTTAGAGACAATGCAAATGTTGGATTGGGTGTAATTCT  
TTTTGAATCCCAGATCCAGTCTGTACTTGAATATGAGCAGAAGATCTACAAGAATGCTGACAG  
GGAACCGTGTTAAGACCCAGCACCCCTATTCCCAGGAGCTTCTGGCCTGACCATCTGCAGCCA  
AAGCACTAACAGGGACAGATATGGGAATGTCCACCTTTGATCCGCATCCTGCACAATAGTGGT  
CCCACCATGGCTGCCACTTTTTTATACTATTTGGAGAAAAGACCTTGTATAAATTCGAGGCC  
GAGTGACTAACGTCTCTGTACACGGAAATGGGTACTTGGTGGCATAGAGAAACACAATTAGC  
CACTTTTTTCAGCTACACTTCTCACTCAGCTGCACCCTACACTTCTCACTCAGGTGCACCCCT  
TCTGCTGTCTTTCCCCAACGTACTGGGTCCCGAGCGTGGTGGGTATTTGCCACACTGGGTGC  
CAGCTCAGCAGCCCCCACCCTCTCTTTATTCTCTCCAAAGCTGGTCTTTCTGACTATCATTGT  
GGTAGGGGGAGGACAGATGCTAAAGGTGGAAGCTGACCTGGAGAAAGAGACACACGGGGTGAC  
TGTGGCAAAGGACAGCTGGAAAAGAACTCTATCACTTCTTCATTGGCAACCACAAGGCACCC  
GAGGCCATGGCACTCCCAGAGGCTGTGCGCAGAGCCAAGCCTCTCAACCTCTTCTGGCCCTGC  
GTCCTGCAGCGAAGTCTCTGCTGTAAGACAGTAGACTCCTTCGATGAGGTGCTCAAAAATGCT  
ACCCGGGGTGGTGGTGTCTGGCTTGCACTCTGGCCAGTTTCAGAGAAAGTTGCAGAGATCAGGG  
GCCAAGGATGTCATAGCCCCAGGTTGTCCTCAGGGTCCCAATCCTAGGGCAGGGTGTGCATGG  
AAGCAAGAACTATGGAAACCTAGCTCCAGTCTGCAGGCTCTGAGCCCCTAGTTCCCTCACTCCA  
GCGGGGCTCCCTCACTGCACAGAACCCACCCCTTCTGTGTGGGCACTGCTGACCACACAGATG  
ACCCAGACCCAAAGAGCCTGGCAGAAGCTCTGTGGTTGGAGCTGGGCTCCGTCTCCAGGTCTG  
GTTCAAGGGGATCAGGAAGGCTCTTTTCCACCTGTGGCTTCACTGGCCCTTTGAGATTTCTTA  
TCTCACC GTTACTTCAGTTACCCTTGCAAGGGGGCCAGGGAGTCAAGAATATACCGTGTTCTC  
CAGGGTTTAAGCCGGCCATGCCTTCCCGAGAGCATAACCAACTTGACAGGGGTGCCCAGTTAC  
CCCACAACTGAAGGAAGGAGATCCTTCCCCGTCCCCAGGAGTGCTCTCAACCAGCCTCAGA  
AAGCTTGAGAAGATGGACCCTTTGCCCACCAGGGTTAATTCCTGGTGGGGCAGCTCGGCTGTG  
ATCAGGGCAACCAAACCTATAGGAAGCCTTCCAGTGTGAGCTGGAATTAGACTGAACATGTGC  
TTGGGCCTGCCTCTCCCTAGACGCAGTTGCGGGGCACTCCAGGGAATGAACCAGCTCAAGTGT  
GTCCCTAACAGCAGCCTGGAGCTACCCCAATCCCTCACAGCCTGACCCTCCTCATTCATCA  
GATCTCGTGCCG

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**FIGURE 456**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA69555  
><subunit 1 of 1, 148 aa, 1 stop  
><MW: 16214, pI: 10.22, NX(S/T): 0

MGTWWHRETQLATFSATLLLTQLHPTLLTQVHPLLLSFPQRTGSRWWVFATLGASSAAPH  
LSLFSPKLVFLTIIIVGGGQMLKVEADLEKETHGVTVAKDSWKRNSITSSLATTRHPRPW  
HSQRLCAEPSLSTSSGPASCSEVSAVRQ

**Important features of the protein:****Signal peptide:**

Amino acids 1-28

**Transmembrane domain:**

Amino acids 64-78

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 103-107

**N-myristoylation sites:**

Amino acids 53-59;94-100

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**FIGURE 457**

CCCGCGCGCCCCTGGCACTCAATCCCCGCCATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTC  
GCGCCGGCCGTTCGGCCCGGCTCTGGGGGCGCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCC  
GGGACCACCAAGGTCCCAGGCTCGACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGCCGGCG  
GAGACAGCTAACGGGACCTCAGAACAGCATGTCCGGATTTCGAGTCATCAAGAAGAAAAAGGTC  
ATTATGAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCC  
CTTGTGACCCCCACTCCAGCAGGGACCCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCT  
CCTTTGGGTCTGGAGTCCCTGCGAGTTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCC  
TTTGGTCTTGGACCACACCGAGGACGGCTCAACATTCATTTCAGGCCTGGAGGACGGCGATCTA  
TATGATGGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTTCAGGTGGACGCTGGG  
CACCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACTCTGTCTGGAGGTATGACTGG  
GTCACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAACCAC  
AGCAGTGGGATGGACGCAGTATTTCTGCCAATTTCAGACCCAGAACTCCAGTGCTGAACCTC  
CTGCCGGAGCCCCAGGTGGCCCGCTTCATTGCGCTGCTGCCCCAGACCTGGCTCCAGGGAGGC  
GCGCCTTGCCCTCCGGGCAGAGATCCTGGCCTGCCCAGTCTCAGACCCCAATGACCTATTCCCTT  
GAGGCCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTCAGCATCACAATTACAAGGCCATG  
AGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACCCGCATCTACAGCATTGGG  
AAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCCGACAAGCCTGGGGAGCATGAG  
CTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAG  
TTGCTTCTGCTCCTGATGCAGTTCCCTGTGCCATGAGTTCCTGCGAGGGAACCCACGGGTGACC  
CGGCTGCTCTCTGAGATGCGCATTACCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATC  
GCCTACCACCGGGGTTTCAGAGCTGGTGGGCTGGGCCGAGGGCCGCTGGAACAACCAGAGCATC  
GATCTTAACCATAATTTTGCTGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAG  
GTGCCCCACATCGTCCCCAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCC  
ACCGTGGCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGT  
GCCAACCTCCACGGGGGTGAGCTCGTGGTGTCTACCCATTTCGACATGACTCGCACCCCGTGG  
GCTGCCCCGCGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTAT  
GCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCC  
GTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTC  
AGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCTGTGACAAGTTCCTCAC  
GAGAATGAATTGCCCCAGGAGTGGGAGAACAAAGACGCCCTCCTCACCTACCTGGAGCAG  
GTGCGCATGGGCATTGCAGGAGTGGTGAAGGACAAGGACACGGAGCTTGGGATTGCTGACGCT  
GTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTATTGGCGT  
CTGCTGACCCAGGGGACTACATGGTGAAGTGGCAGTGGCCAGTGGCGAGGGCTACCATTTCAGTGACACGG  
AACTGTCGGGTACCTTTGAAGAGGGCCCCCTTCCCCTGCAATTTTCGTGCTCACCAAGACTCCC  
AAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGC  
CTGGAGCGGCTAAGGGGACAGAAGGATTGAATACCTGCGGTTTAAGAGCCCTAGGGCAGGCTGG  
ACCTGTCAAGACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAAGTGAGGAAAAGGTGCTCAT  
TAAAGCTACCGGGCACCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 458**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71162
><subunit 1 of 1, 734 aa, 1 stop
><MW: 81677, pI: 6.60; NX(S/T): 6
MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
ESLRVSDSRLEASSSQSFGLGPHRGRLNIHSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
NLLPEPQVARFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
NYKAMRKLMKQVQEQQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG
WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTLPNATVAPETR
AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
NELPQEWENNKDALLTYLEQVRMGIAGVVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY
WRLLTTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
DLRRRLERLRGQKD
```

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**FIGURE 459**

TAAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGAA  
AGAACTGACTGAAACGTTTGAGATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGT  
GGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAGCGA  
TGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTCGCCCCACTTCCACCAAT  
TCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCTGCCCC  
TACAACTCCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGGTCACCT  
GAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAAAACAAAT  
GTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTAATAAACAT  
GAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

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**FIGURE 460**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290  
><subunit 1 of 1, 85 aa, 1 stop  
><MW: 9700, pI: 9.55, NX(S/T): 0  
MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPRFPW  
FRRNFPIPIPIESAPTTPLPSEK

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Homologous region to B3-hordein:**

amino acids 47-85

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**N-glycosylation sites:**

Amino acids 57-61;210-214;220-224;318-322;428-432;472-476

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 80-84

**N-myristoylation sites:**Amino acids 3-9;20-29;39-48;152-161;161-170;262-271;358-364;  
538-544;560-566;637-643**Zinc carboxypeptidases, zinc-binding region 2 signature:**

Amino acids 498-509

**Zinc carboxypeptidases:**

Amino acids 391-411

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**FIGURE 461**

AGCAGGAGCAGGAGAGGGGACA**ATG**GGAAGCTGCCCCGTCCAGGTTTCATGTTCTTATTTCTC  
CTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTGGT  
GCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCCACT  
GAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCATAGC  
ATGGTGCAAAAATTTCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGACACAC  
TACAACATCACTGGGAACACCATCTGCCTCTTTGCGCTGGTAGACAATGAACAACCTGAATTTA  
GAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGATCAACAGC  
CTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCGTAATTCAG  
ATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATGCACAGATAC  
CAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAGTGGTATGAAA  
GAAAATGGGAAGGTGATATCATTTTTTCAAACCTAAAGGAGTCTCAACTGCCAGCTTTGGCAATT  
TACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCCGTAGAGCATGTG  
CAAACTTTTGTGATGGATTCCCTAAGTGGAATTTGTTGAAAGAAAATCGTGAATCAGAAGGA  
AAGACTCCAAAGGTGGAACCT**CTGA**CTTCTCCTTGGAACCTACATATGGCCAAGTATCTACTTTA  
TGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAGGATCACTAGGCCTGC  
CAACCACACACACACGCACGTGCACACACGCACGCACGCGTGCACACACACACGCGCACACAC  
ACACACACACAGAGCTTCATTTCCCTGTCTTAAATCTCGTTTTCTCTTCTTCTTTTAAA  
TTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATTCATACTCTGTAAGCCCAT  
CTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATGCCTCTATGAAAGAGAGGCA  
TTCTTAGAGAAAGATTGTTCCAATTTGTCAATTAATATCAAGTTTGTATACTGCACATGACTT  
ACACACAACATAGTTCCTGCTCTTTTAAGGTTACCTAAGGGTTGAAACTCTACCTTCTTTTCA  
AAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGGATGGTTTTAAACACCTTTGTGA  
AATTGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTCCCTGAACTCAGCAGAAATAGACC  
ATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCCCTATGTAAATCAACAACCTGCATAA  
TAAATAAAAGGCAATCATGTTATA

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**FIGURE 462**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSREFMFLLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDPAAAMEFIAATEVAVIGF
FQDLEIPAVPILHSMVQKFPGVSEFGISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDIES
IDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVVIQHLLIMNKASPEYEENMHRYQKAAKLF
QGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVQHVQNFCDGF
LSGKLLKENRESEGKTPKVEL
```

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

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**FIGURE 463**

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAGG  
GTGCCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGGCC  
ATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTATGGC  
CCTGGAGGAGGCAAGTATTTAGCACCACTGAAGACTACGACCATGAAATCACAGGGCTGCGG  
GTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGGACGTG  
AAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATACATCACA  
AAAGTCTTTGTGCGCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAAGGACCGC  
TATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAGAGGGGCAG  
GTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGCTTTGAATGG  
AATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTCAGCAAACCTCA  
CCCGTGGGTTCGCT**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGTGTGGTGGTGGC  
TGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATAAATAAAGCTTCT  
GCAGAAAA

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**FIGURE 464**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVQVL
GDSWDVKLGALGGNTQEVTLQPGYITKVFAFQAFLRGMVMTSKDRYFYFGKLDGQISSAY
PSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

**Signal peptide:**  
amino acids 1-22

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**FIGURE 465**

CGGACGCGTGGGTCCGGCGGCTGAGGCTGCACCGGGCACGGGTTCGGCCGCAATCCAGCCTGGGCGGAGCCGGAG  
TTGCGAGCCGCTGCCTAGAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGT  
TGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGTTCAGGACATATCCCTGGGC  
AGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCTGGCGCACCGTCAGCCTGGAGGAGCCGGTCTCGAAGC  
CAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACACAGGCTGC  
TGGCCCCAGGATACATAGAAACCCACTACGGCCCAGATGGGCAGCCAGTGGTGTGGCCCCAACACACGGATC  
ATTGCCACTACCAAGGGCGAGTAAGGGGGCTTCCCCGACTCCTGGGTAGTCTCTGCACCTGCTCTGGGATGAGTG  
GCCTGATCACCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAA  
CCCACGAGATCTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAG  
CGGGCATGACCAGCCTTCTGGTGGTCCCCAGAGCAGGGGCAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGG  
AACTGTACATTGTGGCAGACCACACCCCTGTTCTTGACTCGGCACCGAAACTTGAACCACACCAACAGCGTCTCC  
TGGAAGTCGCCAACTACGTGGACCAGCTTCTCAGGACTCTGGACATTAGGTGGCGCTGACCGGCTGGAGGTGT  
GGACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGCTCTGGGCCCTTCTGCAGTGGCGCCGGG  
GGTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGCTGCTCACGGGCGCGCCTTCCAGGGCGCCACAGTGGGCC  
TGGCGCCGTCGAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCG  
GCGCCGACGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCCTCAGCCACGACCCCGACGGCTGCTGCGTGG  
AGGCTGCGGCGCAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCGTTTCCGCGCGTGTTCAGCGCCT  
GCAGCCGCGCCAGCTGCGCGCCTTCTTCCGCAAGGGGGCGCGCTTGCCCTCTCAATGCCCGGACCCCGGAC  
TCCCGGTGCCCGCGCCTCTGCGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGG  
AGTGGCGGACCTCTGCTGCTTTGCTCACAACCTGCTGCTGCGCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTT  
GCGTGCGTGCCTGCTGAAGCGGCTGGAGCGCTGTGCCGCGCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTT  
GCACGGGCACCTCCTCCCACTGTCCCCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGAGTGGCT  
ACTGCTGGGATGGCGCATGTCCACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCTGGCTCCACCCAGCTC  
CCGAGGCTGTTTCCAGGTGGTGAACCTCTGCGGGAGATGCTCATGGAACCTGCGGCCAGGACAGCGAGGGCCACT  
TCCCTGCCCTGTGCAGGGAGGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCAGCCTGCTCGCAC  
CGCACATGGTGCCAGTGGACTCTACCGTTACCTAGATGGCCAGGAAGTGACTGTGCGGGAGCCTTGGCACTCC  
CCAGTGCCAGCTGGACCTGCTTGGCCTGGGCTGGTAGAGCCAGGCACCCAGTGTGGAGCTAGAATGGTGTGCC  
AGAGCAGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTACGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTTT  
GCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCCTTCTGTGACAAGCCAGGCTTTGGTGGCA  
GCATGGACAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCTGCTGGCCATGCTCCTCAGCGTCTCTGCTGC  
CTCTGCTCCAGGGGCGGCCCTGGCTGGTGTGCTACCGACTCCAGGAGCCCATCTGCAGCGATGCAGCTGGG  
GCTGCAGAAGGGACCCCTGCGTGCAGTGGCCCCAAGATGGCCACACAGGGACACCCCTTGGGCGGCGTTCACC  
CCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCTGGACCCTGAGAATCTCATGAGCCAGCAGCC  
ACCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCAAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCT  
GGTGAAGGAGTCTCCTAAATGAACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAACCTTGAACCTG  
CAGGGGCAGAGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGAAGTTTCTTCCCGAGTGGAGCT  
TCGACCCACCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCTGAGGGCTGGAGAACACTGCTTGGGCACACT  
CTCCAGCTCAATAAACCATCAGTCCAGAAGCAAAGGTACACAGCCCTGACCTCCCTCACCAGTGGAGGCTGG  
GTAGTGTGGCCATCCCAAAAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCTTACATGCAATTTCCACGGACCCA  
GCTCTGTGGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCTTGGGGCCCTATGGTTGACTGAGTCCACACTCC  
CCTGCAGCCTGGCTGGCCTCTGCAAACAAACATAATTTGGGGACCTTCTTCTGTTTCTTCCACCCCTGTCTT  
CTCCCTAGGTGGTTCTGAGCCCCACCCCAATCCAGTGCTACACCTGAGGTTCTGGAGCTCAGAATCTGAC  
AGCCTCTCCCCATTCTGTGTGTGTCCGGGGACAGAGGGAAACATTTAAGAAAAGATACCAAGTAGAAGTCAA  
AAGAAAAGACATGTTGGCTATAGGCGTGGTGGCTCATGCCTATAATCCAGCACTTTGGGAAGCCGGGGTAGGAGG  
ATCACCAGAGGCCAGAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTAAAA  
TTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTG  
AGTTCAACACTGCAGTGAGCTATGGTGGCACCCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCCTGTCTCTAA  
AATAAATTTTAAAGGACTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA



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**FIGURE 466**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76788  
><subunit 1 of 1, 813 aa, 1 stop  
><MW: 87739, pI: 6.94, NX(S/T): 5

MGWRPRRRARGTPLL LLLLLLLLLLWVPVGAGVLQGHIPGQPVTPHVVLDGQPWRTVSLEEPVSKPDMGLIVALEAEGQ  
ELLLELEKNHRL LAPGYIETHYGPDGQPVV LAPNHTDHCHYQGRV RGF PDSWVVLCTCSGMSGLITLSRNASYLL  
RPWPPRGSKDFSTHEIFRMEQLLTWKGT CGHRDPGNKAGMTSLPGGPQSRGRREARRTRKYLELYIVADHTLFLT  
RHRNLNHTKQRLLEVANYVDQLLRTLDIQVALTGLEVVWTERDRSRVTQDANATLWAF LQWRRGLWAQRPHDSAQL  
LTGRAFGGATVGLAPVEGMCRAESSGGVSTDHSELPIGAAATMAHEIGHSLGLSHDPD GCCVEAAAESGGCVMAA  
ATGHPFPRVFSACSRRLRAFFRKGGGACLSNAPDPGLPVPPALCGNGFVEAGEECD CGPGQECRDLCCFAHNCS  
LRPGAQCAHGDCCVRCLLKPAGALCRQAMGDCDLPEFCTGTSSHCPPDVYLLDGSPCARGSGYCW DGACPTLEQQ  
CQQLWGP GSHPAPEACFQVVNSAGDAHGNCQDSEGHFLPCAGRDALCGKLQCGGKPSLLAPHMV PVDSTVHLD  
GQEVTCRGALALPSAQLDLLGLGLVEPGTQCGPRMVCQSRRCRKN AFQELQRCLTACHSHGVCNSNHNCHCAPGW  
APPFCDKPGFGGSMDSGPVQAENHDTFLLAMLLSVLLPLLPAGAGLAWCCYRLPGAHLQRCSWGCRRDPACSGPKD  
GPHRDHPLGGVHPMELGPTATGQPWPLDPENSHEPSSHPEKPLPAVSPDPQADQVQMPRSC LW

**Important features of the protein:****Signal peptide:**

Amino acids 1-27

**Transmembrane domain:**

Amino acids 702-720

**N-glycosylation sites:**

Amino acids 109-113;145-149;231-235;276-280;448-452

**Tyrosine kinase phosphorylation site:**

Amino acids 236-244

**N-myristoylation sites:**

Amino acids 29-35;185-191;195-201;308-314;318-324;326-332;338-344;370-376;  
400-406;402-408;454-460;504-510;510-516;517-523;580-586;  
601-607;661-667;687-693;717-723;719-725

**Amidation site:**

Amino acids 200-204

**Neutral zinc metallopeptidases, zinc-binding region signature:**

Amino acids 342-352

**FIGURE 467**

[illegible]

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**FIGURE 468**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623  
><subunit 1 of 1, 97 aa, 1 stop  
><MW: 10160, pI: 6.56, NX(S/T): 0  
MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLPL  
VTKMCHIGCPDIPSLGLGPYVSIACCQTS LCNHD

**Important features of the protein:****Signal peptide:**

amino acids 1-20

**N-myristoylation sites.**

amino acids 6-11 and 33-38

**Prokaryotic membrane lipoprotein lipid attachment sites.**

amino acids 24-34 and 78-88

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**FIGURE 469**

**CATG**GAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTGCAGT  
TTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAAACC  
TAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTTCTCTGGA  
AAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAGACAG  
AAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCACCTCAGCGTGTTGGC  
TTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCAAGCAAGGAAGTAGAATCTTTTGC  
AAGAAAAAACTACGGAGTAACTTTCCCCATCTTCCACAAGATTAAGATTCTAGGATCTGAAGG  
AGAACCTGCATTTAGATTTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAATTTTTGGAA  
GTATCTTGTC AACCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCCCATTGAAGT  
CATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAGAGGATCTA**TG**  
**A**GAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTGGTCTCATTTTA  
AACATTTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTAGTGCGTT  
CTCAGCTCATTGCAACCTCTGCCTTTTTAAACATGCTATTAAATGTGGCAATGAAGGATTTTT  
TTTTAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCAGGATGAGGATGTTACCCAAAG  
CAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAACACTTCTCTGACCATACT  
AAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTGTTCAACTTGACATTTT  
CTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTTGGATTCAAGAGCACTGT  
GTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATGGAATAAAACACAAATGTT  
GAAAAATGTAAAATATATATACATAGATTCAAATCCTTATATATGTATGCTTGTTTTGTGTAC  
AGGATTTTGTTTTTTCTTTTTAAGTACAGGTTCCCTAGTGTTTTACTATAACTGTCACATATGTA  
TGTAACCTGACATATATAAATAGTCATTTATAAATGACCGTATTATAACATTTGAAAAAGTCTT  
CATCAAAAAAAAAAAAAA

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**FIGURE 470**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23909, pI: 9.68, NX(S/T): 0
MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSLE
KYKGKVSLLVVNVASDCQLTDRNYLGLKELHKEFGPSHFVLAFFPCNQFGESEPRPSKEVESFA
RKNYGVTFPIFHKIKILGSEGEPAFRELVDSKKEPRWNFWKYLVNPEGQVVKFWRPEEPIEV
IRPDIAALVRQVIKKKEDL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-31

**Glutathione peroxidases signature 2.**

amino acids 104-112

**Glutathione peroxidases.**

amino acids 57-82

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**FIGURE 471**

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCCATTCTCCGGCTGCGAGAAAGGACGCGCGCCCTGCG  
TCGGGCGAAGAAAAGAAGCAAACTTGTGGGAGGGTTTCGTCATCAACCTCCTTCCCGCAAACTAAACCTCCT  
GCCGGGGCCATCCCTAGACAGAGGAAAGTTCTGTCAGAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGC  
GCTGGCTGTGGAATTAGATCTGTTTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCAACGTCGCGGGC  
ACCGGGTTGGCGCTGCCCAGTGGAAACCGACAGTTTGGAGCCCTCGGCTGCAAGTGGCCTCTCCTCCCCGCGGTT  
GTTGTTCACTGTGCGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGGTCCGAAGAGCGCTGCG  
CTCCTACTCGGTTCTGCTTCTTCTCTCTCGGTTCCCTACTGTGAAATCGCAGCGACATTTACAAAGGCCTCCG  
GGTCTACCGAGACCGATCCGACGCTTTGGCCCGGTCGTGCCTATTGCATCGGGAGCCCCGAGCACCGGCGAA  
GGACTGGCGGGTGGGGTAGGGAGGTGGCGCGCGGGCATGGCGAGGTTCCCGAAGGCCGACCTGGCCGCTGCAGG  
AGTTATGTTACTTTGCCACTTCTTCACGGACCAAGTTTCACTTCGCCGATGGGAAACCCGGAGACCAAATCCTTGA  
TTGGCAGTATGGAGTTACTCAGGCCTTCCCTCACACAGAGGAGGAGGTGGAAGTTGATTACACGCGTACAGCCA  
CAGGTGGAAGAAAGAACTTGGACTTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGA  
GCCCAGAAGCTTACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGATACAGACCA  
CAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTTATGGTGAACATAGACCAAAT  
GGAAAAAGATAAAGTGAAGATTGATGGAATATTGTCCAATCTCATCGGCAAGCTGCAAGAGTGAATCTGTCTT  
CGATTTTCCATTTTATGGCCACTTCTACGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGT  
CGTACATCGAATGCTAACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTGATCCCACTGTATCCAGAAA  
TTCAACTGTCAGATATTTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTCCAGGATAATTA  
TAACCTGGGAAGCTTACATTCCAGGCAACCCTGCTCATGGATGGACGAATCATCTTTGGATACAAAGAAATTC  
TGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAGTGAAGTTCGGACTGTCCGATGCATTTGTCTGTCTT  
CAGGATCCAACAAATTTCCAATGTTTGAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAA  
AATTACCAACATTTTCGGCTGTGGAGATGACCCCATTAACCATGCCTCCAGTTTAAACAGATGTGGCCCCCTGTGT  
ATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAACTTCAAAGATGTTCCAGTGGATTTGATCGTCATCG  
GCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAAGAGAAGATGTGTGAGAATACAGAACCAGTGGAAAC  
TTCTTCTCGAACCACCACAACCGTAGGAGCGACAACCACCCAGTTCAAGGTCTTAACCTACCACCAGAAGAGCAGT  
GACTTCTCAGTTTCCCACAGCCTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGC  
TTCTACAGATGACAGTGCAGCTGAGAAGAAAGGGGGAACCTCCACGCTGGCCTCATCATTTGGAATCCTCATCCT  
GGTCTCTCATGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCAACATCAGCAGCCAGCATCTT  
CTTTATTGAGAGACGCCCAAGCAGATGGCCTGCGATGAAGTTTAGAAGAGGCTCTGGACATCCTGCCTATGCTGA  
AGTTGAACCAAGTTGGAGAGAAAGAAGGCTTTATTGTATCAGAGCAGTGCTAAAATTTCTAGGACAGAACAACACC  
AGTACTGGTTTACAGGTGTTAAGACTAAAATTTTGCCTATACCTTTAAGACAAACAACAACACACACACAAAC  
AAGCTCTAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCAGGAAACAAAGGGTAAACAA  
AAACTAAAATTTATACAAGATACCATTTTCACTGAACATAGAATTCCTAGTGAATGTCATCTATAGTTCACT  
CGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTATAATGCTTTTGGCTTAGGTGCAGGGTTGCAAG  
GGATCAGAAAAAAAATCATAATAAGCTTTAGTTCATGAGG

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**FIGURE 472**

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVTAQAFPHTEEEVEVD SHAYSH  
RWKRNLDFLKAVDTNRASVGQDSPEPRSFDTLLDDGQDNNTQIEEDTDHNYISRIYGPSDS  
ASRDLWVNIDQMEKDKVKIHGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVV  
HRMLTATQYIAPLMANFDPVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQATLLMD  
GRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKIT  
NISAVEMTPLPTCLQFNRCGPCVSSQIGFNCWSCSKLQRCSSGFDHRQDWVDSGCPEESKEK  
MCENTEPVETSSRTTTTVGATTTQFRVLTTRRAVTSQFPTSLPTEDDTKIALHLKDNGASTD  
DSAAEKKGGTLHAGLIIGILILVLIVATAILVTVMYHHPTSAASIFFIERRPSRWPAMKFRR  
GSGHPAYAEVEPVGEKEGFIVSEQC

**Important features of the protein:****Transmembrane domain:**

amino acids 454-478

**N-glycosylation sites.**

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 297-301, 492-496, 503-507

**N-myristoylation sites.**amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,  
455-461

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**FIGURE 473**

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACCCCG  
CGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCCCTGAGCCTCGGGCTCCGGCCCCGGACCT  
GCAGCCTCCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGGC  
TTTAAAAGTGCTACTAGAACAAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCTATTT  
GTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGG  
AACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGGCTTCGGC  
TATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTC  
CAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCAAATTGTTCA  
GCCACAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAACTTGTC  
GGCTTTCAAGACATGGAGTGTGTGCTTGTGGAGACCCTCCTCCTCTTACGAACCGCACTGT  
GCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCCACGGGACACGGCGCTG  
GCTGCCGTTATCTGCAGCGCTCTGGCCACCCTCCTGCTGGCCCTGCTCATCCTCTGTGTATC  
TATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTGCGAGGACATTCAG  
TACAACGGCTCTGAGCTGTGCTGTTTTGACAGACCTCAGCTCCACGAATATGCCACAGAGCC  
TGCTGCCAGTGCCGCCGTGACTCAGTGCAGACCTGCGGGCCGGTGCCTTGCTCCCATCCATG  
TGCTGTGAGGAGGCCTGCAGCCCCAACCCGGCGACTCTTGTTGTGGGGTGCATTCTGCAGCC  
AGTCTTCAGGCAAGAAACGCAGGCCAGCCGGGGAGATGGTGCCGACTTTCTTCGGATCCCTC  
ACGCAGTCCATCTGTGGCGAGTTTTTTCAGATGCCTGGCCTCTGATGCAGAAATCCCATGGGTGGT  
GACAACATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACATTCATTCTCTCAAT  
CCAGAAGCTTCAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCT  
GTTCAGTCCAGTCTCATTCTGAAAACCTTACAGCAGCTACTGATTATCTAGATATAACAAC  
ACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAG  
AGTGGCGCTGTCTATCCACCCAGCCACTCAGACGTCCCTCCAGGAAGCTTAAAGAACCTGCTTC  
TTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTACTCCTTTGTTAGGCTTATGGACTGA  
GCAGTCTGGACCTTGATGGCTTCTGGGGCAAAAATAAATCTGAACCAAACCTGACGGCATTG  
AAGCCTTTTCAGCCAGTTGCTTCTGAGCCAGACCAGCTGTAAGCTGAAACCTCAATGAATAACA  
AGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTCTTACATGAGAAGCTTCTCTGCCAC  
AAAAGTGACTTCAAAGACTGATGGGTTGAGCTGGCAGCCTATGAGATTGTGGACATATAACAA  
GAAACAGAAATGCCCTCATGCTTATTTTCATGGTGAATGTGGTTTTTACAAGACTGAAGACCCA  
GAGTATACTTTTTCTTTCCAGAAATAATTTTCATACCGCTATGAAATATCAGATAAATTACCT  
TAGCTTTTATGTAGAATGGGTTCAAAGTGAGTGTCTTCTATTTGAGAAGGACACTTTTTCATC  
ATCTAAACTGATTTCGCATAGGTGGTTAGAATGGCCCTCATATTGCCTGCCTAAATCTTGGGTT  
TATTAGATGAAGTTTACTGAATCAGAGGAATCAGACAGAGGAGGATAGCTCTTTCAGAAATCC  
ACACTTCTGACCTCAGCCTCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTA  
GGGAATGTGGTGCAGAAAGGGCAGCCCATTTGCCAGAAATTAACACATATTGTAGAGACTTGTA  
TGCAAAGGTTGGCATATTTATATGAAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCC  
TCTGCCTGAGCTTAGAAGGTTATAGAAAAAGGGTATTTATAAACATAAATGACCTTTTACTTG  
CATTGTATCTTATACTAAAGGCTTTAGAAATTACAACATATCAGGTTCCCCTACTACTGAAGT  
AGCCTTCCGTGAGAACACACCACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTT  
GGATGAAGCAGCTGTAACCTGCCCTAGTGTAGTTTGACCAGGACATTGTGCTGCTCCTTCCAAT  
TGTGTAAGATTAGTTAGCACATCATCTCCTACTTTAGCCATCCGGTGTGGATTAAAGAGGAC  
GGTGTCTCTTTCTATTAAAGTGCTCCATCCCCTACCATCTACACATTAGCATTGTCTCTAGAG  
CTAAGACAGAAATTAACCCGTTCAAGTCAAAAGCAGGGAATGGTTCATTTACTCTTAATCTT  
TATGCCCTGGAGAAGACCTACTTGAACAGGGCATATTTTTTTAGACTTCTGAACATCAGTATGT  
TCGAGGCTACTATGATATTTTGGTTTGAATTGCCCTGCCCAAGTCACTGTCTTTAACTTTT  
AACTGAATATTAAATGTATCTGTCTTCTCCT



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**FIGURE 474**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210
><subunit 1 of 1, 417 aa, 1 stop
><MW: 45305, pI: 5.12, NX(S/T): 6
MALKVLLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVCRLHRFKEDWGFQKCKPCLDCAVVNRQKANC SATSDAICGDCLPG
FYRKTKLVGFQDMECVPCGDP PPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
VLLALLILCVIYCKRQFMEKKPSWSLSRQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD
SVQTCGPVRLLP SMCCEEACSPNPATLGC GVHSAASLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-25

**Transmembrane domain:**

Amino acids 169-192

**N-glycosylation sites:**

Amino acids 105-109;214-218;319-323;350-354;368-372;379-383

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 200-204;238-242

**Tyrosine kinase phosphorylation site:**

Amino acids 207-214

**N-myristoylation sites:**

Amino acids 55-61;215-221;270-276

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 259-270

**TNFR/NGFR family cysteine-rich region proteins:**

Amino acids 89-96

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**FIGURE 475**

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATG**GCAATG  
GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCCAA  
GCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATGAAG  
CTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGGGTAT  
CGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGACGCAA  
TCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACTGACAAATGC  
AACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCCGCCGACG  
CTCAGCGGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTATCGGCAGG  
TCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGCAGAATGACA  
GTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTGCACCACCGAG  
GGCACCACCAGCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGGGGTACCTCTGC  
AACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCTCCCCGAGCACTA  
CAGGTCCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGCA**TAG**ACCGCCCCT  
CCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGCCCCTATCACATAGC  
TCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

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**FIGURE 476**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576  
><subunit 1 of 1, 251 aa, 1 stop  
><MW: 26935, pI: 7.42, NX(S/T): 2  
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSLD  
TGYRAPVTILVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQAPD  
PPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSPVPYIRTCHRPSC  
TTEGTTSPWTAIDLQSGSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 233-251

**N-glycosylation sites.**

amino acids 120-124, 174-178

**N-myristoylation sites.**

amino acids 15-21, 84-90

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**FIGURE 477**

CCCACGCGTCCGGGACAGATGAACTTAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGGGAAAGGACAAAA  
AGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCTACTGCTGTTCTTTTATGCTGGGAGCTGTGGCTGTAAC  
CAACTAGGAAATAACGTATGCAGCAGCTATGGCTGTGAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCCTGTT  
TCTTTTTCTTTTTTGGGGAGTGTCTTGGCAGGTTCTGGGTTTGGACGTTATTCCGGTGAAGTGGGAAACAGAGAA  
AGGATCCTTTGTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACAGGGT  
GGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCACAAATGAGAACTGGA  
CCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTCCAAATTTTAATGGATGATCCCTTTTCAGAT  
TTACCGGGCTGAGCTGAGAGTCAGGGATATAAATGATCAGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAAA  
AATATCAGAAAATACAGCTGAAGGGACAGCATTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGG  
TATCCAAAACCTACAGGATCAGCCCCAAGCTTTTTTCCATATTAACTTAGTGGCGGTGATGAAGGCATGATATA  
TCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCTTAACCTCACAGCGCTGGA  
TGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATCGTTGTCTTGGACGTCAATGACAATGCCCCACA  
GTTTGGCCAGGCTCTGTATGAGACCCAGGCTCCAGAAAACAGCCCCATTGGGTTCTTATTGTTAAGGTATGGGC  
AGAAGATGTAGACTCTGGAGTCAACGCGGAAGTATCCTATTCATTTTTTGTATGCCTCAGAAAATATTTCGAACGAC  
CTTTCAAATCAATCCTTTTTCTGGGGAAATCTTTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAATTCTTACAA  
AATAAATATACAGGCAATGGACGGTGGAGGCCCTTTCTGCAAGATGTAGGGTTTATGTTGGAAGTATTGGACACCAA  
TGACAATCCCCCTGAAGTATCGTATCATCATTTTTCCAAGCTCTGTTGCTGAGAATTCTCCTGAGACGCGCTGGC  
TGTTTTTAAGATTAATGACAGAGACTCTGGAGAAAATGGAAGATGGTTTGCTACATTCAAGAGAATCTGCCATT  
CCTACTAAAACCTTCTGTGGAGAATTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGA  
GTACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAAACATAACGGTCTCGGT  
CTCCGACGTCAATGACAACGCCCCCGCCTTCAACCAACCTCTACACCTGTTCTGTCGTCGCGAGAACACAGCCC  
CGCCCTGCACATCGGCAGCGTCAGCGCCACAGACAGAGACTCGGGCACCAACGCCCCAGGTCACTCTCGCTGCT  
GCGGCCCCAAGACCCGACCTGCCCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCCGCCCT  
CAGGTCTGCTGGACTACGAGGCCCTGCAGGCTTTTCGAGTTCCGCGTGGGCGCCACAGACCGCGGCTCCCCCGCGCT  
GAGCAGAGAGGCGCTGGTGCGCGTGTGGTGTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACCCGCTGCA  
GAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCGGGCGGCGAGCCGGGCTACCTGGTGACCAAGGTGGTGGC  
GGTGGACGGCGACTCGGGCCAGAACGCTGGCTGTGCTACAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTCCG  
TGTGTGGGCGCACAATGGGGAGGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGCGCAAGCACAGGCTCGT  
GGTGTGTTGCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGACGGCTT  
CTCCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCCGCCCCAGGCCAGGCCGAGGCCGACTTGCTCACCCTCTA  
CCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCCTCTCGGTGCTCCTGTTCTGTTGGCGGTGCGGCTGTG  
CAGGAGGAGCAGGGCGGCTCGGTGGTCTGCTCGGTGCCCGAGGGTCTTTTCCAGGGCATCTGGTGGACGT  
GAGGGGCGCTGAGACCTGTCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCCGGGACCAAGTGTG  
CAAGTTCTTGAAACAGTTATTTTCGGATATTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAATTCACCTT  
CCGAAATAGCTTTGGATTTAATATTCAGTAAAGTCTGTTTTTAGTTTCATATACTTTTGGTGTGTTACATAGCCA  
TGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTATTATGCAACTTCAAGCATTATTTTCAAGTAGTATA  
CCCCGTGGTTTTTACAATGTTTTCATCATTTTTTTGCAATTAACAACCTGGGTTTAAATTAATGAGTATTTTTT  
CTAAATGATAGTGTAAAGGTTTTAATCTTTCCAAGTGGCCCAAGGAATTAATTACTATTATATCTCATTACAGAA  
ATCTGAGGTTTTGATTCATTTTCAGAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTGTACTTGCTCTA  
TTTAAGAAGGCATATCTACATTTCCAAACTCATTCTAATCTTATATATTCGTGTTTGAACCATGTCATTTA  
TTTCTACATCATGTATTTAAAAAGAAATATTTCTCTACTACTATGCTCATGACAAAATGAACAAAAGCATATTGT  
GAGCAATACTGAACATCAATAATACCCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTT  
GGCCAATATTTTCTTATGTTAACTTTTGTGATGTATAAAACAGACTATGCCTTAAATTGAATAAAATATATA  
TCTGCCTGAAAATGAATAAAAAATAAACATTTTGAATGTGAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 478**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976
><subunit 1 of 1, 800 aa, 1 stop
><MW: 87621, pI: 4.77, NX(S/T): 7
MAVRELCFPRQRQVLFLFLFWGVSLAGSGFGRYSVTEETEEKGSFVVNLAKDLGLAEGELAARG
TRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVRDI
NDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGLNGIQNYTISPNSFFHINISGGDEGM
IYPELVLDKALDREEQGELSLTLTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYETQAP
ENSPIGFLIVKVWAEVDVSGVNAEVSYSFFDASENIRTTTFQINPFSGEIFLRELLDYELVNSY
KINIQAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFNSVAENSPETPLAVFKINDRDSGEN
GKMVCYIQENLPFLKPSVENFYILITEGALDREIRAEYNITITVTDLGTPLRKTEHNITVLV
SDVNDNAPAFQTQSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQDPHPLASLV
SINADNGHLFALRSLDYEALQAFEFVVGATDRGSPALSREALVRVLVLDANDNSPFVLYPLQN
GSAPCTELVPRAAEPGYLVTKVAVDGDGSGQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLL
SERDAAKHRLVVLVKDNGEPPRSATATLHLLLVLDGFSQPYLPLPEAAPAQAEADLLTVYLV
VALASVSSFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFGHLVDVRGAETLSQSYQYEV
LTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

```

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 687-711

**N-glycosylation sites.**

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

**Glycosaminoglycan attachment site.**

amino acids 28-32

**Tyrosine kinase phosphorylation sites.**

amino acids 394-402, 578-585

**N-myristoylation sites.**amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,  
217-223, 324-330, 325-331, 471-477, 568-574, 759-765**Amidation site.**

amino acids 781-785

**Aminoacyl-transfer RNA synthetases class-II signature 1.**

amino acids 117-138

**Cadherins extracellular repeated domain signature.**

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

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**FIGURE 479**

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCCC  
GAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTC**CATG**GGACCTGTGCGGTTGG  
GAATATTGCTTTTCCCTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGGAGG  
ACGATGACACAGAACGCTTGCCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAGCTAC  
AGGCGGAACCTGAGTCGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCTGGATA  
CAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGGCCTTAG  
AGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCACTGAGAT  
ATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGGGGTGAAGG  
TGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACATACCTCAAGA  
AGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTACTTCCACCATC  
AGGAGCAGCCCCTACAAAATTTTCTCTGTGAAGGTCATGTGCTCCCAGCTGCTGAAACTGCAT  
GTCTACAGGAACTTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAACAGAAGGGGAGG  
AAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAGATGACCAAGACAG  
GAAGCCACCCCAAACCTTGACCGAGAAGATCTTT**TGA**CCCTTGCCTTTGAGCCCCCAGGAGGGGA  
AGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAGCTTTTCAAGGTGTGTT  
TATGAGTGA CTCCACCAAGCTTGTAGCTGTTCTCTCCCATCTAACCTCAGGCAAGATCCTGG  
TGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGGTCCTGCTCCTAGAGATG  
AACTCTATCCAGCCCCTTAATTGGCAGGTGTATGTGCTGACAGTACTGAAAGCTTTCCTCTTT  
AACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGCTGTGGGCTTTGGGGAAGTC  
ACTTAGCTCCTTAAGGTCTGTTTTTAGACCCTTCCAAGGAAGAGGCCAGAACGGACATTCTCT  
GCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCAGCAAACCGTGAAGGAGAATGG  
GACACTGGGTCATGGCCTGGAGTTGCTGATAATTTAGGTGGGATAGATACTTGGTCTACTTAA  
GCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGTGCTCAACTTTCTATATCGCTATT  
AAACTTTTTTCTTTTTTCTA

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**FIGURE 480**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256
><subunit 1 of 1, 248 aa, 1 stop
><MW: 28310, pI: 4.63, NX(S/T): 0
MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVLE
LGQVLDTGKRKRHVPYSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMATLKGL
VQKGVKVDLGIPLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQPLQNFLCEGHVL
PAAETACLQETWTGKEITDGEEKTEGEEEEEEEEEEEEEGGDKMTKTGSHPKLDREDL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 106-110

**N-myristoylation site.**

amino acids 115-121

**Amidation site.**

amino acids 70-74

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**FIGURE 481**

GGCGTGTGCAAGGCGGGGTCCGGCCCCGCGCAGGTCGGGTAAGCGCGTCTAGGGCGCTGCGCGG  
CGCAGCGAAAATGGCGGGCTTCCAGGTGGGCGCGCAAGGCCGTGGTCCTGCTTTGTGCTCTGA  
CCTGCTGCTGCTGCTGCTACTGCTACCACCGCTGGGTCTGCGCGGCCGAAGGCTCGCCCCG  
GACGCCCCGACGAGTCTACCCACCTCCCCGGAAGAAGAAGGATATTCGCGATTACAATGA  
TGCAGACATGGCGCGTCTTCTGGAGCAATGGGAGAAAGATGATGACATTGAAGAAGGAGATCT  
TCCAGAGCACAAAGAGACCTTCAGCACCTGTGCACTTCTCAAAGATAGACCCAAGCAAGCCTGA  
AAGCATATTGAAAATGACGAAAAAAGGGAAGACTCTCATGATGTTTGTCACTGTATCAGGAAG  
CCCTACTGAGAAGGAGACAGAGGAAATTACGAGCCTCTGGCAGGGCAGCCTTTTCAATGCCAA  
CTATGACGTCCAGAGGTTTATTGTGGGATCAGACCGTGCTATCTTCATGCTTCGCGATGGGAG  
CTACGCCTGGGAGATCAAGGACTTTTTGGTCCGTCAAGACAGGTGTGCTGATGTAACCTCTGGA  
GGGCCAGGTGTACCCCGGCAAAGGAGGAGGAAGCAAAGAGAAAAATAAAACAAAGCAAGACAA  
GGGCAAAAAAAGAAGGAAGGAGATCTGAAATCTCGGTCTTCCAAGGAAGAAAATCGAGCTGG  
GAATAAAAGAGAAGACCTGTGATGGGGCAGCAGTGACGCGCTGTGGGGGGACAGGTGGACGTG  
GAGAGCTCTTTGCCAGCTCCTGGGGTGGGAGTGGTCTCAGGCAACTGCACACCGGATGACAT  
TCTAGTGTCTTCTAGAAAGGGTCTGCCACATGACCAGTTTGTGGTCAAAGAATTACTGCTTAA  
TAGGCTTCAAGTAAGAAGACAGATGTTTTCTAATTAATACTGGACACTGACAAATTCATGTTT  
ACTATAAAATCTCCTTACATGGAAATGTGACTGTGTTGCTTTTTCCATTTACACTTGGTGAG  
TCATCAACTCTACTGAGATTCCACTCCCCCTCCAAGCACCTGCTGTGATTGGGTGGCCTGCTCT  
GATCAGATAGCAAATTCTGATCAGAGAAGACTTTAAAACTCTTGACTTAATTGAGTAAACTCT  
TCATGCCATATACATCATTTTCATTATGTTAAAGGTAAAATATGCTTTGTGAACTCAGATGTC  
TGTAGCCAGGAAGCCAGGGTGTGTAAATCCAAAATCTATGCAGGAAATGCGGAGAATAGAAAA  
TATGTCACCTTGAAATCCTAAGTAGTTTTGAATTTCTTTGACTTGAATCTTACTCATCAGTAAG  
AGAACTCTTGGTGTCTGTGTCAGGTTTTATGTGGTCTGTAAAGTTAGGGGTTCTGTTTTGTTCC  
TTATTTAGGAAAGAGTACTGCTGGTGTGAGGGGTTATATGTTCCATTTAATGTGACAGTTTT  
AAAGGATTTAAGTAGGGAATCAGAGTCCTTTGCAGAGTGTGACAGACGACTCAATAACCTCAT  
TTGTTTCTAAACATTTTTCTTTGATAAAGTGCCTAAATCTGTGCTTTCGTATAGAGTAACATG  
ATGTGCTACTGTTGATGTCTGATTTTGCCGTTTCATGTTAGAGCCTACTGTGAATAAGAGTTAG  
AACATTTATATACAGATGTCATTTCTAAGAACTAAAATTCTTTGGGAAAACCCCTCAAAAAA  
AAAAAAAAAAAAAAAAAAAAA



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**FIGURE 482**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92289
><subunit 1 of 1, 234 aa, 1 stop
><MW: 26077, pI: 8.13, NX(S/T): 1
MAASRWARKAVVLLCASDLLLLLLLLLPPPGSCAAEGSPGTPDESTPPPRKKKKDIRDYND
ADMARLLEQWEKDDDDIEEGDLPEHKRPSAPVDFSKIDPSKPESILKMTKKGKTLMMFVTV
SGSPTEKETEEITSLWQGSLEFNANYDVQRFIVGSDRAIFMLRDGSYAWWEIKDFLVGQDRC
ADVTLEGQVYPGKGGGSKEKNKTKQDKGKKKKEGDLKSRSSKEENRAGNKREDL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-32

**N-glycosylation site:**

Amino acids 201-205

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 85-89

**Tyrosine kinase phosphorylation site:**

Amino acids 50-59

**N-myristoylation sites:**

Amino acids 30-36;138-144;153-159;176-182

**Amidation site:**

Amino acids 207-211

**FIGURE 483**

[illegible]

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**FIGURE 484**

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPRL  
AWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVILNV  
QFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLDAQNYPW  
LTNHTVQLQLRSLAHNLSVVATNDVGVTASLPAPGPSRHPSLISSDSNNLKLNNVRLPRENM  
SLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIYRVSSV  
SSDEIWL

**N-glycosylation sites:**

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,  
251-255, 280-284

**Glycosaminoglycan attachment site:**

amino acids 23-27

**Casein kinase II phosphorylation sites:**

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

**N-myristoylation sites:**

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

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**FIGURE 485**

AGAGTTCCTTTTTCTAGGTCGATTAGGTTATACATTGTTGAAGTATAGTTTCGAGTTAGAATT  
GGTCATTTTATTTTCAGTGTTTCACAGAAATCGAAGAAGACAGAAATGGCGCTTCTGTGGTGG  
ATATCTACAGTAGCAATACTGTTGTTTACTTCGACGATTTTGGGAACATACGTTGAAGCTGGT  
GCCGCTAAGTCTAACGAAGAAGAGATTGTGAACAAAAGCGAATTGGAAGATTTCCACGAGGG  
TCGAGAAAGGATGCATCGGGGTGCCACAAGCCGGGCTACCCTGTACCCCTCATTCTCGCTGC  
CCTCCACCTCCCCATGTGCAGCGTCCTCGTCCTATTCTGCATGCTTAGTCTAACACCATCAGG  
CTCGTTTATCTTTTCTGTCATTGATCTCACCAGGAGCAAATCACTAGTGCGTGCTTCTGATTC  
ACGTAACGTAGTATGTAAATAAATGTCAGTGATATTATGAATTGGTAAAACATTTCTGTTATC  
TAAATAAAACAGTGAAGTTTGTGTGACTAAAAAAA

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**FIGURE 486**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96855
><subunit 1 of 1, 84 aa, 1 stop
><MW: 9274, pI: 9.70, NX(S/T): 1
MALLWWISTVAILLFTSTILGTYVEAGAAKSNEEEIVNKSEFGRFPRGSRKDASGCHKPG
YPVPPHSRCPPPPHVQRPRPILHA
```

**Signal peptide:**

Amino acids 1-21

**N-glycosylation site:**

Amino acids 38-42

**N-myristoylation site:**

Amino acids 27-33

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**FIGURE 487**

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCCGGGGCG**ATG**TGGAGCGCG  
GGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGGGC  
GGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTCAAT  
ACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCAGCAA  
TCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCGGCTCG  
GAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACGCATGTG  
CTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCAGGAGGTG  
AGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCTGCTCTGGA  
CAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTGTTCTGTCA  
GTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGGCATGCCCAGT  
GCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTAGTGTGGAGCCC  
TCTGCAGGTCACGATGAACT**CTGA**GTGTGTGGATGGATGGGTGGATGGAGGGTGGCAGGTGGG  
GCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCTCAAGTGCCTTTGTG  
ATTAAAGAATGTTGGTCTATGAAA

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**FIGURE 488**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857  
><subunit 1 of 1, 221 aa, 1 stop  
><MW: 23598, pI: 6.96, NX(S/T): 0  
MWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGSG  
SGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSN  
NQEVSAFGEDGEGDDLDLWTVRCSGQHWEREA AVR FQHVGT SVFLSVTGEQYGSPIRGQHEVH  
GMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**Glycosaminoglycan attachment site.**

amino acids 62-66

**N-myristoylation sites.**amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,  
91-97, 190-196**Endoplasmic reticulum targeting sequence.**

amino acids 218-223

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**FIGURE 489**

CAGCAGCCGAGACAGCAGCTGAGACGGCAGCGGCAGCTTCTCAGGGCCGGAGCCAGTTCTTGGAGGAGACTCTGC  
ACAGGGCA**ATGG**ATCACTGTGGTGCCCTTTTCCTGTGCCTGTGCCTTCTGACTTTGCAGAATGCAACAACAGAGAC  
ATGGGAAGA**ACT**CTCTGAGCTACATGGAGAATATGCAGGTGTCCAGGGGCCGGAGCTCAGTTTTTCTCTCGTCA  
ACTCCACCAGCTGGAGCAGATGCTACTGAACACCAGCTTCCAGGCTACAACCTGACCTTGCAGACACCCACCAT  
CCAGTCTCTGGCCCTTCAAGCTGAGCTGTGACTTCTCTGGCCTCTCGCTGACCAGTGCCACTCTGAAGCGGGTGCC  
CCAGGCAGGAGGTCAAGCATGCCCGGGGTCAACACGCCATGCAGTTCCCGCCGAGCTGACCCGGGACGCCTGCAA  
GACCCGCCCCAGGGAGCTGCGGCTCATCTGTATCTACTTCTCCAACACCCACTTTTTCAAGGATGAAACAACCTC  
ATCTCTGCTGAATAACTACGTCTCTGGGGGCCAGCTGAGTCATGGGCACGTGAACAACCTCAGGGATCCTGTGAA  
CATCAGCTTCTGGCACAAACAAAGCCTGGAAGGCTACACCTGACCTGTGTCTTCTGGAAGGAGGGAGCCAGGAA  
ACAGCCCTGGGGGGGCTGGAGCCCTGAGGGCTGTCTACAGAGCAGCCCTCCCACTCTCAGGTGCTCTGCCGCTG  
CAACCACCTCACCTACTTTGCTGTTCTCATGCAACTCTCCCCAGCCCTGGTCCCTGCAGAGTTGCTGGCACCTCT  
TAGGTACATCTCCCTCGTGGGCTGCAGCATCTCCATCGTGGCCTCGCTGATCACAGTCCTGCTGCACTTCCATTT  
CAGGAAGCAGAGTGACTCCTTAACACGTATCCACATGAACCTGCATGCCTCCGTGCTGCTCCTGAACATCGCCTT  
CCTGCTGAGCCCCGATTCGCAATGTCTCCTGTGCCCGGTTCAGCATGCACGGCTCTGGCCGCTGCCCTGCACTA  
CGCGCTGCTCAGCTGCCCTCACCTGGATGGCCATCGAGGGCTTCAACCTCTACCTCCTCGGGCGTGTCTACAA  
CATCTACATCCGCAGATATGTGTTCAAGCTTGGTGTGCTAGGCTGGGGGGCCCCAGCCCTCCTGGTGTGCTTTT  
CCTCTCTGTCAAGAGCTCGGTATACGGACCCTGCACAATCCCCGTCTTCGACAGCTGGGAGAATGGCACAGGCTT  
CCAGAACATGTCCATATGCTGGGTGCGGAGCCCCGTGGTGCACAGTGTCTGGTGCATGGGTACGGCGGCCCTCAC  
GTCCCTCTTCAACCTGGTGGTGTGCTGGCCTGGGCGCTGTGGACCCTGCGCAGGCTGCGGGAGCGGGCGGATGCACC  
AAGTGTACAGGGCTGCCATGACACTGTCACTGTGCTGGGCTCACCGTGTGCTGGGAACCCACCTGGGCCCTTGGC  
CTTCTTTTCTTTTGGCGTCTTCTGCTGCCCCAGCTGTTCTCTTACCATCTTAACTCGCTGTACGGTTTCTT  
CCTTTTCTGTGGTCTGCTCCCAGCGGTGCCGCTCAGAAGCAGAGGCCAAGGCACAGATAGAGGCCCTTCAGCTC  
CTCCCAAACAACACAG**TAG**TCCGGGCCCTCCTGGCCTGGAATCCTCAGCCTCTCTGGCCGCCAGTAGCCTGAGGCT  
ACGGCTCCTGCTAGAGAGGGTGGCAGGCTGCTGCTGGACCCAGAGGCCACTGTGACCGCCAAGGGGCCTTTT  
CACTTCCACGGCCTCTCCAGGCACTGAGGGGAAGGCATTGCTCTACCTCTCCCTGACATTTTGTCTCCGGGGCAGA  
TCCAACCTTACCTGGGGCAGCAAACCTTGTCTGCTGCTGCTGCTGATGACCTTGGGCCTGCCACTTCTC  
GCCTGGGCATCAGGAAGCCAAGTTTCAAGGACTGTCTTTGAGTCTGTCTGTATGACCTTGGGCCTGCCACTTCTC  
ACAGACCCTAGGTATCCACAGCTGTGACATGGGGGCAAGCAGCTTTGTTTCAGCCTAACCCAGGAGCTTAGTAAA  
AATTGCATAAGACCAGGGGGAAGAGTGTACAGCTGGGGTGGGAATTCGCCGCGGCTCCACCTGCTTGCTAGGGGC  
AGGATCTCATTCAGGCTGCCCTGGAAGCACCTGCTTGGCCCTGCCACCTTCCCTCAGGGGAGGGCCAGATGGCAT  
CCTGGCTTGGGGCGGGTGGGACCTACCCAGGCTCTGAGACTTTACTGGCCTATGCTGAGGCCCTCTTTTCTTTA  
ACTCCCTAAATTATGATGACTCCAAGTCCAAGCCCACCTTCCCAAAGATTGGGAGGTTCCGCCGTTCCAGAGG  
CTCCTCCTGCGGTGCTCCCAAGACTTCCATAGACCATCTGGACCACTAGCCCATCCCGCAGTTTTCTTGGGGCA  
GAGGAAAACGCTTCTTTCTCTCCAGCTGAATCAGCTGGATCCCACTGTCTGGCTGTTTGGTGATTGGGCAAGA  
TTGAATTTGCCCAGGTAGGCGTGAGAGTGTGGGTTTTAAATTGCAAGCTCAGGCCATAGTTTACAGAAATCACCC  
TTACCCACAGACCTTCATGAGACAGTGCTCATGAAGCCAGTGCCTTTCCAGAACGAACACTAGGCGGCACCGTTG  
GTCCACACTCAGAGGCCCTTGGCGCCAAGACTGCATCTAGAATCGCTCAAACACCTGTTTGCAGACCCCATGCAC  
CAGCTGGAGGGGGCCGTAAGTGCAGGACTGCGCCTACTGAGTGACCCATTTCTCCAGGAGGAAAGGCAAGACAG  
CTTACACGGCCATTTGTCTCTTTTCCCAATGCGGCGGTGCACTTTGCTCTTGGGGGCTGCACCCAGACATAGC  
TGGCACACAGAGCAGGGTGTCTAGGTGGTGGTGTCTAGGGCCCTGCCCCAGGCCACTGGGCCGTTTTGATGACCT  
CAAAGGTACAGGCAGAAAATAGGAGCAGGATTTCCCTGGGGAAAAGTTATCCTGGGACATCTTCTGCTCTTCT  
GTACATTTCTAGATGCAAATAACTCCTTACCAGGCAGTGAGTGGCGTAGGCTCTGGAGCCAGGCTGCCTGGGCT  
CCAATGCCAGCTCTGCCACTTGTAGCTGTGAGACTGTGGACAAACCACTCAGCCTCTGTGTGCTCAGTTTTCC  
TATTTGTAAAATAGAGACCATAGTGGTACCTATTTTGAAGACTAAGTAAAGAATTCAAATAAAGAGACTTGGCA  
CAGAGTAAGTGCTCAGTAAAAA



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**FIGURE 490**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96860
><subunit 1 of 1, 528 aa, 1 stop
><MW: 59000, pI: 8.73, NX(S/T): 9
MDHCGALFLCLCLLTQLNATTETWEELLSYEMNQVSRGRSSVFSSRQLHQLEQMLLNTS
FPGYNLTQLQPTIQSLAFKLSCDFSGLSLTSATLKRVPQAGGQHARGQHMQFPALTRD
ACKTRPRELRLICIYFSNTHFFKDENNSSLNNYVLGAQLSHGHVNNLRDPVNISFWHNQ
SLEGYTLCVFWKEGARKQPWGGWSEPGCRTEQPSHSQVLCRCNHLTYFAVLMQLSPALV
PAELLAPLTYISLVGCSISIVASLITVLLHFHFRKQSDSLTRIHMNLHASVLLLNIAFLL
SPAFAMSPVPGSACTALAAALHYALLSCLTWMAIEGFNLYLLGRVYNIYIRRYVFKLG
LGWGAPALLVLLSLSVKSSVYGPCITPVFDSWENGTFQNMISICWVRSPVHSLVMGYG
GLTSLFNLVVLAWALWTLRRLRERADAPSVRACHDTVTVLGLTVLLGTTWALAFFSFGVF
LLPQLFLFTILNSLYGFFLFLWFCSQRCRSEAEAKAQIEAFSSSQTTQ
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-21

**Transmembrane domains:**

Amino acids 244-264;290-309;316-344;358-376;411-431;468-491

**N-glycosylation sites:**Amino acids 18-22;58-62;65-69;146-150;147-151;173-177;  
179-183;394-398;400-404**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 274-278

**N-myristoylation sites:**86 GLSLTS  
101 GGQHAR  
157 GAQLSH  
255 GCSISI  
311 GSACTA  
420 GGLTSL  
467 GTTWAL**Prokaryotic membrane lipoprotein lipid attachment sites:**

Amino acids 246-257;318-329

**Eukaryotic thiol (cysteine) proteases histidine active site:**

Amino acids 410-421

**G-protein coupled receptors family 2 proteins:**

Amino acids 273-302;314-343

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**FIGURE 491**

CTTGGCTGCCCCGACAACAAGCTCGCCACCTGCGCTGGGCGCATCCACCATCCAAGGCCAGCT  
GAGGGGCACCAGACAGAGGATGAGGAGAGAGAGTGCACACGGGCTGCCCTGAGAGACATTTT  
CATGGACATCCTCATGCTGCTTCTGCTTTTGTGTGTAATATATGGGAGATTTTCCCAAGATGA  
ATACTCCCTCAATCAAGCTATCCGGAAAGAATTTACAAGAAATGCCAGAACTGCTTGGGTGG  
CCTGAGAAACATCGCTGACTGGTGGGACTGGAGTCTGACCACACTTCTGGATGGCCTGTACCC  
GGGAGGCACCCCGTCAGCCCGTGTGCCGGGGGCTCAGCCTGGAGCTCTTGGAGGAAAATGCTA  
CCTAATAGGCAGTTCCGTAATTAGGCAGCTAAAAGTTTTTCCTAGGCATTTATGCAAGCCTCC  
CAGGCCATTTTCAGCACTCATCGAAGACTCTATTCCCTACATGTAGTCCCGAAGTTGGAGGCCC  
TGAGAACCCCTACCTGATAGACCCAGAGAACCAAAACGTGACCCTGAATGGTCCTGGGGGCTG  
TGGGACAAGGGAGGACTGTGTGCTCAGCCTGGGCAGAACCAAGGACTGAAGCCCACACAGCCCT  
GTCCCGACTCAGGGCCAGCATGTGGATTGACCGCAGCACCAGGGCTGTGTCTGTGCACTTCAC  
TCTCTATAACCCCTCCAACCCAACTCTTCACCAGCGTGTCCCTGAGAGTGGAGATCCTCCCTAC  
GGGGAGTCTCGTCCCCTCATCCCTGGTGGAGTCATTACAGCATCTTCCGCAGCGACTCAGCCCT  
GCAGTACCACCTCATGCTTCCCCAGCTGGTCTTCCTGGCACTCAGCCTGATCCACCTCTGTGT  
TCAACTCTACCGTATGATGGACAAGGGCGTCCCTCAGCTACTGGCGAAAGCCAAGGAAGTGGCT  
GGAGGTAGCCTCTCTTGTGTCATTTTCTTTTGAAAAATTAACAATAAACTGTTTATATCTTGAA  
AAAATAATTTAAATAAGAAATTGATTATGCACTAGCTACTGCCAACATTATTGCAGTTTTTCTC  
CCTCTGTAGTGTTAATCTCAAAACAGCATTTGAGATCAGGTATCATTTAGTGTTGTTACAGTT  
ACCGTCATGTACCACACGAATTCAGCCAAGGTGGTGGTCCCATAAGATCATATGGTGTCTAAG  
AAATTTCTGTCACCTAATGACATCTTGATTCTGACCTTGTATGTAGGCCTAGGCTAAATATGT  
CTGTTTGTATCTTAGCTTTTAATAAAGAAGTTAAAAATAAAAAA

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**FIGURE 492**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96861
><subunit 1 of 1, 300 aa, 1 stop
><MW: 33649, pI: 9.26, NX(S/T): 1
MRRESRTRAALRDISMDILMLLLLLLCVIYGRFSQDEYSLNQAIRKEFTRNARNCLGGLRN
IADWWDWSLTLLDGLYPGGTPSARVPGAQPGALGGKCYLIGSSVIRQLKVFPRHLCKPP
RPFSAIEDSIPTCSPEVGGPENPYLIDPENQNVTLNGPGGCGTREDCVLSLGRTRTEAH
TALSRLRASMWIDRSTRAVSVHFTLYNPPTQLFTSVSLRVEILPTGSLVPSSLVESFSIF
RSDSALQYHMLLPQLVFLALSLIHLVCVQLYRMMDKGVLSYWRKPRNWLEVASLVSFSEK
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-30

**Transmembrane domain:**

Amino acids 250-267

**N-glycosylation site:**

Amino acids 153-157

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 2-6

**N-myristoylation sites:**

Amino acids 56-62;75-81;79-85;80-86;88-94;92-98;160-166

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**FIGURE 493**

TCTCAGGGCTTCATACAGGAAATCTATTGCTGTGTCAAGTTCAGAGAAAAGCTTCTGTTCGT  
CCAAGTTACTAACCAGGCTAAACCACATAGACGTGAAGGAAGGGGCTAGAAGGAAGGGAGTGC  
CCCACTGTTGATGGGGTAAGAGGATCCTGTACTGAGAAGTTGACCAGAGAGGGTCTCACCATG  
CGCACAGTTCCTTCTGTACCTGTGTGGAGGAAAAGTACTGAGTGAAGGGCAGAAAAGAGAAA  
ACAGAAATGCTCTGCCCTTGGAGAACTGCTAACCTAGGGCTACTGTTGATTTTGACTATCTTC  
TTAGTGGCCGAAGCGGAGGGTGCTGCTCAACCAACAACCTCATTAATGCTGCAAACTAGCAAG  
GAGAATCATGCTTTAGCTTCAAGCAGTTTATGTATGGATGAAAAACAGATTACACAGAACTAC  
TCGAAAGTACTCGCAGAAGTTAACACTTCATGGCCTGTAAAGATGGCTACAAATGCTGTGCTT  
TGTTGCCCTCCTATCGCATTAAAGAAATTTGATCATAATAACATGGGAAATAATCCTGAGAGGC  
CAGCCTTCCTGCACAAAAGCCTACAGGAAAGAAACAAATGAGACCAAGGAAACCAACTGTACT  
GATGAGAGAATAACCTGGGTCTCCAGACCTGATCAGAATTCGGACCTTCAGATTTCGTCCAGTG  
GCCATCACTCATGACGGGTATTACAGATGCATAATGGTAACACCTGATGGGAATTTCCATCGT  
GGATATCACCTCCAAGTGTTAGTTACACCTGAACTGACCCTGTTTCAAACAGGAATAGAACT  
GCAGTATGCAAGGCAGTTGCAGGGAAGCCAGCTGCGCAGATCTCCTGGATCCCAGAGGGCGAT  
TGTGCCACTAAGCAAGAATACTGGAGCAATGGCACAGTGACTGTTAAGAGTACATGCCACTGG  
GAGGTCCACAATGTGTCTACCGTGACCTGCCACGTCTCCCATTTGACTGGCAACAAGAGTCTG  
TACATAGAGCTACTTCCTGTTCCAGGTGCCAAAAAATCAGCAAAATTATATATTCATATATC  
ATCCTTACTATTATTATTTTGACCATCGTGGGATTCATTTGGTTGTTGAAAGTCAATGGCTGC  
AGAAAATATAAATTGAATAAAACAGAATCTACTCCAGTTGTTGAGGAGGATGAAATGCAGCCC  
TATGCCAGCTACACAGAGAAGAACAATCCTCTCTATGATACTACAAACAAGGTGAAGGCATCT  
CAGGCATTACAAAGTGAAGTTGACACAGACCTCCATACTTTATAAGTTGTTGGACTCTAGTAC  
CAAGAAACAACAACAACGAGATACATTATAATTACTGTCTGATTTTCTTACAGTTCTAGAAT  
GAAGACTTATATTGAAATTAGGTTTTCCAAGGTTCTTAGAAGACATTTTAATGGATTCTCATT  
CATACCCTTGATATAATTGGAATTTTGTATTCTTAGCTGCTACCAGCTAGTTCTCTGAAGAACT  
GATGTTATTACAAAGAAAATACATGCCCATGACCAAAATATTCAAATGTGCAGGACAGTAAAT  
AATGAAAACCAAATTTTCTCAAGAAATAACTGAAGAAGGAGCAAGTGTGAACAGTTTCTTG  
TATCCTTTTCAGAATATTTTAATGTACATATGACATGTGTATATGCCTATGGTATATGTGTCAA  
TTTATGTGTCCCCTTACATATACATGCACATATCTTTGTCAAGGCACCAGTGGGAACAATACA  
CTGCATTACTGTTCTATACATATGAAAACCTAATAATATAAGTCTTAGAGATCATTTTATATC  
ATGACAAGTAGAGCTACCTCATTCTTTTTAATGGTTATATAAAATTCCATTGTATAGTTATAT  
CATTATTTAATTAAAAACAACCCTAATGATGGATATTTAGATTCTTTTAAGTTTTGTTTATTT  
CTTTTAAGTTTTGTTTGTGGTATAAACAATACCACATAGAATGTTTCTTGTTCATATATCTCT  
TTGTTTTTGTAGTATATCTGTAGGATAACTTTCTTGAGTGGAATTGTCAGGTCAAAGGGTTTTGT  
GCATTTTACTATTGATATATATGTTAAATTGTGTCAAATATATATGTCAAATTCCTCCAACA  
TTGTTTAAATGTGCCTTTCCCTAAATTTCTATTTTAATAACTGTACTATTCCTGCTTCTACAG  
TTGCCACTTCTCTTTTTAATCAACCAGATTAAATATGATGTGAGATTATAATAAGAATTATA  
CTATTTAATAAAAAATGGATTTATA

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**FIGURE 494**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96866
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39069, pI: 8.13; NX(S/T): 10
MLCPWRTANLGLLLILTIFLVAEAEAGAAQPNNSLMLQTSKENHALASSSLCMDEKQITQN
YSKVLAEVNTSWPVKMATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE
TNCTDERITWVSRPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLVTPELTL
FQNRNRTAVCKAVAGKPAAQISWIPEGDCATKQEYWSNGTVTVKSTCHWEVHNVSTVTCH
VSHLTGNKSLYIELLPVPGAKKSAKLYIPYIILTIIILTIVGFIWLLKVNGCRKYKLNKT
ESTPVVEEDEMOPYASYTEKNNPLYDTTNKVKASQALQSEVDTDLHTL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-24

**Transmembrane domains:**

Amino acids 78-98;267-286

**N-glycosylation sites:**Amino acids 31-35;60-64;69-73;116-120;122-126;185-189;  
218-222;233-237;247-251;298-302**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 112-116

**N-myristoylation sites:**

Amino acids 103-109;259-265

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**FIGURE 495**

CCAGGTGCACAGCGCATCGCCCCGAGGCTGTACCGCCCTGCCCGCCACCCAGCTGTCCTG  
GACCCAGGGGCAGGGAGAGGCTGGACGCCAGGTGCGCGGACACAGAAGCGTCTAAGCACAGCT  
TCCTCCTTGCCGCTCCGGGAAGTGGGCAGCCAGCCAGGAACCAAGTACCACCTGCACCA**ATGGG**  
GCTGTCCCGGAAGGAGCAGGTCTTCTTGGCCCTGCTGGGGGCTCGGGGGTCTCAGGCCTCAC  
GGCACTCATTTCTCCTCCTGGTGGAGGCCACCAGCGTGCTCCTGCCACAGACATCAAGTTTGG  
GATCGTGTTTGATGCGGGCTCCTCCACACGTCCCTCTTCTGTATCAGTGGCCGGCGAACA  
GGAGAATGGCACGGGTGTGGTCAGCCAGGCCCTGGCCTGCCAGGTGGAAGGGCTGGAATCTC  
CTCCTACACTTCTAATGCTGCACAGGCTGGTGAGAGCCTGCAGGGCTGCTTGGAGGAGGCGCT  
GGTGCTGATCCCAGAGGCCAGCATCGGAAAACACCCACGTTCTTGGGGGCCACGGCTGGCAT  
GAGGTTGCTCAGCCGGAAGAACAGCTCTCAGGCCAGGGACATCTTGCAGCAGTCACCCAGGT  
CCTGGGCCGGTCTCCCGTGGACTTTTGGGGTGCCGAGCTCCTGGCCGGGCAGGCCGAAGGTGC  
CTTGGTTGGATCACTGTCAACTACGGCTTGGGGACGCTGGTCAAGTACTCCTTCACTGGAGA  
ATGGATCCAGCCTCCGGAGGAGATGCTGGTGGGTGCCCTGGACATGGGAGGGGCTCCACCCA  
GATCACGTTTCGTGCCTGGGGGCCCCATCTTGGACAAGAGCACCCAGGCCGATTTTCGCCTCTA  
CGGCTCCGACTACAGCGTCTACACTCACAGCTACCTGTGCTTTGGACGGGACCAGATGCTGAG  
CAGGCTCCTCGTGGGGCTGGTGCAGAGCCGCCGGCTGCCCTGCTCCGTACCCGTGCTACCT  
CAGCGGCTACCAGACCACACTGGCCCTGGGCCGCTGTATGAGTCACCCTGTGTCCACGCCAC  
GCCCCCGCTGAGCCTCCCCAGAACCTCACAGTTGAAGGGACAGGCAACCCTGGAGCCTGCGT  
CTCAGCCATCCGGGAACTTTCAACTTCTCCAGCTGCCAGGGCCAGGAGGACTGCGCCTTTGA  
CGGGGTCTACCAGCCCCCGCTGCGGGGCCAGTTCTATGTGGAGGCCAGCTACCCTGGGCAGGA  
CCGCTGGCTGCGGGACTACTGTGCCTCAGGCCTGTACATCCTCACCTCCTGCACGAGGGCTAC  
GGGTTCAGCGAGGAGACCTGGCCAGCCTCGAGTTCCGAAAGCAGGCGGGCGGTGTGGACATT  
GGCTGGACACTGGGCTACATGCTGAACCTGACCGGGATGATCCCGGCCGATGCGCCGGCTCAG  
TGGCGGGCAGAGAGCTACGGCGTCTGGGTGGCCAAAGTGGTGTTCATGGTGCTGGCCCTGGTG  
GCGGTGGTGGGGCTGCCTTGGTCCAGCTCTTCTGGTTGCAGGACT**TAGT**GGGAAGGCGGAGGT  
GGGCCCCACAGAGCCCACAGGCAGCTGCGTCCCGGATGCTGGAGGCTTCTGAGCCCTGAGC  
GCCGTGGGGCCTTGCTCTGTGGCTCTGCCCACGGTCAGGTGACAGCCACCTCCAGGGCACCGT  
CAGGGTGGTGCTGGCCACAGAGGCTGCATGACCTCCCTCCCGGCGTCCCTCCCCAACCTCC  
TTCCGCAACTGGGCTTCCAGGGCCGTAGGTGCCTTTCTGCACACAGGCCGCCAGGACTCGTGG  
TGTCTCCAGGCTGTGTGACTGCAGGGCCACATGCTGCCTGCAAACAGGGCAAGACCACGGAGG  
CACAGGGGTCTGCTCCTGATGGGGCCTCAGGAGGGGCGGAGAGGGGTGGAAGGGAGGGAGCT  
GCCCCACCTGGACCCCCGCTCTCCCTGCTGTTGCTGAGCAGATGGATGGAGTCCAGGCCTGG  
GGGCTTCTGCTGGGCCAGCCCGGCTCCACACCCACTTGGAGGGTGAGACTGCAGTGGGGGT  
TGTTTTTATTAAAGCATCATGGACACAGCAAAAAAAAAAAAAA

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**FIGURE 496**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96870
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49377, pI: 4.98, NX(S/T): 5
MGLSRKEQVFLALLGASGVSGLTALILLVEATSVLLPTDIKFGIVFDAGSSHTSLFLYQ
WPANKENGTVVVSQALACQVEGPGISSYTSNAAQAGESLQGCLEEALVLIPEAQHRKTPT
FLGATAGMRLLSRKNSSQARDIFAAVTQVLGRSPVDFWGAELLAGQAEGAFGWITVNYGL
GTLVKYSFTGEWIQPPPEMLVGALDMGGASTQITFVPGGPILDKSTQADFRLYGSDYSVY
THSYLCFGRDQMLSRLLVGLVQSRPAALLRHPCYLSGYQTTLALGPLYESPCVHATPPLS
LPQNLTVEGTGNPFGACVSAIRELFNFSSCQGQEDCAFDGVYQPPLRGQFYVEASYPGQDR
WLRDYCASGLYILTLLHEGYGFSEETWPSLEFRKQAGGVDIGWTLGYMLNLTGMIPADAP
AQWRAESYGVVWAKVVFMVLALVAVVGAALVQLFWLQD
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-21

**Transmembrane domain:**

Amino acids 428-449

**N-glycosylation sites:**

Amino acids 67-71;135-139;304-308;325-329;410-414

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 133-137

**N-myristoylation sites:**Amino acids 50-56;123-127;165-171;207-213;234-240;  
259-265;311-317;314-320;331-337;398-404;  
413-419;429-435**GDA1/CD39 family of nucleoside phosphatases proteins:**

Amino acids 43-59;202-215

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**FIGURE 497**

GCCTTATAAAGTAGCCTCTGCATCTGCCTGCCTCGGGCAGAGGAGGGCTACCCTGGGGCTGAG  
AGTTCACCTGTCTCAGGAACCACCTGAGCCACAGATCCTGTGGGCAGCGGCCAGGGCAGCCA  
**TGG**CCTTGGGCAAGTAGGCTGGGCCTGCTGCTGGCACTGCTGCTGCCCCGTGGTCGGTGCCTCCA  
CGCCAGGCACCGTGGTCCGACTCAACAAGGCAGCATTGAGCTACGTGTCTGAAATTGGGAAAG  
CCCCCTCTCCAGCGGGCCCTGCAGGTCAGTGTCCCTCATTTCTGGACTGGAGTGGAGAGGCGC  
TTCAGCCCACCAGGATCCGGATTCTGAATGTCCATGTGCCCCGCCTCCACCTGAAATTCATTG  
CTGGTTTCGGAGTGCGCCTGCTGGCAGCAGCTAATTTTACTTTCAAGGTCTTTCGCGCCCCAG  
AGCCCCCTGGAGCTGACGCTGCCTGTGGAAGTGTGGCTGACACCCGCGTGACCCAGAGCTCCA  
TCAGGACCCCTGTGGTCAGCATCTCTGCCTGCTCTTTATTCTCGGGCCACGCCAACGAGTTTG  
ATGGCAGTAACAGCACCTCCACGCGCTGCTGGTCCTGGTGCAGAAGCACATTAAAGCTGTCT  
TGAGTAACAAGCTGTGCCTGAGCATCTCCAACCTGGTGCAGGGTGTCAATGTCCACCTGGGCA  
CCTTAATTGGCCTCAACCCCGTGGGTCTGAGTCCAGATCCGCTATTCCATGGTCAGTGTGC  
CCACTGTCACCACTGACTACATTTCCCTGGAAGTCAATGCTGTTCTCTTCTGCTGGGCAACC  
CCATCATCCTGCCCACGGATGCCACCCCTTTTGTGTTGCCAAGGCATGTGGGTACCGAGGGCT  
CCATGGCCACCGTGGGCCTCTCCCAGCAGCTGTTTGACTCTGCGCTCCTGCTGCTGCAGAAGG  
CCGGTGGCCTCAACCTGGACATCACAGGGCAGCTGAGGTCCGATGACAACCTGCTGAACACCT  
CTGCTCTGGGCCGGCTCATCCCGGAGGTGGCCCCGCCAGTTTCCCGAGCCCATGCCTGTGGTGC  
TCAAGGTGCGGCTGGGTGCCACACCTGTGGCCATGCTCCACACAAACAACGCCACCCTGCGGC  
TGCAGCCCTTCGTGGAGGTCTGGCCACAGCCTCCAACCTCGGCTTTCCAGTCCCTCTTCTCCC  
TGGATGTGGTAGTGAACCTTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGGACCA  
CGTCTGTGCTGGGGGATGTCCAGCTCACGGTGGCCTCCTCCAACGTGGGCTTCATTGATACAGAT  
CAGGTGCGCACACTGATGGGCACCGTTTTTTGAGAAGCCCCCTGCTGGACCATCTCAATGCTCTC  
TTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTTGCCCTGAGATCTTT  
GTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAGAGCT**TGA**GGCAAGACCACT  
GGGAGGCCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCATTTCAAGCCACTGGGGA  
AACTGAGGCAAAACCATACTTAGTCATCACCAACAAGCTGGACTGCTTAGCTGGGCTGTTTTA  
TCTTCCCTGAGTGCCCTGGGTCTCCCTCCCTCACTTCTGCCCTTTCCCTTCCTCCTCCTCTTCT  
CCTCCCTCTTCCCTCATCTCCCCCTCCTTCTCTGCCCCACCCAGGGGGGAGCAGACTGCT  
CCTCCAGGCTGTATAGACCTGCCCTCTTGCAATTAACAACCTTCTCTTGAGCTGC



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**FIGURE 498**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96872
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49158, pI: 8.72, NX(S/T): 4
MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQRALQVTVPHFLDWS
GEALQPTRIRILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT
RVTQSSIRTPVVSISACSLFSGHANEFDGSNSTSHALLVLVQKHIKAVLSNKLCLISISNL
VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVTSDYISLEVNAVLFLLGNPIILPTDAT
PFVLPRHVGTEGSMATVGLSQQLFDSALLLLQKAGALNLDITGQLRSDNLLNTSALGRL
IPEVARQFPPEMPVVLKVRLGATPVAMLHTNNTLRLQPFVEVLATASNSAFQSLFSLDV
VVNLRQLSVSKVKLQGTTSVLGDVQLTVASSNVGFIDTDQVRTLMGTVFEKPLLDHLNA
LLAMGIALPGVVNLHYVAPEIFVYEGYVVVISSGLFYQS
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**Transmembrane domain:**

Amino acids 217-236

**N-glycosylation sites:**

Amino acids 96-100;151-155;293-297;332-336

**N-myristoylation sites:**

Amino acids 8-14;149-155;189-195;249-255;252-258;283-289

**LBP / BPI / CETP family proteins:**

Amino acids 22-50; 251-287

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**FIGURE 499**

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCC**ATG**AAAGC  
CCTTATGCTGCTCACCCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCACTC  
CTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGGACA  
GCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCTGTGG  
CACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTGACATA  
TAACACCACCTGCTGCAACAAGGACAAGTGAACAGCGCAGGACCCCGGCCCACTCCAGCCCT  
GGGCCTTGCTCTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCAC**TGAG**ACTCATT  
CCATTGGCTGCCCCCTCCTCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCTCTGTATCC  
CCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTGTTCCGAGTG  
GTCTCCTCATCCATCCTTCCACCTCACACCCTTCACTCTCCTTTTTCTGGGTCCCTTCCCAC  
TTCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCTATACTCTGCTG  
TCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTGTTGTCCCCAGTG  
AAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCAAACCCAGGCTCCC  
ATATGTACCCCATCCCCCATACTCACCTCTTCCATTTTGAGTAATAAATGTCTGAGTCTGGA  
AAAAAAAAAAAAAAAAAAAA

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**FIGURE 500**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878
><subunit 1 of 1, 125 aa, 1 stop
><MW: 13821, pI: 8.60, NX(S/T): 2
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSNL
RCGTPEEPCQEAFNQTNRKLGITYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGWLLH
```

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**N-glycosylation sites.**

amino acids 77-81, 88-92

**N-myristoylation site.**

amino acids 84-90

**Ly-6 / u-PAR domain protein signature.**

amino acids 85-98

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**FIGURE 501**

GGAGCCTCCTAATGCAGTCTTCTGCACAGTCCTGGGGACTGACTGACTGAATCACACCTCTGG  
GGCTGGGGGCTGCTGACATGTGTGCCTTTTCCTTGGCTGCTTCTTCTCCTGCTGCTCCAGGAGG  
GCAGCCAAAGGAGACTCTGGAGATGGTGTGGATCCGAGGAAGTGGTTGCGGTCTTCAGGAGT  
CCATCAGCCTCCCCCTGGAAATACCACCAGATGAAGAGGTTGAGAACATCATCTGGTCCTCTCAC  
AAAAGTCTTGCCACTGTGGTGCCAGGGAAAGAGGGACATCCAGCTACCATCATGGTGACCAAT  
CCACACTACCAGGGCCAAGTGAGCTTCCTGGACCCCAGCTATTCCCTGCATATCAGCAATCTG  
AGCTGGGAGGATTCAGGGCTTTACCAAGCTCAAGTCAACCTGAGAACATCCCAGATCTCTACC  
ATGCAGCAGTACAATCTATGTGTCTACCATCCTAACTATGCTTCTGAGAAGCCTTCAACAGCC  
TTCTGCCTCCTGGCCAAGGGATTGCTCATCTTCTTGCTCTTGGTAATTCTGGCCATGGGACTC  
TGGGTCATCCGAGTCCAGAAAAGACACAAAATGCCAAGGATGAAGAACTCATGAGAAACAGA  
ATGAAATTGAGGAAGGAGGCAAAGCCTGGCTCCAGCCCTGCCTGACTGCTCCTTGGGAACCCC  
AGTCCTGAGCTTGGTTTCTTCCCAGCACCCAGAGAATCCTTCCTCAGCTCTCTTCTTTCCAGG  
GGAAGGAGGTGCTCAGGGGTGGGTATCCAGAGAGCCATACTTCTGAGGGAAGACTGGCTGGCA  
ATAAAGTCAAATTAAGTGACCACA

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**FIGURE 502**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96879
><subunit 1 of 1, 198 aa, 1 stop
><MW: 22584, pI: 9.40, NX(S/T): 1
MCAFPWLLLLLLLQEGSQRRLLWRWCGSEEVVAVLQESISLPLEIPPDEEVENIIWSSHKS
LATVVPKGEGHPATIMVTNPHYQGQVSFLDPSYSLHISNLSWEDSGLYQAQVNLRTSQIS
TMQQYNLCVYHPNYASEKPSTAFCLLAKGLLI FLLL VILAMGLWVIRVQKRHKMPRMKKL
MRNRMKLRKEAKPGSSPA
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-18

**Transmembrane domain:**

Amino acids 144-165

**N-glycosylation site:**

Amino acids 99-103

**N-myristoylation site:**

Amino acids 106-112

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**FIGURE 503**

ACGGGCCCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGGCTGCAGCTCTGCAG  
TCGGGGCCGTTTCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCTAC  
CGCACCCAGGTTTCGGCCCGTAGGCGTCTGGCAGCCCGGCGCCATCTTCATCGAGCGCC**ATGGC**  
CGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTCTGCT  
GACCGCGGGCCCTGCCCTGGGCTGGAACGACCCCTGACAGAATGTTGCTGCGGGATGTAAAAGC  
TCTTACCCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACAGTTGAA  
ATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAAGTCATACAGTGTGAGAACAA  
AGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCATACAAATT  
TGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGTACTAAGAGG  
TTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAACTGAAGGAGTC  
TGGAAAGCAGCACGGCTTTGCCTCTTCTCTGATTATTATTATAAGTGGTCCTCGGCGGATTC  
CTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTTTGTAGTCTATAA  
GCTGTTCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATCCTCCATTTTCCCA  
CCGTTACCAGAGATTCACCAACTCAGCAGGACCTCCTCCCCCAGGCTTTAAGTCTGAGTTCAC  
AGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTTGGCAGTGCTTTTACAGGACAACA  
AGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAAGTGGTGGAACTAGGATA  
TTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGGTACTACCCGTCCTATCC  
TCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCATGGAGGCTCGGGCAGCTA  
TTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAGGATATGGTGGTACCAGGAG  
ACG**ATAA**AGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAATTTTGGATTTTTCATCACTTT  
CTCTTTAGAAAAAAAGTACTACCTGTTAACAATTGGGAAAAGGGGATATTCAAAGTTCTGTG  
GTGTTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAGGCTAAAAGTTGATGTGTGACAA  
AATACTTATGTGTTGTATGTCAGTGTAAATGCAGATGTATATTGCAGTTTTTGAAGTGATC  
ATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAACCTGTGATGCCCTAAGAAGCATTAA  
GAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAAAATTTAGTTTTGGTGGTTGTAGC  
TGATGAGTTATTACCTCATAGAGACTATAATATTCTATTTGGTATTATATTATTTGATGTTTG  
CTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAATTATGCTAATTTGTGAGTTCTGATCAC  
TTTTGAGCTCTGAAGCTTTGAATCATTCAAGTGGTGGAGATGGCCTTCTGGTAACTGAATATTA  
CCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTAGAAGGTTGTTGTGAATGACTCTGTGCTGG  
CAAAAATGCTTGAAACCTCTATATTTCTTTCGTTTATAAGAGGTAAAGGTCAAATTTTCAAC  
AAAAGTCTTTTAATAACAAAAGCATGCAGTCTCTGTGAAATCTCAAATATTGTTGTAATAGT  
CTGTTTCAATCTTAAAAAGAATCA

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**FIGURE 504**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889  
><subunit 1 of 1, 339 aa, 1 stop  
><MW: 36975, pI: 7.85, NX(S/T): 1  
MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIQ  
LKCVGGTAGCDSYTPKVIQCQNKGDGYDVQWECKTDLDIAYKFGKTVVSCGYESSEDQYVL  
RGSCGLEYNLDYTELGLQKLKESGKQHGFAFSFDYYYKWSSADSCNMSGITIVVLLGIAFVV  
YKFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGSAFTG  
QQGYENSGPGFWTGLGTGGILGYLFSGNRAATPFSDSWYYPSYPPSYPGTWNRAYSPLHGGSG  
SYSVCSNSDTKTRTASGYGGTRRR

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 171-190

**N-glycosylation site.**

amino acids 172-176

**Glycosaminoglycan attachment sites.**

amino acids 244-248, 259-263, 331-335

**Tyrosine kinase phosphorylation site.**

amino acids 98-106

**N-myristoylation sites.**amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,  
270-276, 278-284, 312-318

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**FIGURE 505**

GCAAAAGGAAGGGAGGGAAGCACTCCATCATCTCACTGGGAAGAACGGGCACGGGCATACCTGC  
AGCTACTGGGGTTCCACTGGGCTTGAGGGTCGATTTTTTCACCTTTTGAAGGACAAGATGCATT  
GGAAGATGTTGCTGCTTCTGCTGTTGTATTACAATGCTGAGGCTTCTATGTGCCACAGGTGGA  
GCAGGGCTGTGCTCTTCCCTGCCGCCACCGGCCAAAGAGGTCCTCATCACTGCCATTGAACC  
CAGTCCTGCAGACCTCCCTGGAGGAGGTGGAGCTGCTCTACGAGTTCCTGCTGGCCGAACCTG  
AGATCAGCCCTGACCTGCAGATCTCCATCAAGGACGAGGAGCTGGCCTCCTTGCGGAAGGCCT  
CAGACTTCCGCACCGTCTGCAACAACGTATCCCCAAGAGCATCCCAGACATCCGCCGGCTCA  
GCGCCAGCCTCTCCAGCCACCCTGGCATCCTCAAGAAAGAAGACTTTGAAAGGACAGTGCTGA  
CCCTGGCCTACACAGCCTACCGCACAGCCCTGTCCCACGGCCATCAGAAGGACATCTGGGCGC  
AGTCCCTCGTTAGCCTCTTCCAGGCCCTGAGGCACGACTTGATGCGCTCCTCACAGCCGGGAG  
TACCTCCCCTGAGAGACTGGCCACACAGGACCTCAGAGCAGGGACCAGCACAGTAATCCAGA  
AAGTCTTCATTCTCTACTCCATTTACAGAGACCAGCAACAAAACACTTACCGCTGACACAGAG  
CAGCAGAGATCAAACAGTAACCCCGATGCTCTTTTCTCCTTGATTTTCTGGAAGACACATC  
TGATTCATGCCATCATGTGACCTGGGCTGGAAGAAAGGGCTGGAATGGTCATTCAAGACGCCT  
CCATGGGCAGAATGGTTTGCCTATGGCAGGCAGAAATCTGATATGCTTCAACCCAGAGCAGTG  
GCCACACACTCAAGAGTGAGAACAGGCGTGAGCCACCGTGCCTGGCCCAGGATCTAAAACTT  
TCTAAGTTTCTCCATCGTTGGCATCCTCACAGCTATCTCCAATGTCACTCAAGAGACATCAA  
CAGACATTTAACTGCTGCAGACTTCATTGCTCTGTACCTCACCTTGAATCTAACAAATCAAA  
GTATTTCTGCAGGTCCAATGGTCTAAAATCAAATGCTTGTTAAATGACTTTTTTACAACACCCCTT  
ACTTTCCTAATCCATTTCAATCTTATTTTTTTTATTGTGGTAAAAACACATCACGTAAAATG  
TACCATCTTAACCATTTTTTAAGCATATGGTACAGCAGTGTTAACTCCATGCATGTTGTGAAAC  
AGACCCCGGAACCTTCTCATCTTGTAATTCTGAAGTCTATACCCACCGAACAACCTCCTCTT  
TTCCCCTTCCCCCTGCCTGCCCCAGCTCTTGGCACCATTATTCTGCTTTCTGTTTTTGAGAGT  
CTGACTACTTAAGATACCTCATACAAGCGGGATCTGGCTTACATTTCTTGAGCATTGTATTCT  
GGAAAAGTGTTTCCTTCTCTGAAAAATGGGTAGAGTTCTGAAGGAGAACTACTGGTCTTATT  
GTACACTTGCTGTACCTATTTTTATTTAACAAATATTCATCTATGGTATAATAAAGATGTCAT  
GGTTGGAAAAAAAAAAAAAAAAAAAAAAAAA



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**FIGURE 506**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96893
><subunit 1 of 1, 173 aa, 1 stop
><MW: 19733, pI: 8.78, NX(S/T): 0
MHWKMLLLLLLYNAEASMCHRWSRAVLFPAAHRPKRSSSLPLNPVLQTSLEEVELLYEF
LLAELEISPDQLQISIKDEELASLRKASDFRTVCNNVIPKSIPDIRRLSASLSSHPGILKK
EDFERTVLTLAYTAYRTALSHGHQKDIWAQSLVSLFQALRHDLMRSSQPGVPP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-17

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 36-40;84-88;105-109

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**FIGURE 507**

GGCGGCGGGCTGCGCGGAGCGGCGTCCCCTGCAGCCGCGGACCGAGGCAGCGGCGGCACCTGC  
CGGCCGAGCAATGCCAAGTGAGTACACCTATGTGAAACTGAGAAGTGATTGCTCGAGGCCTTC  
CCTGCAATGGTACACCCGAGCTCAAAGCAAG**ATG**AGAAGGCCAGCTTGTATTAAAAGACAT  
CCTCAAATGTACATTGCTTGTGTTTGGAGTGTGGATCCCTTTATATCCTCAAGTTAAATTATAC  
TACTGAAGAATGTGACATGAAAAAATGCATTATGTGGACCCTGACCATGTAAAGAGAGCTCA  
GAAATATGCTCAGCAAGTCTTGAGAAGGAATGTCGTCCCAAGTTTGCCAAGACATCAATGGC  
GCTGTTATTTGAGCACAGGTATAGCGTGGACTTACTCCCTTTTGTGCAGAAGGCCCCCAAAGA  
CAGTGAAGCTGAGTCCAAGTACGATCCTCCTTTTGGGTTCCGGAAGTTCTCCAGTAAAGTCCA  
GACCCTCTTGGAACCTCTTGCCAGAGCACGACCTCCCTGAACACTTGAAAGCCAAGACCTGTCG  
GCGCTGTGTGGTTATTGGAAGCGGAGGAATACTGCACGGATTAGAACTGGGCCACACCCTGAA  
CCAGTTCGATGTTGTGATAAGGTTAAACAGTGCACCAGTTGAGGGATATTGAGAACATGTTGG  
AAATAAAACTACTATAAGGATGACTTATCCAGAGGGCGCACCACTGTCTGACCTTGAATATTAT  
TCCAATGACTTATTTGTTGCTGTTTTATTTAAGAGTGTTGATTTCAACTGGCTTCAAGCAATG  
GTAAAAAAGGAAACCCTGCCATTCTGGGTACGACTCTTCTTTTGAAGCAGGTGGCAGAAAAA  
ATCCCACTGCAGCCAAAACATTTTCAAGGATTTTGAATCCAGTTATCATCAAAGAGACTGCCTTT  
GACATCCTTCAGTACTCAGAGCCTCAGTCAAGGTTCTGGGGCCGAGATAAGAACGTCCCCACA  
ATCGGTGTCATTGCCGTTGTCTTAGCCACACATCTGTGCGATGAAGTCAGTTTGGCGGGTTTT  
GGATATGACCTCAATCAACCCAGAACACCTTTGCACTACTTCGACAGTCAATGCATGGCTGCT  
ATGAACTTTCAGACCATGCATAATGTGACAACGGAAACCAAGTTCCTCTTAAAGCTGGTCAAA  
GAGGGAGTGGTGAAAGATCTCAGTGGAGGCATTGATCGTGAATTT**TGA**ACACAGAAAACCTCA  
GTTGAAAATGCAACTCTAACTCTGAGAGCTGTTTTTGGACAGCCTTCTTGATGTATTTCTCCAT  
CCTGCAGATACTTTGAAGTGCAGCTCATGTTTTTAACTTTTAAATTTAAAAACACAAAAAAAT  
TTTAGCTCTTCCCACTTTTTTTTTTCTATTTATTTGAGGTCAGTGTTTGTGTTTTGCACACCAT  
TTTGTAATGAACTTAAGAATTGAATTGGAAGACTTCTCAAAGAGAATTGTATGTAACGAT  
GTTGTATTGATTTTAAAGAAAGTAATTTAATTTGTAAACTTCTGCTCGTTTACACTGCACAT  
TGAATACAGGTAACTAATTGGAAGGAGAGGGGAGGTCACTCTTTTGATGGTGGCCCTGAACCT  
CATTCTGGTTCCTGCTGCGCTGCTTGGTGTGACCCACGGAGGATCCACTCCCAGGATGACGT  
GCTCCGTAGCTCTGCTGCTGATACTGGGTCTGCGATGCAGCGGCGTGAGGCCTGGGCTGGTTG  
GAGAAGGTCACAACCCTTCTCTGTTGGTCTGCCTTCTGCTGAAAGACTCGAGAACCAACCAGG  
GAAGCTGTCTGGAGGTCCCTGGTCCGAGAGGGACATAGAATCTGTGACCTCTGACAACTGTG  
AAGCCACCCTGGGCTACAGAAACCACAGTCTTCCCAGCAATTATTACAATTCTTGAATTCCTT  
GGGGATTTTTTACTGCCCTTTCAAAGCACTTAAGTGTTAGATCTAACGTGTTCCAGTGTCTGT  
CTGAGGTGACTTAAAAAATCAGAACAAACTTCTATTATCCAGAGTCATGGGAGAGTACACCC  
TTTCCAGGAATAATGTTTTGGGAAACACTGAAATGAAATCTTCCAGTATTATAAATTGTGTA  
TTTAA

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**FIGURE 508**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96897
><subunit 1 of 1, 362 aa, 1 stop
><MW: 41736, pI: 8.80, NX(S/T): 3
MRRPSLLLKDILKCTLLVFGVWILYILKLNVTTEECDMCKMHYVDPDHVKRAQKYAQOVL
QKECRPKFAKTSMAALLFEHRYSDLLPFVQKAPKDSEAESKYDPPFGFRKFSSKVQTLLE
LLPEHDLPEHLKAKTCRRCCVIGSGGILHGLELGHNTLNQFDVVIRLNSAPVEGYSEHVGN
KTTIRMTYPEGAPLSDLEYYSNDLFVAVLFKSVDFNWLQAMVKKETLPFWVRLFFWKQVA
EKIPLQPKHFRILNPVVIKETAFDILQYSEPQSRFWGRDKNVPTIGVIAVVLATHLCDEV
SLAGFGYDLNQPRTPPLHYFDSQCMAAMNFQTMHNVTTETKFLCLKLVKEGVVKDLSSGIDR
EF
```

**Important features of the protein:****Transmembrane domains:**

Amino acids 11-27;281-297

**N-glycosylation sites:**

Amino acids 30-34;180-184;334-338

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 2-6;109-113;223-227

**N-myristoylation sites:**

Amino acids 146-152;150-156;179-185;191-197

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**FIGURE 509**

GGGCGGACGCAGTGCAGTAAGAGCAGATGGGCGGACCCAAATTTCTTCGGCTTCACGATTTTG  
CCGAGGTCTAGCCCTGCATCCAGCCTTGAAACAGGGTGGGGAGGAGGCAGAAAGGGGAGGGAC  
TGCACTCCCTCTGAGCGTGCTAGCTCCGACTGCCTGACGGATCACCTTCCGCTCCAACATGG  
CTAGTTCTCTCAACGCCGTGACTCAAGCCTGTTGTGCCAGGCAGGGCGCACTCAGCAGCGCAGC  
CCCACAGGTGGCGAAGGCTCCGCGAGAGGGTTCCCGCCAGGCTAGACAGTGGAGTGCCGCACA  
GCGCGCCTTCCAGCCTCGCAGCCGCCACCTAGCGGTTCCGACCCGGCGCCAGCAGGCCTGCT  
TGGTCGATCTTCGAGCCAAAGATGCGGCGAGGCTGGAAGATGGCTCTGTCTGGGGGGCTGCGG  
TGCTGCCGCCGGGTACTGTCCTGGGTGCCAGTGCTCGTTATTGTCCTCGTCGTGCTCTGGTCC  
TACTATGCCTACGTCTTTGAACTCTGCCTGGTTATTTACCTCATACTCTACCATGCCATCTTT  
GTGTTCTTTACCTGGACCTACTGGAAGTCTATCTTTACACTCCCACAGCAGCCAAACCAGAAG  
TTCCACTTGTCTACACAGACAAGGAGCGCTATGAAAATGAAGAAAGACCTGAGGTCCAGAAG  
CAGATGCTTGTTGATATGGCCAAAAAGCTACCGGTTTACACAAGAAGTGAAGTGGAGGTCAG  
TTCATCCAAAGGCAGCTAGAGAGGCAGCTCAGCAAGTATCTCAGAAAGGCTAAGTCATATATG  
TTCTCAAACTAGCCCTTTTTTTTTCCTCCCATCTTCTGAAAACCACTATGGAGATTTTTCTCCA  
CATTTTATTTCTAAAAAATTTTAAACACATATCAAAGCTGGAAGAATTGTATAGTAAACAAAC  
TGTATACCCCAAACCTGGATTCTTCTGCTAACATTTTTCTGTGTTGCTATATCACATATCTATC  
CACATATGCATACCTCTATTTATCTTTCGTCAAGCCATCTTATGTTTCTGATGCATTTCAAAG  
TAAATAGCTGACATCAGTAAGACATCTACCTAAATATTTTATTCTGTTTTGTTAAATTTACA  
TACAAAAACATGCATAATCTTAAGGGTACCATTCCATGTATTTTGAAGTGTACACATCTGT  
GTAACATAACCCCAATAAAATTGCCATCACCTCAG

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**FIGURE 510**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA98564
><subunit 1 of 1, 143 aa, 1 stop
><MW: 17255, pI: 9.99, NX(S/T): 0
MRRGWKMALSGGLRCCRRVLSWVPVLVIVLVVLWSYYAYVFELCLVIYLILYHAIFVFFT
WTYWKSIFTLPQQPNQKFHLSYTDKERYENEERPEVQKQMLVDMAKKLPVYTRTGSGGQF
IQRQLERQLSKYLRKAASYMFSN
```

**Important features of the protein:****Transmembrane domain:**

Amino acids 24-45

**N-myristoylation sites:**

Amino acids 11-17;12-18

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**FIGURE 511**

CAGCCGGGGCG**ATG**GCGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCG  
CGGCGAGTGCCCTTTCCCTGGCCGGCGCCAGTCTGGTCCTGAGCCTGCTGCAGAGGGTGCGCA  
GCTACGCGCGGAAATGGCAGCAGATGCGGCCCATCCCCACGGTGGCCCGCGCCTACCCACTGGTG  
GGCCACGCGCTGCTGATGAAGCCGGACGGGCGAGGTAAGGGCCGGCGCTCCTCCTGGAGCGCA  
ACGGGGTCCGCAGCCCCGTTCCCAACCCTCCGATCAGCCAGGAACCCGCTGCTTGTGGCGCTGG  
CCGCAGGAGAGAGGAGCCTGTACCCCTGTGGAGAATGCACTCCCAGTTCTAGTCGTTGCCCT  
TGGCACCCGCGACACTGCTAGTGCCCATCCCAAAGTGAGCATTTTCTTTGTGTGTAGCACA  
GGATGCGGTATTTCCAAACCCCTGCCCTCGGTCTTTTCCACCTCACCGCTGCTCAGCTCTCA  
AAGCCCTGCCGTTTCTCCTGCCTTGGCTTGGGAAGCCT**TAG**GAACAGAAGCTCCCTGGGAGC  
ACAGAGCGGTTTTAAACTGGCCAACACCTTAACGCCAGAGCCGCCCTCCTCTCGCTGCCACT  
TTGGAATAAGAGACTAGAGATTCAGTGGACGCTTCCTCCCGGCATCACAAGACTTGACTGC  
TGCTTCAGTTCCTCGCTTGACCTTCATACTTTAGCCCTTTAAAGGATGTTACATAATAACAATT  
AAGAGACGGCAGGGCCTTCAGGCAGACTTCTTTGGAGGGTGTCAAACGCCTGTTTTATTAAAG  
AGTGAATTTTTTAATTAAAATCATGTTTTAAACAGAGATGGACATTTTATTGATGGAAAAA  
ATCACGTTAAGTTAGAAAGCTCTCAAAAGTACCTGGTATTTACAACCTCCCTGTCAGGGAGGGC  
GAACTCGATCTCAGAGTTTTATTTTCATCAGGGATTACGTTGAGGTACCCAGAAATGAGAAGA  
TTTGCCCAAAATGGCATATTTTAAATTGGCCCAGACCAGAACCCAGTTTCTCTGGGATTAT  
TTGTTAGTAATCGTTTTACAGGCTGAGCATTAACCTCAAAAGCTTGAAGACTTTTTTCTC  
ATTTTCACTTGTTTTCTCTAATAAAAAATAATGCTGTAATTTCAACTTCACAAGATGAGGCCTC  
ATGGAAGAGTGTTTACCAAAATATTAAAAATACTTTGACAGAAAAAATCAAGCGAACTCTTT  
GCCAACCAAATATCATCATGACTGATGTAACAAGTAATCCAACACAGATATGAAAATCACTGG  
TAAAAATCATCTCAGTTAATTCTAAAAGCAGAGCTAACCACCCCTTTTGTCTTAAGGCTTTAT  
GGTATTAAAAAATAAACTGTACAAAAATATAGATTTTCCCCTATCCCCTACCCCTGGAAAGTA  
ATATACTGAAGTCTCATCATACTGTTTTGGGGATTCCAGTAATTAAAATCTCTAGTGAACAAA  
GACCTGTTTTCAAAACAACCTGTGAGCTGACTGGACTATTTAAAGTAATTCTCCTTGTAGTCAC  
TTTCAGAGTGAAGACAATGACGAATACTGTCTTTTACAAAGGGACTTTTTATTCCACCAACAA  
ATTCTGGATTTTGGCATCAGGAAAACCACTGTTCAATTTCACACTATATCCAAGTTGTTTG  
AGAAATTATTTAAAACCTCTTAACTTAGAGGGTTTTCTTCTCCTTACTTGTTAAAGTGACT  
ATATTACAGAGTCACTTTAAGGATTAAATTTATTGCATGCAAAGTTTCTAGATCACTGTCTAG  
AAGTCAGTTAGAGTAAGTTCTTTAGTTGTCAATCAAGCATTTAGTAAGGCCCTGCTTTGTGCC  
CAGTGTTGACCTCAACAAAGTTGGGGATATCAGAATATTCTAAGATACAGTCGTTGTTCCCAA  
GAATCTTGCTTTTACATACAAGAGGTGTTGCGTTTCATTTTGCGGCTAATGTCCAAACGCTG  
GCCTCAGCCATTTACCTTGAAGATTGCAGTTGGCTTCCAACCTGGCCTCTAAACTCTAATCTA  
GCATTTTCCAGTCCATTGTGACAAAGTCTGCCCTCCCCAGCTACTCCCAGCTGTTGGACCTGC  
TGCCTTAGAACCACAGATTGGTACCTCGTGCC

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**FIGURE 512**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA107443
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19353, pI: 10.97, NX(S/T): 0
MAGLWLGLVWQKLLWGAASALSLAGASLVLSLLQRVASYARKWQQMRPIPTVARAYPLV
GHALLMKPDGRGKGRSSWSATGSAAPFPPSDQPGTRCLWRWPQERGACHPVENALPVLV
VAPWHPPTLLVPHPKVSIFFVCSTGCGISKPLPSVFSHLTAAQLSKPCRFLLPWLGKP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-25

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 75-79

**N-myristoylation sites:**

Amino acids 3-9;17-23;145-151

**Amidation site:**

Amino acids 73-77

**Leucine zipper pattern:**

Amino acids 8-30

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**FIGURE 513**

GGCGGCTGGACGAGGACGCTCAGAGCCCAGCTCTCGAGAGTTCAAGCAACCGACGGTTCC  
CCACTGCTCCCAGGAGCGGTTACCTGGGCACTCTGTGCCCCCTCCTTCCTGTTTCGGGCCCCA  
GGCCGAGGACCTGCCAGTAGGGCTCAGTTGCCTGGAGCCCGTTCAGCCCATCCCCAGTT  
CACTTTGCTTGTGGGATCTCCCCGTTGCTCCTGCCCGTGGACTGAGTGGCAGGCCATCCT  
ACAAGCACCCGGACACTTGACATCAGTGGTGTCAAGACAACCTCTAAGAAGGTTTTCCGTG  
ATCCTGCAAGCCCTGCCTTCCTTCCTGGGATCCTGCCTTCAATTTGATTGCACAGGTACC  
ACAGCAAGCCAGTGCTGTGTGCTCCGAGTTCCAGGGCGTCCCTCCAGCTCAGCCACTGCAC  
TGAGAACATGGACTCTCTGTGGGGCCAGGAGCCGGGAGTCACCCCTTTGGGGTCCACAA  
CACCCGGCTGTCCCCAGACTTGTGTCCAGGGAAGATAGTGTTGAGGGCCCTCAAGGAGAG  
CGGGGCAGGGATGCCTGAGCAGGACAAGGACCCTAGAGTCCAAGAGAATCCTGGTGATCA  
GAGAAGGGTCCCCGAGGTACCCGGGGATGCACGGTCTGCATTTCCGCCCCCTGCGGGACAA  
TGGAGGCCTCTCTCCCTTTGTGCCCCGGGCCCGGGCCTCTGCAGACAGACCTCCATGCCCA  
GAGGTGAGAAATCAGATATAACCAGACATCCCAGACCTCCTGGACGAGCTCCTGCACCAA  
CCGAAATGCCATCTCCAGCTCCTACAGCTCCACGGGAGGCTTGCTGGGGCTAAAGCGGAG  
GAGGGGGCCAGCCTCATCCCACTGCCAGCTGACCCTCAGTTCCCTCAAAGACAGTGAGTGA  
GGACAGGCCTCAGGCTGTCTCTTCAGGTACACCCAGTGTGAAAAGGCAGCAGATATAGC  
ACCAGGGCAGACACTCACCTCAGGAATGACTCCTCCACATCCGAGGCCTCTAGGCCCAG  
TACACACAAGTTTCCCCTGCTGCCACGCAGGCGAGGGGAGCCTTTGATGCTGCCACCTCC  
CTTAGAGCTGGGGTACCGGGTCACTGTTGAAGACCTGGACCGGGAGAAGGAGGCGGCCTT  
CCAGCGCATCAACAGTGCAGTGCAGGTTGAGGACAAGGCCATCTCGGACTGCAGACCCTC  
ACGGCCTTCCCACACTTTGTCTCACTTGCAACAGGGGCTTCTGGTCTGCCTGCCGTTTC  
TAAAGCACCCAGTATGGATGCACAGCAGGAGACACACAAGTCCCAAGACTGCCTGGGCCT  
ACTGGACCCCTTAGCATCTGCTGCAGGGGTCCCCTCTACAGCTCCCATGTCTGGGAAGAA  
GCACAGACCACCAGGCCCCCTGTTCTCCTCCTCAGATCCCCCTTCCCTGCCACCTCTTCTGA  
TTCCCAGGACTCAGCCCAGGTACCTCGCTGATTCTGCCCCCTTCCCAGCTGCAAGCAT  
GGATGCGGGCATGAGAAGAACAAGGCATGGCACTTCTGCTCCTGCAGCTGCCGCAGCAGC  
CCCTCCCCGCTCCACATTGAACCCACGTTGGGGTCACTACTGGAGTGGATGGAGGCCCT  
TCACATTTCTGGGCCTCAGCCACAGCTGCAGCAGGTGCCAGAGGTGAGAACCAGAGATC  
CCAGACCTCCTGGACCAGCTCGTGCCCCAAATGAATGCCATCTCGAGCCCCCTACAGCTC  
TACGGGAGGCCTCCCGGAACAAAAGCGGAAGAGGGGCCAGCCTCATCCCACTGCCAGCTG  
ACCCTCAGTTCCCTCAAACACAGTGAGTGAGGACGGACCTCAGGCTGTCTCTTCGGGTAC  
ACCCAGTGTGAAAAGACGGCAGATACAGCACCAGGGCAGACACTCGCCTCCAGGGGTGGC  
TCCCCAGATCCCAGGCCTCTAGGCCCCGTATATGCAAGTTTCCCCTGCTGCCACGCAGG  
CGAGGGGAGCCTTTGATGCTGCCACCTCCCTTAGAGATGGGGTACCGGGTCACTGCTGAA  
GACCTGGACCGGGAGAAGGAGGAGGCATTCCAGCGCATCAACAGTGCAGTGCAGGTTGAG  
GACCAGGCCATCTAGGACTGCAGACCCTCACGGCCTTCCCACACTTTGTCTCACTTGCA  
ACAGGGGCTTCTGGTCTGCCTGCCGTTTCTAAAGCACCCAGTATGGATGCACAGCAGGAG  
ACACACAAGTCCCAAGACTGCCTGGGCCTAGTGGCCCCCTGCATCTGCTGCACAGGCCT  
GTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAACGGCATAAACCCGGGAGGCAGAGC  
TTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGT  
CTC



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**FIGURE 514**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA107786
><subunit 1 of 1, 428 aa, 1 stop
><MW: 45450, pI: 9.28, NX(S/T): 3
MDSLWGPAGAGSHPFVHNTRLSPDLCPGKIVLRALKESGAGMPEQDKDPRVQENPGDQRR
VPEVTGDARSAFRPLRDNGGLSPFVPGPGPLQTDLHAQRSEIRYNQTSQTSWTSSCTNRN
AISSYSSTGGLLGLKRRRGPASSHCQLTLSSSKTVSEDRPQAVSSGHTQCEKAADIAPG
QTLTLRNDSSSTSEASRPSTHKFPLLPRRRGEPLMLPPPPELGYRVTVEDLDREKEAAFQR
INSALQVEDKAISDCRPSRPSHTLSSLATGASGLPAVSKAPSMDAQQETHKSQDCLGLLD
PLASAAGVPSTAPMSGKKHRPPGPLFSSSDPLPATSSDSQDSAQVTSLIPAPFPAASMDA
GMRRTRHGTSAPAAAAAAPPRSTLNPTLGSLLEWMEALHISGPQPQLQQVPRGQNQRSQT
SWTSSCPK
```

**Important features of the protein:****N-glycosylation sites:**

Amino acids 105-109;187-191

**Glycosaminoglycan attachment site:**

Amino acids 38-42

**N-myristoylation sites:**

Amino acids 15-21;130-136;180-186;307-313;361-367

**Amidation site:**

Amino acids 315-319

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 106-117

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**FIGURE 515**

GTCAGGGCCAGGGTGAGCGCCCCGACTCCGAGCTGTCCCCGCTCCCGGCGCGGCGCTCCGCTCT  
CAGCCACCTCACGGCTGCCAGGAGTGCGCGGGAGTTTGCCCCGGAGCGCGGGGAAGTTTCCTC  
CGAAGCTGCGCTCCTGGAACAGCAGCACCTGCAAGCGCCCCGGCAGCGGCCCGCGAGGTTACTT  
TATGGAATTGGGCTCTTAGAGAAACAAGAAAAGACTGAAGTTTACGGGAAAACAAATCATGTG  
GTCTTCAGATTCTGAAATAAGGAGAAATGCAGCCATCTGAAATGGTCATGAACCCCAACAAG  
TCTTCCTCTCTGTGCTGATATTTGGAGTAGCTGGGCTACTCCTCTTCATGTATTTGCAAGTCTGG  
ATTGAAGAACAACATACAGGGAGAGTGGAGAAGAGAAGAGAACAAAAAGTAACTTCAGGATGG  
GGACCAGTGAAGTACTTGCGGCCTGTACCCAGAATCATGAGTACAGAAAAAATCCAGGAACAT  
ATCACCACCAGAACCCCAAGTTTTCACATGCCTGAGGATGTACGAGAAAAAAGGAAAAATCTT  
CTACTCAATTCTGAGAGATCTACTAGGCTCTTAACAAAGACCAGTCATTACAAAGGAGGGGAT  
CAAGCTTTAAGTAAGTCCACAGGGTCACCAACAGAGAAGTTGATTGAAAAACGTCAAGGAGCT  
AAGACTGTTTTTAACAAGTTCAGCAACATGAATTGGCCAGTGGACATTCACCTTTAAACAAA  
AGTTTAGTCAAAGATAATAAATGGAAGAAAAGTGGAGAGACCCAAGAGAAACGAAGGTCTTTC  
CTTCAGGAGTTTTGCAAGAAATACGGTGGGGTGAGTCATCATCAGTCACATCTTTTTTCATACA  
GTATCCAGAACTATGTAGAAGATAAACACAAAATCTTATATTGTGAGGTACCTAAGGCTGGC  
TGTTCCAATTGGAAAAGAAATCTGATGGTACTAAATGGATTGGCTTCCTCTGCATACAACATC  
TCCCACAATGCTGTCCACTACGGGAAGCATTGGAAGAAGCTAGATAGCTTTGACCTAAAAGGG  
ATATATACCCGCTTAAATACTTACACCAAAGCTGTGTTTGTTCGTGATCCCATGGAAAGATTA  
GTATCAGCCTTTAGGGACAAATTTGAACACCCCAATAGTTATTACCATCCAGTATTCGGAAAG  
GCAATTATCAAGAAATATCGACCAAATGCCTGTGAAGAAGCATTAAATTAATGGATCTGGAGTC  
AAGTTCAAAGAGTTTATCCACTACTTGCTGGATTCCCACCGTCCAGTAGGAATGGACATTCAC  
TGGGAAAAGGTCAGCAAACCTCTGCTATCCGTGTTTGATCAACTATGATTTTGTAGGGAAATTT  
GAGACTTTGGAAGAAGATGCCAATTACTTTTTACAGATGATCGGTGCTCCAAAGGAGCTGAAA  
TTTCCCACTTTAAGGATAGGCACTCTCCGATGAAAGAACCAATGCTCAAGTCGTGAGACAG  
TATTTAAAGGATCTGACTAGAACTGAGAGACAATTAATCTATGACTTTTATTACTTGGACTAT  
TTAATGTTTAATTATACAACCTCCACTTTTGTAGTTTGCATTCAATTTCTAAAACCTGTATAT  
ACTTAATGATGATAAGTTCAAATCAGCTGTAATTTTTCTATAATTCTCTGTATGACAGAAATT  
TAACCAAGTGCAGTTGTCTTGATTTAATGTAGATTTTTTACCAAATAGTATGACACCAATTGGC  
ACAAAGTTATAGGAAAATCACCTACAGGAGATGTAAACAACCTGAGTTGCTCTAAAATGTTTG  
GAAAAGAGCTGCTTTTGCATTATGAATTATATTGTTGAAGCAATAACCTAGCCAGCTGTTGCA  
TTAGCTAAAGCAGCCTCTTGCAATGGTAGGAAAAAAGGATCTCAAATAGCATGAGTGTATGTC  
TATATCCTGAAATTTATTGTCTAAAATGCATGAATATATTTTGTAGCAGTCTGTGGCATATTAA  
TCAAACCTGTTGAATTGTTTTCTTACACCCTGGAAATCTTCTATCAACTATAATGATAAATCC  
ATTTTGAAGTGATATTTTGGACTTAGGCATTTTACTTTAGATTGGAAGGCATTATGTGATTTACA  
ATATGAGAATATAGCAGAAAAACCA

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**FIGURE 516**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108682
><subunit 1 of 1, 443 aa, 1 stop
><MW: 52021, pI: 9.63, NX(S/T): 4
MQPSEMVMNPKQVFLSVLIFGVAGLLLFMYLQVWIEEQHTGRVEKRREQKVTSGWGPVKY
LRPVPRIMSTEKIQEHITNQNPKEFMPEDVREKKENLLLNSESTRLLTKTSHSQGGDQA
LSKSTGSPTEKLEKROGAKTVFNKFSNMNWPVDIHPLNKSIVKDNKWKKTETQEKRRS
FLQEFCKKYGGVSHHQSHLFHTVSRIYVEDKHKILYCEVPKAGCSNWKRIIMVLNGLASS
AYNISHNAVHYGKHLKKLDSFDLKGITYRLNTYTKAVFVRDPMERLVSAFRDKFEHPNSY
YHPVFGKAIKKYRPNACEEALINGSGVKFKEFIHYLLDSHRPVGMDIHWEKVSCLCPC
LINYDFVGKFETLEEDANYFLQMIGAPKELKFPNFKDRHSSDERTNAQVVRQYLKDLTRT
ERQLIYDFYLDYLMFNYYTPLL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-24

**N-glycosylation sites:**

Amino acids 159-163;243-247;324-328;437-441

**Glycosaminoglycan attachment site:**

Amino acids 53-57

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 177-181

**Tyrosine kinase phosphorylation site:**

Amino acids 329-337

**N-myristoylation sites:**

Amino acids 116-122;236-242

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**FIGURE 517**

GGAACCTCCAGGCACCCCTGTGTGGCCGCACTGCTCCCTCTGGCCCAACCATGCTCTGTCCAGCCACCTGCTGC  
CCGCTTGGTCTGTCTCTGGCAGGGTCTCAGGCTGGGCTGGGTCCTCCCAACCACTGCAGGAGCCCTGGCCAGG  
CCGTGTGCAACTTCGTGTGTGACTGCAGGGACTGCTCAGATGAGGCCAGTGTGGTTACACGGGGCCCTCGCCCA  
CCCTGGGCGCCCCCTTCGCCTGTGACTTCGAGCAGGACCCCTGCGGCTGGCGGGACATTAGTACCTCAGGCTACA  
GCTGGCTCCGAGACAGGGCAGGGGCGCACTGGAGGGTCTGGGCTCACTCAGACCACACACTGGGCACCGACT  
TGGGCTGGTACATGGCCGTGGAACCCACCGAGGGAAGAGGGCATCCACCGCAGCCCTGCGCTCGCCAACCCCTGC  
GAGAGGCAGCCTCCTCTTGCAAGCTGAGGCTCTGGTACCACGCGGCTCTGGAGATGTGGCTGAACTGCGGGTGG  
AGCTGACCCATGGCGCAGAGACCCCTGACCCCTGTGGCAGAGCACAGGGCCCTGGGGCCCTGGCTGGCAGGAGTTGG  
CAGTGACCACAGGCCGCATCCGGGGTGAATTCCGAGTGACCTTCTGTGCCACCCGAAATGCCACCCACAGGGGCG  
CTGTGGCTCTAGATGACCTAGAGTTCTGGGACTGTGGTCTGCCACCCCCCAGGCCAACTGTCCCCGGGACACC  
ACCACTGCCAGAACAAGGTCTGCGTGGAGCCCCAGCAGCTGTGCGACGGGGAAGACAACCTGCGGGGACCTGTCTG  
ATGAGAACCACTCACCTGTGGCCGCCACATAGCCACCGACTTTGAGACAGGCCTGGGCCCATGGAACCGCTCGG  
AAGGCTGGTCCCGGAACCAACCGTGTGGTGGTCTGAGCGCCCTCCTGGCCACGCCGTGACCACAGCCGGAACA  
GTGCACAGGGCTCCTTCTGGTCTCCGTGGCCGAGCCTGGCACCCCTGCTATACTCTCAGCCCCGAATTCCAAG  
CCTCAGGCACCTCCAACCTGCTCGCTGGTCTTCTATCAGTACCTGAGTGGGTCTGAGGCTGCTCCAGCTGCTGT  
TCCTGCAGACTCTGGGGCCCGGGCGCCCCCGGGCCCCCGTCTGCTGCGGAGGCGCCGAGGGGAGCTGGGGACCG  
CCTGGGTCCGAGACCGTGTGACATCCAGAGCGCCTACCCCTTCCAGATCCTCCTGGCCGGCAGACAGGCCCGG  
GGGCGTCTGGGTCTGGACGACCTCATCCTGTCTGACCACTGCAGACCAGTCTCGGAGGTGTCCACCCTGCAGC  
CGCTGCCTCCTGGGCCCCCGGGCCCCAGCCCCCAGCCCTGCGGCCAGCTCGCGGCTCCAGGATTCTGCAAGC  
AGGGGCATCTTGCTGCGGGGACCTGTGTGTGCCCCGGAACAACCTGTGTGACTTCGAGGAGCAGTGCCGAGGGG  
GCGAGGACGAGCAGGCCTGTGGCACCACAGACTTTGAGTCCCCGAGGCTGGGGCTGGGAGGACGCCAGCGTGG  
GGCGGCTGCAGTGGCGGCGTGTCTCAGCCCAGGAGAGCCAGGGGTCCAGTGCAGCTGCTGCTGGGCACTTCCTGT  
CTCTGCAGCGGCTGGGGGAGCTAGGCGCTGAGGCCCCGGTCTCACACCCCTCCTTGGCCCTTCTGGCCCCA  
GCTGTGAACTCCACCTGGCTTATTATTTACAGAGCCAGCCCCGAGAGGTCTCCTGTAACCTTTGAGCGGGACACAT  
GCAGCTGGTACCCAGGCCACCTCTCAGACACACACTGGCGCTGGGTGGAGAGCCGCGGCCCTGACCCACGACCACA  
CCACAGGCCAAGGCCACTTTGTGCTCCTGGACCCACAGACCCCTGGCCTGGGGCCACAGTGCCACCTGCTCT  
CCAGGCCCCAGGTGCCAGCAGCACCACGGAGTGTCTCAGCTTCTGGTACCACCTCCATGGGCCCCAGATTGGGA  
CTCTGCGCCTAGCCATGAGACGGGAAGGGGAGGAGACACCTGTGGTGCAGGTCAGGCACCCAGGGCAACCGCT  
GGCAGGAGCCTGGGCCACCTTTCCACAGCCTGGCTCCCATGCCAGTACCAGCTGCTGTTGAGGGCCCTCC  
GGGACGGATACACGGCACCATGGCGCTGGACGATGTGGCGCTGGGTGGAGAGCCGCGGCCCTGCTGGGCCCTAATTACT  
GCTCCTTTGAGGACTCAGACTGCGGCTTCTCCCCTGGAGGCCAAGGTCTCTGGAGGCGGCGGCCAATGCTCGG  
GCCATGCTGCCTGGGGCCCCCAACAGACCATAACCTGAGACAGCCCAAGGGCACTACATGGTGGTGGACAAA  
GCCCAGACGCACTACCCCGGGGCCAGACGGCCTCCCTGACCTCCAAGGAGCACAGGCCCTGGGCCAGCTGCTT  
GTCTGACCTTCTGGTACCACGGGAGCCTCCGACGCCAGGCACCCCTGCGGGTCTACCTGGAGGAGCGCGGGAGGC  
ACCAGGTGCTCAGCCTCAGTGCCACGGCGGGCTTGCCTGGCGCCTGGGCAGCATGGACGTGCAGGCCGAGCGAG  
CCTGGAGGGTGGTGTGAGGAGTGGCGCAGGCGTGGCACACTCCTACGTGGCTCTGGATGATCTGCTCCTCC  
AGGACGGGCCCCTGCCCTCAGCCAGGTTCTGTGATTTTGAAGTCTGGCCTGTGTGGCTGGAGCCACCTGGCCGGG  
CCGGCCTGGGCGGATACAGCTGGGACTGGGGCGGGGAGCCACCCCTCTCGTTACCCCCAGCCCCCTGTGGACC  
ACACCCTGGGCACAGAGGCAGGCCACTTTGCTTCTTTGAAACTGGCGTCTGGGCCCCGGGGCGCGGCCCT  
GGCTGCGCAGCGAGCCTCTGCCGGCCACCCAGCCTCCTGCCCTCCGCTTCTGGTACCACATGGGTTTCTGTAGC  
ACTTCTACAAGGGGAGCTGAAGGTACTGCTGCACAGTGTGAGGCCAGCTGGCTGTGTGGGCGCAGGCGGGC  
ATCGGGGACACAGTGGCTGGAGGCCAGGTGGAGGTAGCCAGTGCCAAGGAGTTCCAGATCGTGTGTTGAAGCCA  
CTCTGGGCGGCCAGCCAGCCTGGGGCCATTGCCCTGGATGACGTGGAGTATCTGGCTGGGCAGCATTGCCAGC  
AGCCTGCCCCAGCCCCGGGAACACAGCCGCACCCGGGTCTGTGCCAGCTGTGGTTGGCAGTGCCTCCTATTGC  
TCATGCTCCTGGTGTGCTGGGACTTGGGGACGGCGTGGCTGCAGAAGAAGGGGAGCTGCCCTTCCAGAGCA  
ACACAGAGGCCACAGCCCCCTGGCTTTGACAACATCCTTTTCAATGCGGATGGTGTACCCCTCCCGGCATCTGTCA  
CCAGTGATCCGTAGACCACCCAGACAAGGCCCGCTTCTCAGCTGACATCCAGCACTTGGTCAGACCCTAGCC  
AGGGACCGACACCTGCCCCGCCAGGCTGGGACAGGCTGCAGGTCTCAGGATATGCTGAGGCTGGGCGTTCCC  
TGCCCTGTGCTGACTCTGTTGCTCTGTGAATAAACACCCCTGGCCCATGAGGGCCGCCCCAAAAA

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**FIGURE 518**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108684
><subunit 1 of 1, 1137 aa, 1 stop
><MW: 122776, pI: 6.00, NX(S/T): 4
MPLSSHLLPALVLFFLAGSSGWAVPNHCRSPGQAVCNFVCDRCDCSDEAQCQYHGASPTL
GAPFACDFEQDPCGWRDISTSGYSWLRDRAGAALEGPGPHSDHTLGTDLGWYMAVGTHRG
KEASTAALRSPTLREAASSCKLRWLWYHAASGDVAELRVELTHGAETLTWQSTGPGWPGW
QELAVTTGRIRGDFRVTF SATRNATHRGAVALLDLEFWDCGLPTPQANCPPGHHHCQNKV
CVEPQQLCDGEDNCGDLSDENPLTCGRHIATDFETGLGPWNRSEGWSRNRHAGGPERPSW
PRRDHSRNSAQGSFLVSVAEPGTPAILSSPEFQASGTSNCSLVFYQYLSGSEAGCLQLFL
QTLGPGAPRAPVLLRRRRRGELGTAWVRDRVDIQSAYPFQILLAGQTGPGGVVGLDDLILS
DHCRPVSEVSTLQPLPPGPAPAPQPLPPSSRLQDSCKQGHLCAGDLCVPPEQLCDFEEQ
CAGGEDEQACGTTDFESPEAGGWEDASVGRQLQWRRVSAQESQGSAAAAGHFLSLQRAWG
QLGAEARVLTPLLGPSPGSCELHLAYYLQSQPREVSCNFERDTCWYPGHLSDTHWRWVE
SRGPDHDHTTGQGHFVLLDPTDPLAWGHSALHLSRPQVPAAPTECLSFWYHLHGPGQIGTL
RLAMRREGTEETHLWSRSGTQGNRWHEAWATLSHQPGSHAQYQLLFEGLRDGYHGTMALDD
VAVRPGPCWAPNYCSFEDSDCGFSPGGQGLWRRQANASGHAAGWPPTDHTTETAQGHYMV
VDTSPDALPRGQTASLTSKEHRPLAQFACLTFWYHGSLSRSPGTLRVYLEERGRHQVLSLS
AHGGLAWRLGSMQVQAERAWRVVFEAVAAGVAHSYVALDDLLQDGPQPGSCDFESGL
CGWSHLAGPGLGGYSWDWGGGATPSRYPQPPVDHTLGTGTEAGHFAFFETGVLGPGGRAAWL
RSEPLPATPASCLRFWYHMGFPEHFYKGEKLVLLHSAQQQLAVWGAGGHRHQRHLEAQVE
VASAKEFQIVFEATLGGQPALGPALDDVEYLAGQHCQQPAPSPGNTAAPGSVPAVVGSA
LLLLMLLVLLGLGGRRLQKKGSCFFQSNTEATAPGFDNILEFNADGVTLPASVTSDF

```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**Transmembrane domain:**

Amino acids 1075-1092

**N-glycosylation sites:**

Amino acids 203-207;281-285;339-343;756-760

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 514-518;1100-1104

**N-myristoylation sites:**

Amino acids 32-38;55-61;61-67;106-112;116-122;336-342;350-356;409-415;  
 523-529;540-546;678-684;707-713;791-797;870-876;921-927;  
 937-943;954-960;1036-1042;1071-1077

**Amidation site:**

Amino acids 1093-1097

**Cell attachment sequence:**

Amino acids 191-194

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**FIGURE 519**

GCAGGGGAGCTCCGAGTGTCCACAGGAAGGGAACCTATCAGCTCCTGGCATCTGTAAGGATGCT  
GTCCATGCTGAGGACAATGACCAGACTCTGCTTCCTGTTATTCTTCTCTGTGGCCACCAGTGG  
GTGCAGTGCAGCAGCAGCCTCTTCTCTTGAGATGCTCTCGAGGGAATTGAAACCTGTGCCTT  
CTCCTTTTCTTCCCTGCCTAGAAGCTGCAAAGAAATCAAGGAACGCTGCCATAGTGCAGGTGA  
TGGCCTGTATTTCTCCGCACCAAGAATGGTGTGTCTACCAGACCTTCTGTGACATGACTTC  
TGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCACGAGAATGACATGCGTGGGAAGTGCAC  
GGTGGGTGATCGCTGGTCCAGTCAGCAGGGCAACAAAGCAGACTACCCAGAGGGGGATGGCAA  
CTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCC  
TGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCATGTGCCCCAACAAGTCCCCCAT  
GCAGCATTTGGAGAAACAGCGCCCTGCTGAGGTACCGCACCAACACTGGCTTCTCCAGAGACT  
GGGACATAATCTGTTTGGCATCTACCAGAAATACCCAGTGAAATACAGATCAGGGAAATGTTG  
GAATGACAATGGCCCAGCCATACCTGTGGTCTATGACTTTGGTGATGCTAAGAAGACTGCATC  
TTATTACTCACCGTATGGTCAACGGGAATTTGTTGCAGGATTCGTTCAAGTTCCGGGTGTTTAA  
TAACGAGAGAGCAGCCAACGCCCTTTGTGCTGGGATAAAAGTTACTGGCTGTAACTGAGCA  
TCACTGCATCGGTGGAGGAGGGTTCTTCCACAGGGCAAACCCCGTCAGTGTGGGGACTTCTC  
CGCCTTTGACTGGGATGGATATGGAACCTCACGTTAAGAGCAGCTGCAGTCGGGAGATAACGGA  
GGCGGCTGTACTCTTGTTCTATAGATGAGACAGAGCTCTGCGGTGTCAGGGCGAGAACCCATC  
TTCCAACCCCGGCTATTTGGAGACGGAAAACTGGAATTCTAACAAGGAGGAGAGGAGACTAA  
ATCACATCAATTTGCA

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**FIGURE 520**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108701
><subunit 1 of 1, 325 aa, 1 stop
><MW: 36212, pI: 8.68, NX(S/T): 1
MLSMLRTMTRLCLLFFSVATSGCSAAAASSLEMLSREFETCAFSFSSLPRSCKEIKERC
HSAGDGLYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGNKA
DYPEGDGNWANYNFTGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSALLR
YRTNTGFLQRLGHNLFGLIYQKYPVKYRSGKCWNDNGPAIPVVYDFGDAKKTASYYSYGQ
REFVAGFVQFRVFNNERAAANALCAGIKVTGCNTEHHCIGGGGFFPQGKPRQCGDFSADFWD
DGYGTHVKSSCSREITEAAVLLFYR
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-26

**Glycosaminoglycan attachment site:**

Amino acids 86-90

**N-myristoylation sites:**

Amino acids 23-29;88-94;127-133;136-142;265-271

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**FIGURE 521**

GATCAGTGTGTGAGGGAAGTCCCATCATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCT  
GTGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAGGTCA  
TTCTAGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTCACTCAAAGCCTTCGTTAATTGACTACA  
GGAAGCCTTCTGCATTGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAAGAAAATGAAATATTTGTTG  
ACCTAGCTCTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAATGATTTTTTTGTTGAAA  
TAAGAGGAACTTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAAACCA  
ACTACGATGTAATGCTTATAGACCCCTGTGATTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTG  
TGCTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAAACTTCCAGCTCCACTTTCTCTATG  
TACCTGTGCCATGACAGGACTAACAGACAGAATGACCTTTCTGGAAAGAGTAAAAATTCATGCTTTTCAGTTT  
TGTTCCACTTCTGGATTACGACTATCATTTTTGGGAAGAGTTTTATAGTAAGGCATTAGGAAGGCCCA  
CTACATTATGTGAGACTGTGGGAAAGCTGAGATATGGCTAATACGAACATATTGGGATTTTGAATTTCTCAAC  
CATACCAACCTAACTTTGAGTTTGTGGAGGATTGCATGTAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAA  
ATTTTGTCCAGATTACAGGGAAGATGGTATTGTGGTGTCTCTGGGGTCACTGTTTCAAAATGTTACAGAAG  
AAAAGGCTAATATCATTGCTTCAGCCCTTGCCAGATCCCACAGAAGGTGTTATGGAGGTACAAAGGAAAAAAC  
CATCCACATTAGGAGCCAATACTCGGCTGTATGATTGGATACCCAGAAATGATCTTCTGGTATCCCAAAACCA  
AAGCTTTTACTCATGTTGGAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTC  
CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAA  
CTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCTCTTATAAAGAGAATGCTATGA  
GATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTCTATGC  
GCCACAAAGGAGCCAAGCACCTGCGATCAGCTGCCATGACCTCACCTGGTTCAGCAGTACTCTATAGATGTGA  
TTGGGTTCTGCTGACCTGTGTGGCAACTGCTATATCTTGTTCACAAAATGTTTTTATTTTCTGTCAAAAAT  
TTAATAAACTAGAAAGATAGAAAAGAGGGAATAGATCTTTCCAAATTCAAGAAAGACCTGATGGGGTAATCCTG  
TTAATTCAGCCACATAGAATTTGGTGAAACCTTGCTATTTTCATATTATCTATTCTGTTATTTTATCTTAGCT  
ATATAGCCTAGAATTCATGATCATGAGGTTGTGAGTATATCTCATTTCTTCGTTGTATTTTCTAGGTGTCTTT  
ACTCTCTTCTCTCACTTTGTGACACAAGGACATGAATACATCTAAATTTTCTATTTCTGATATGACTGTTTTGA  
TGATGTCATTACTTCTATAACCTTAAGTGATAGGGTGACATGCAATATGATTATTCCTGGTGTGCGCCCAACAC  
ATGGATATAAAGAGGTAAAAACTTAAATTCACAAAATTCAGTAAACCACACAAATCAGGTAAGTGTCTATGA  
GATTAGCTGGCTATGAGAAACATAATGATGTTTCTTTTCAATTTAAATAAGCCTTTCTACATAGCCAGCATCAG  
TGATCTCAGAAAATAAATTGCTAATAATGATGACATGGCATTATGCTTAGAAAAGTTTGCTGTATTTCCATAGAC  
CTCATCTAGATGTCATGGCTACATTTCTGCCATCACTCAACCAATACTTTTTTCTGTTTTCTTGATGATAAAAA  
GACCTTTCTCATGATTGCCATCAAATAACAAAAGAACTATTTTTTTCTCACATAGAGAACATGTCAGTAAGAT  
ATTCAAGGTGAACAGATATTTTGGGATTAGTAATTTTGAATATGTGGTGATAATTACTGAGTTTATAAAAT  
TTATTTGATAGTACCTTAAAGAAGATTTATATGTTTATTCTTTAAAAATGATGAATACTCATAATTCTTATCTC  
TATAATCAAAAGTATAATTTACTGTAGAAAAATAAAGAGATGCTTGTCTGAAAGTAAGATCAGTGAAGTCTTT  
TCAGTCTCAATCTTTGAGAATTGTAAATTCATCAAATAATTGCTTACATAGTAAAAATTTAAGGTATTAGAAAAC  
CTGCATAACAAATAGTATTATATATTAATATTTTGATATGTAAAGCTCTACACAAAGCTAAATATAGTGAATA  
ATGTTTACACTAGTAAGCAAATATGTTAATCTTCTCATTTTTTTACTGTCTATATAATCTTAGTGATATGCCTATT  
AATAGTTTTTAAATAAAATAATTGGCTTATCTGGCTTTTGAATTTTGAATTTCTTACAGATGTTGATTAGGTA  
TATCTACAAATTAATTTCAATTTTAAATGATGATATAAAATAAATAAAGTATTTTCTGTGTATGTATACA  
ATAAATATAAATAAAATTTGTTTACTGTTTTGAAAGTTTCTTAAGTTTTA



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**FIGURE 522**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108720  
><subunit 1 of 1, 527 aa, 1 stop  
><MW: 60284, pI: 8.31, NX(S/T): 3  
MRSDKSALVFLLQLFCVGCFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSK  
PSLIDYRKPSALKFEVVHMPQDRTEENEI FVDLALNVLPGLSTWQSVIKLNDFVEIRGT  
LKMMCESFIYNQTLMKKLQETNYDVMLIDPVI PCGDLMAELLAVPFVLTLRISVGGNMER  
SCGKLPAPLSYVPVPM TGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYSKALGR  
PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGHCKPAKALPKEMENFVQSSGED  
GIVVFSLSLGFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQNDL  
LGHPKTKAFITHGGMNGIYEAIYHGVPMVGVPIFGDQLDNIAHMKAKGA AVEINFKTMTS  
EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSA AHD  
LTWFQHYSIDVIGFLLTCVATAIFLFTKCF LFSCQKFNKTRKIEKRE

**Important features of the protein:****Signal peptide:**

Amino acids 1-21

**Transmembrane domain:**

Amino acids 489-510

**N-glycosylation sites:**

Amino acids 131-135;313-317;518-522

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 67-71;340-344

**Tyrosine kinase phosphorylation sites:**

Amino acids 122-131;136-144

**N-myristoylation sites:**

Amino acids 19-25;276-282;373-379;377-383

**Amidation site:**

Amino acids 338-342

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**FIGURE 523**

GGCTGCGGGGTCGGCACGGAAGATGCACGCGAGGCTCCTGGGGCTCTCGGCCCTGCTGCAGGC  
GGCCGAACAGAGCGCGCGCCTTTACACCGTGGCTTACTACTTCACCACAGGACGGCTTCTGTG  
GGGGTGGCTGGCCCTTGCTGTCCTCCTGCCCCGGTTCTTGGTCCAGGCCCTGAGCTACCTGTG  
GTTCCGAGCAGACGGGCATCCAGGGCATTGCTCCTTGGTGATGCTGCACCTCCTACAGCTTGG  
TGTTTGGGAAGCGGCACTGGGACGCTGCACTGACCAGTCTGCAGAAGGAACTGGAGGCTCCCCA  
CCGAGGCTGGCTGCAGCTGCAGGAGGCCGACCTGTGCGGCCCTTCGACTCTTGGAGGCCCTGCT  
GCAGACTGGGCCCCACCTGCTGCTTCAGACATATGTTTTTCTAGCCTCAGACTTCACAGATATT  
GTGCCAGGGGTGAGCACCCTGTTTTCTGGTCTCACTCTCCTGGGCACTGGTGTCTTACACT  
CGTTTCATGGGCTTCATGAAGCCAGGCCACCTGGCCATGCCATGGGCGGCCCTCTTCTGCCAG  
CAGCTCTGGAGGATGGGCATGTTGGGAACCCGCGTGCTGAGTCTGGTTCTGTTCTACAAAGCC  
TACCACTTTTGGGTTTTTGTGGTTGCAGGTGCCACTGGCTGGTGATGACATTCTGGCTTGTG  
GCCAGCAGAGTGACATCATCGACAGCACCTGCCACTGGAGGCTGTTCAACCTGCTCGTGGGG  
GCCGTGTACATCCTCTGCTACCTCAGCTTCTGGGACAGCCCTTCTAGAAATAGGATGGTCAG  
TTCTACATGGTCATGCTGTTGGAGAACATCATCCTGTTGCTGTTGGCCACCGACTTTCTCCAG  
GGGCGATCGTGGACCAGCCTGCAGACCATAGCTGGGGTCTGTCTGGATTTCTGATTGGCAGT  
GTCTCACTGGTAATTTATTACAGCCTGCTGCATCCAAAATCCACAGACATCTGGCAGGGCTGC  
CTAAGGAAGTCTGTGGCATTGCAGGAGGTGATAAACAGAGAGAAGAGATTCTCCCCGGGCC  
ACAGATCTAGCTGGGAAGAGAACCAGAGAGCTCAGGCTCATGCCAAGGGGCAAGTTATGAACCA  
ACCATTTTAGGGAAGCCCCCTACCCCTGAGCAGGTCCCCCAGAGGCTGGGCTGGGGACCCAG  
GTTGCTGTGGAGGACTCTTTCCTCAGTCATCACCCTGGCTGTGGGTGAAACTTGCCCTAAAA  
ACAGGAAATGTGTCTAAGATCAATGCCGCCCTTTGGAGATAACAGTCCTGCCTATTGTCCACCT  
GCATGGGGGTTGAGTCAACAGGACTACCTGCAGAGAAAGGCCTTGTCTGCCCAGCAAGAGCTC  
CCATCCTCATCCCGTGACCCCTCAACCTTAGAGAACAGCTCTGCGTTTGAAGGTGTCCCTAAA  
GCAGAGGCCGACCCATTGGAAACCTCAAGTTACGTATCTTTTGCCAGCGATCAGCAGGATGAA  
GCACCTACCCAGAACCCAGCACGCCACGCAGGGGGAGGGCACCCCAAAGGAAGGAGCTGACGCT  
GTTTCTGGGACACAGGGGAAGGGGACAGGTGGGCAGCAGAGAGGAGGGGAAGGACAGCAGAGT  
TCCACGTTGTACTTCAGCGCCACTGCAGAAGTGGCCACATCCTCACAACAAGAAGGCAGCCCA  
GCTACTCTGCAAACGGCCCACTCTGGAAGGAGGCTGGGAAAGAGCAGCCCTGCCCAGCCTGCA  
TCGCCCCACCCAGTGGGCTTGGCGCCCTTCCCCGACACCATGGCCGACATTAGCCCCATCCTA  
GGCACAGGCCCATGTAGAGGCTTCTGCCCCAGTGCAGGCTTCCCTGGAAGAACCCTCAGTATC  
TCAGAGCTAGAGGAGCCGCTGGAGCCCAAAGGGAGCTAAGTCACCATGCAGCTGTTGGTGTG  
TGGGTGTCATTGCCACAGCTGAGGACTGCCCATGAGCCCTGCCTCACGTCCACCCCTAAGTCT  
GAGTCTATCCAAACGGACTGCAGCTGCAGGGAACAGATGAAGCAAGAGCCGAGTTTTTTCATC  
**TGA**CCACAGTCATGGTGGGATAAGACAACAGGCTGACAAACCAAGCTGGCCATTTGGTACCGT  
GAGAAAGGAAATCCCACTTCTGACACCTGTGTCCTTGGGCACATCACTGTCACCTCTGAATCT  
CCATCTGCATCCCTGAAAAATGAAGAAACAGGGCTGGATGATTTTGCAGGTCCAATGCAAACA  
TCACAGACCCACCCATGCATAGGAGAGACTCTAACATACTTTAGAGGAGGAGAAAGAGATTCT  
CAGTCAAAATTGTCTGCTACCTTTTATGAGCTGTAGGTTCCCTTATTTTATCTTTTTGCTGTG  
GCTTCTAGGAAACACAAAGGTAAAACCCAGATTCTTATTTTATTTGAGGTTCTTGTTACAATT  
AGCTTTGCCTCACATTTAGCGGTTATGAATCTCATTTTAATATATTCTAACTGTATTATGTTA  
TGAAATCTCTTGGAAGATAATTTGCATGCTTTCTGGGAGTAGGTAAGGCCTGTGTGCTTGTA  
ATAACTAACATAACTGAAAGTGCAAATGTCA

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**FIGURE 524**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108726
><subunit 1 of 1, 686 aa, 1 stop
><MW: 74981, pI: 6.60, NX(S/T): 2
MHARLLGLSALLQAAEQSARLYTVAYYFTTGRLLWGWLALAVLLPGFLVQALSYLWFRAD
GHPGHCSLVMHLHLLQLGVWKRHWDAALTSLQKELEAPHRGWLQLQEQADLSALRLLEALLQ
TGPHLLLQTYVFLASDFTDIVPGVSTLFSWSSLSWALVSYTRFMGFMKPGHLAMPWAALF
CQQLWRMGMLGTRVLSLVLFYKAYHFVWFVAGAHWLVMTFWLVAQQSDIIDSTCHWRLE
NLLVGAVYILCYLSFWDSPSRNRMVTFYVMVLENIILLLLATDFLQASWTSLOQTIAGV
LSGFLIGSVSLVIYYSLHHPKSTDIWQGCLRKSCGIAGGDKTERRDSPRATDLAGKRTE
SGSCQGASYEPTILGKPPTPEQVPPEAGLGTQVAVEDSFLSHHHWLWVKLALKTGNVSKI
NAAFGDNSPAYCPPAWGLSQQDYLQKALSQQQELPSSSRDPSTLENSSAFEGVPKAEAD
PLETSSYVSFASDQQDEAPTQNPAAATQGEQTPKEGADAVSGTQGGGTGGQQRGGEGQQSS
TLYFSATAEVATSSQQEGSPATLQTAHSGRRLGKSSPAQPASPHVGLAPFPDTMADISP
ILGTGPCRGFCPSAGFPGRTLSISELEEPLEPKRELSHHAAGVWVWVSLPQLRTAHEPCLT
STPKSESIQTDSCREQMKQEPSFFI
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-17

**Transmembrane domains:**

Amino acids 35-50;269-287;293-313

**N-glycosylation sites:**

Amino acids 416-420;467-471

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 344-348

**N-myristoylation sites:**Amino acids 188-194;288-294;299-305;335-341;338-344;362-368;  
390-396;473-479;529-535;536-542;558-564;603-609;  
643-649**Amidation sites:**

Amino acids 354-358;568-572

**Leucine zipper pattern:**

Amino acids 112-134

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**FIGURE 525A**

AGTGCCCTCTGTCAATTTAATCTCCACGGAGTCCTGAAGGTGCTTCCCAGGTTTGTCCCCATCACACAGATGAGGC  
AATCGTTCTGTTAAGACTGTCTTGGGTCAATATGTCAGCAATGAAATCGGTGCTGCCATTACTAAACCCCTTACT  
GTGTGCTGGCATTGTGTATGCATGATGTGTGCGTGCACACGTGTGTGTTGCGTGTACATGTGCATGTGTGTG  
TTGTGTGCTGTGTGTGCACATGTAGAAAGAAAGTGATGTGTGGGAATGGAGAATTCCAACCCAGGAGGAGACTG  
TGCTGGGGCTGCCACGAGAAGTGGTGACACTTCGAGAAACGGGTCCAAATGCACGTTGCCTTCAGTTCTCTG  
TGTGACCTTGGGCAAGTCACTTCAGCTCCCTGAGCTTTGTTTTTAAAAATATTTTTTAAATGTATAAAACCATGG  
ACCATTACATATGAAGAGAAATGTGTGTGCAACATTCAGTTAATAATCACAAGGTGGAGGAGTGCCTGCTCAGA  
CCCAGAGCTGACACAGGGAACCTCTCCAGAAGGCTGCAGGGCTTCCCTCCCAACCCCTCAACGGCCCACTTGCTG  
AGCCCGTGCTTATCTGTTCAGTGGAAATGCCATGTGCCACGTTCCTCAGAAGTAAAGCCACTAGGTAAGTGTGAC  
ACTCTGTGCCAGCTTGGTGCAAGCCCCCTGTGTGTGCTATCTTATTGACCTCCCAATAGCATGGTAAGGTCA  
GTACTGTCACTTCCCCCACTTTGAAGATGAGGAGAGCACAAATCTAGATGGAAATGGAGGTACGCAGTGGAAA  
TAGGATCCAGACAGATTAATCCAATCTCAAGCCTGAATTCCTCCATTCCACGCTACGCTGAAGCTCAATCTCTC  
TTCCTGGTTGATTCTCCCCACTTCCCCACCCCAAGATATATCCCATCGCTGCTTGGTGGACAGTAGCCATGACTG  
GGTTTTGGTAAAGGTTGCTGAATAATCAGGCTGCTGGTTAGTTTTTACATTTACCTTTCCAGTGAAATGGGGC  
CCCATGAAAAAGGCAGCTCAAGTTGTAAATTACTCAAAGGAAGGACAGAAAGTCTTCTGTTTGCACCTACCCTA  
AGGATTTGGGGTAGACACTGGGAATTTACTAATTATGAATTCAGTGCTTTCCTTGCTGAAAGAGAGGGCTGGAA  
TCAACGCTGAGTGAAGGCATCAAGTTTAAGCTGCTAATTACTTCTGATCATGCAGAATAAAAGCTACGTCCTT  
GAAATACACCAGGCAGCTAAACATAATCTTTCGCTTCCGTAGTGTTGGTTAAGGAATCCAGATGTTACTGCAAT  
AACCCTCCATAAACAAGGAACACCCAGCTGTGAGAACTGGCTTCTCAGCATTCGTCCCAGCAGAGGCTCTTC  
CGGGGCCAGCCCTGGAAGAACCCTCAGGGTTCTGATGGTTGCCCTGTTTCAGCACAGCCCTTATTGGCAGGCAG  
ACGGCTACGGGCACAGCCACAGGCTGAAGGTGAGTCCAGCACACAACCTTCTGACAGTGAACAGGAGTAAACATG  
GGACCCACCCGAAACCTTTGTCTGTGACTTCTTAGCAATGGAGGCAGCTCTAGGCTCTGGAGAGTTCGGGTAT  
AGGAGACCATGACTTGAGCAGACTGATATAAGTGAATGCAACATATTTAGATGGCACAACCTAATTTAGATTT  
ATCAGTGCTAATATAGAAAAAGCTAGTATTTATTGGGGCTTATTAGATTTTTAGTCTGAATCCTCACAACCTTACG  
AGGGGGTTCGTTTTACAGACTATGATCTTGCATGATTTCCCCAAGATGCTCATTAGTATATGGTGAAAGTAGA  
ATTTGAATACAGAAGACCTGGTTCTGCTACTTTCTGTTCTATTGTTTCAACCAGCCTTTCTCTTTCAA  
ACAACTTCAGTGCAATTCATGGTTTTGGAAAATAAACTTGATTTTGAGATTCAGACAATAAGTGCATTTTTAATG  
TTTATTCTTTTATCTTGAAAACTGATATATTTATGAAATGATATGTGCTCACTCAGTGTCAACACTTCAAACAA  
CACAGACAGTACAATGACAAATTGGAGATCAGCTCTAATCTCGGCCCAATTTAATGCATTGCTGAATATTCTT  
CTGAACATAGTCCATCCCACTGTCCCATGACACAAGACGCTCCAAGGGGCTGAAGATAGAGGGACTTCTGCAG  
TCAAGAGAGCTGGGAAACTCTTGGACAGTCACAATGTGCATTTGGGTATTAAAGGCTCTGCAAGGTTCTGCACCA  
AATAAACCCCTTGATTGGCTTGATCCAATGCCATGTTTCCAAAACCTACTTGCCCGTGGGACACCTTAGTCCATA  
ACACAGGTTGGCATTCTTCTAGAGAGTGTGCTGTGAAAAACACTGGTCTCACAGCACCGTGCATTCACGCA  
GGTATTTACCAAGCAGGGACTTTGGGCCAGGTCCGTGCTAGGCTCTGCAGGTGGACCAGCCAGCCCTGACCTCCA  
TGGTGTCTCTTCTCATGGGAGAGGCTGCACAGCAGTCATTGAGAAAACGAAGAAACACACAGGTACTTTCAGATG  
CTGATAATGACTACCATGTGCTAAAAGAGCTCCAGGTGTTGTCTGTTTGGAGACAATCTTCTCGACAATGAGATA  
GAATGAACCATGCAAACTTTGGGGGCTACGATGGTTTTAGGAAAGAGCTAGAGTGAAAAATCCTTTGACATATAT  
ACATACAAATAAAGATACATGTGTATAATTTTATGTAATTGACATCACATTATATGCTGGCACCTGCCCTTTTTTG  
CTTAATGAAATGTCAAAGGTAATATTACCAATCAATCAATATATTTACCATCGTGTTTAATTTCTGCAGAGCA  
CTTATTCAAGCACATACTGCATTTTCTTAGTCACTCACTGGTGGGAATAGAAAGTTTTCTCAGGCATGCATTTT  
TCCCACTTCTGAAATGATCTCCTTAGAATAAATCCCCAAATGTATTGCTGGGTTCAAAGGCATGAACATTTTA  
CATTTTTATACAATAATGTCAAACCTACCTTCCGGAATGATGCTCACTTTACTTTCCCTCCAAGACTGTGTGAAA  
ATGCCATTTTCTAAATGCTTACTATGACTGGTTTCCAACCTACATTTAATTTCTGTTCAATCTGATAGGCAAA  
AAATGATATTTAATTTTTATTTGATTGATAATGACCTTGAACGTGCCATTAGCCTTTTGCATGTATTCTTTTAT  
GAAACATCTGTTCTATCCTTCGTCAATGTTCCCTCTCATATGTTAACTTTTCTTATTGATTGTAGAGCACTT  
TGATATTGTGAATATTAGCTTTTGTGATCAGAATTATGGAATTGTTGTTGCTTTAGTTTTGCTTATCAAGTTT  
AAAGCCATTTCAGAGATGTTGTAAATGTGTATGTTGTTAAATTTATGTCTTATTTGTGTTTTCTGATGCTCATAT  
GTTTAGAATGGTCAAGCAATCCCACTTATGATTACATAAATATCTCCCATATTGCTCTTAGCATTTTTTTCTC  
TTTTCATGTAACCCCTTTGTTCTTTAGGAATTTACTTTGCGGTAAGAAATGGGCTGGCTTCCAGTTTTATGTTT  
CCAAATGGTGATTGAGCTGTCCATTTCCATATCTCCCTTATTAGAAATGACCACTATATTATGTTCTAAAATA  
TCTGCGTACTTGTGTCCCTTCCATAATCTCAGTTCATCTCTTTGAGCTATCTTTGATTCTTTTCAAACCAC  
ACTGCTTTACTGAACGTGTCATCTTATACATTTTAACTACTCAGCAAGACAAGTTTCTCAATGCCACTCTTTT  
TCAGAGTTTTTCTGGTGGTTGTAAGATGTTTATTCTCTGGATAAACTTTAGAACTACTCTTTTGTCCAAGGTA  
AAATATATCCCACATTGAGATCATACTGAATATACAGACTAATTTCAGGAAAAATGTATGCTTTTATTGCATTGA  
GTCTTCTTATCCAATAAAAAAGATATGAATTTCCATGTATTGAATCTTCACTGAGACTTATTTTTGGCTTTTCA

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**FIGURE 525B**

CATGTCCTGCAAATGTATTGTTAAATTTATTTTATAGGTATTTAGGGGAAATGATTTTCTAAAGTTTGTATTTTC  
TAGCTTGTTATAATTTACATATGAGATAGTCATTGTTGTATATTATTTATAACTGATCATATTACTGTATTTGTA  
TTGTTTAAATAGTTTTTCTATTATTTTGGGTTTTCCTGGAATACAACCTTATTATCTACAAATTATGATTGTTTT  
GCCTTTTCCAATGTTTCATAACTGTTTTTATATTCTTGTCTGATTGCTTTGTTTCAGCACTTCTAGAATAAAGTCAT  
GCAATACTAATGA

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**FIGURE 526**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108728  
<subunit 1 of 1, 100 aa, 1 stop  
<MW: 10922, pI: 8.81, NX(S/T): 0  
MSAMKSVLP LLNPYCVLAFVYACMCVRAHVVCVYMCMCVLCACVCTCRKKVMCGNGEFQ  
PRRRLCLGLPREVVTLRETGSKCTLPSSSLCDLGQVTSAP

**Important features of the protein:****Signal peptide:**

Amino acids 1-28

**N-myristoylation sites:**

Amino acids 80-86;94-100

**Prokaryotic membrane lipoprotein lipid attachment sites:**

Amino acids 13-24;34-45

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**FIGURE 527**

GTGAGACTTCTTTCTTCATTGTGGCTAGCTTTGAAAAGACCCTCTGAACTTCCTAAAGATATC  
AAGATGATATCACCAGACTTGCCCTTTTTGACAATTGTCTTGATCATAGTTAGTTGGACAACCT  
TGTGGAGCACTAGCCATACTTCTTTCTTATCTTTACTATGTGTTTAAGGTTGTTTCATCTGCAA  
GCCAGCTTAACAACCTTTTAAGAATAGCCAGCCTGTGAATCCCAAACACTCTAGAAGAAGTGAA  
AAGAAATCCAATCATCATAAAGACTCCTCAATACACCATCTTCGTTTATCTGCCAACGATGCT  
GAAGATAGCCTTCGCATGCACAGTACTGTGATTAACCTTACTAACATGGATTGTATTACTCAGC  
ATGCCTTCTCTAATTTATTGGCTAAAGAATCTTAGGTATTATTTTAAACTTAATCCTGATCCA  
TGTAACCTTTGGCATTTATCCTTATTCCGACTATGGCAATTCTTGGAATACTTACACTGTT  
TCAATAAAATCAAGTAAATTGTTGAAGACTACTTCACAATTTCCACTTCCTCTGGCTGTTGGT  
GTGATTGCTTTTGGGTCAGCACATTTATATAGGCTTCCATGCTTTGTCTTCATTCCTCTTTTA  
CTCCATGCATTATGCAACTTTATGTAAGATTGGACTTAAGGAATGATGAAGATAATTTATGTG  
TTTAGGGCCAGTGATAAGAGGGAACACACAGATCCATCAGTATGGACAGCAAGATCCTTTGGA  
GAAGACAAGTCTATTTTTACAATATTGAAAATAGGAAATTAGTTTGTAAATGTTTGAGGGAAG  
TAGTTGAAGCATGGTTTTGTTTTGTGGTGTGGAATCCATGTACTAATCATTTTTGAAAAATTC  
ATGAAGGGATATATGGTGATCACTATCATTGAGGACTCCTGTGCATATAAAATAGTCTGTTTT  
ATCAACTGTAAA

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**FIGURE 528**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108738  
><subunit 1 of 1, 196 aa, 1 stop  
><MW: 22225, pI: 9.90, NX(S/T): 0  
MISPDLPFLTIVLIIVSWTTCGALAILLSYLYYVFKVVHLQASLTTFKNSQPVNPKHSRR  
SEKKSNNHKDSSIHHLRLSANDAEDSLRMHSTVINLLTWIVLLSMPSLIYWLKNLRYFFK  
LNPDPCKPLAFILPTMAILGNTYTVSIKSSKLLKTTSQFPLPLAVGVIAFGSAHLYRLP  
CFVFIPLLLHALCNFM

**Important features of the protein:****Signal peptide:**

Amino acids 1-25

**Transmembrane domains:**

Amino acids 91-108;128-143;167-186

**N-myristoylation site:**

Amino acids 141-147



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**FIGURE 529**

GCGAGCCGGGTCCCACCATGGCCGCGAATTATTCCAGTACCAGTACCCGGAGAGAACATGTCA  
AAGTTAAAACCAGCTCCCAGCCAGGCTTCCTGGAACGGCTGAGCGAGACCTCGGGTGGGATGT  
TTGTGGGGCTCATGGCCTTCCTGCTCTCCTTCTACCTAATTTTCACCAATGAGGGCCGCGCAT  
TGAAGACGGCAACCTCATTGGCTGAGGGGCTCTCGCTTGTGGTGTCTCCCGACAGCATCCACA  
GTGTGGCTCCGGAGAATGAAGGAAGGCTGGTGCACATCATTGGCGCCTTACGGACATCCAAGCTT  
TTGTCTGATCCAACTATGGGGTCCATCTTCGGCTGTGAACTGCGGAGGCACGTGGAGATG  
TACCAATGGGTAGAACTGAGGAGTCCAGGGAGTACACCGAGGATGGGCAGGTGAAGAAGGAG  
ACGAGGTATTCTTACAACACTGAATGGAGGTGAGAAATCATCAACAGCAAAAACCTTCGACCGA  
GAGATTGGCCACAAAAACCCAGTGCCATGGCAGTGGAGTCATTATGGCAACAGCCCCCTTT  
GTCCAAATTGGCAGGTTTTTCCTCTCGTCAGGCCTCATCGACAAAGTCGACAACTTCAAGTCC  
CTGAGCCTATCCAAGCTGGAGGACCCCTCATGTGGACATCATTGCGCGTGGAGACTTTTTCTAC  
CACAGCGAAAATCCCAAGTATCCAGAGGTGGGAGACTTGCCTGTCTCCTTTTCTATGCTGGA  
CTGAGCGGCGATGACCCTGACCTGGGCCCAGCTCACGTGGTCACTGTGATTGCCCGGCAGCGG  
GGTGACCAGCTAGTCCCATTCTCCACCAAGTCTGGGGATACCTTACTGCTCCTGCACCACGGG  
GACTTCTCAGCAGAGGAGGTGTTTCATAGAGAACTAAGGAGCAACTCCATGAAGACCTGGGGC  
CTGCGGGCAGCTGGCTGGATGGCCATGTTTCATGGGCCTCAACCTTATGACACGGATCCTCTAC  
ACCTTGGTGGACTGGTTTCTGTTTCCGAGACCTGGTCAACATTGGCCTGAAAGCCTTTGCC  
TTCTGTGTGGCCACCTCGCTGACCCTGCTGACCGTGGCGGCTGGCTGGCTCTTCTACCGACCC  
CTGTGGGCCCTCCTCATTGCCGGCCTGGCCCTTGTGCCCATCCTTGTTGCTCGGACACGGGTG  
CCAGCCAAAAAGTTGGAGTGAAGAACCCCTGGCACCCGCCGACACCTGCGTGAGCCCTGAGG  
CTGGTTGTACAATGCCCACGCCTGCCTGGCTGCTTTCACCTGGGAGTGCTTTCGATGTGGGCA  
CCTGGGCTTCCTAGGGCTGCTTCTGAGTGGTTCTTTCACGTGTTGTGTCCATAGCTTTAGTCT  
TCCTAAATAAGATCCACCCACACCTAAGTCACAGAATTTCTAAGTCCCCAACTACTCTCACA  
CCCTTTTAAAGATAAAGTATGTTGTAACCAGGACGTCTTAAATGATTCTTTGTGTACCTTTTC  
TGTCATATTAGAAACCGTTCTGTGCCTGCTGGGAGTAATTCCTTTAGCAATTAAGTATTTGG  
TAGCTGAATAAGGGGTCAGAACTTCTGAAACCAGAGATCTGTAATCATCTCTATTGGCCTGGG  
GTGCCTGTGCTATAAATGAGTTTCTTACATGAAAAACACAGCCAGCCCAAGATGACTTATCT  
GGGTTTAGGATTCAATAGTATTTCACTAACTGCTTATTACATGAGCAATTTTCATCAAATCTCCA  
AACTCTTAAAGGATGCTTTCGGAAAACACGCTGTATACCTAGATGATGACTAAATGCAAAATC  
CTTGGGCTTTGGTTTTTTCTAGTAAGGATTTTAAATAACTGCCGACTTCAAAAGTGTTCTTA  
AAACGAAAGATAATGTTAAGAAAAATTTGAAAGCTTTGGAAAACCAAATTTGTAATATCATTG  
TATTTTTTTATTAAAAGTTTTGTAATAAATTTCTAAATTATCA

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**FIGURE 530**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108743  
><subunit 1 of 1, 400 aa, 1 stop  
><MW: 44876, pI: 8.32, NX(S/T): 2  
MAANYSSSTSTRREHVKVKTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIFTNEGRALKT  
ATSLAEGLSLVVSPDSIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPVAVKLRRHVE  
MYQWVETEEESREYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHKNPSAMAVESFMA  
TAPFVQIGRFFLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDDFFYHSENPKEYPEVGDLR  
VSFSYAGLSGDDPDLPAPHVTVIARQRGDQLVPFSTKSGDTLLLLLHHGDFSAAEEVFHRE  
LRNSMKTWGLRAAGWMAMFMGLNLMTRILYTLVDWFPVFRDLVNIGLKAFACVATSLT  
LLTVAAGWLFYRPLWALLIAGLALVPILVARTRVPAKKLE

**Important features of the protein:****Transmembrane domains:**

Amino acids 34-53;365-388

**N-glycosylation site:**

Amino acids 4-8

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 140-144

**Tyrosine kinase phosphorylation sites:**

Amino acids 99-107;220-227

**N-myristoylation sites:**

Amino acids 35-41;93-99;310-316

**Cell attachment sequences:**

Amino acids 221-224;268-271

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**FIGURE 531**

AAAAAAAAAAAAAAAAAAGAAGCTCTTATGCCAGGAACCTGGAATGGAGACCAAATATATATTG  
GTTATATCATAGTATCACAGGGTTACTTTGGCATTGTTGGGAACTTGAGAGAAATGCGGCAATAA  
CTGTTACTTTAAAAGCTTGGGTGCTGTGATTCTGCCTTCAGCCTCAGCCACTTTGTGGTGCT  
TTGCGTGGCATCAGTACCTCCACTGATTCTTCTGTCTTTCCTCTCTCTCTTCCCCCCTCTT  
CCCTTCTGTTTTTCTCAGATCTAAGGGTTATAATGGAGGGGCAAACCTGCCTGGCTATTTCAGA  
TAAGACTTCACTGAGTGACTGTTTCAGCCCATGATTTACCCTGCAGTTTAACAGGCTCAGGAAT  
TAGGTCGCATCAGTTGAGCGCGGGTCACTTAGGCCTATTAATCATCATCAGACGGCAATTAAAG  
GACCATTTCTGCCTTTTTCACTATTACATCCCCGCCTGTAGCCAGCCTGCCATACAGTAGA  
TACTCAATAAATATTTGCTGAATGATAACCAATAA

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**FIGURE 532**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108758  
<subunit 1 of 1, 100 aa, 1 stop  
<MW: 10316, pI: 8.52, NX(S/T): 0  
MGNNCYFKSLGAVILPSASATFVVLCVASVPPLILLSFLSLFPPSFPSVFLRSKGYNGGA  
NCLAISDKTSLSDCSAHDLPCLTGTSGIRSHQLSAGHLGL

**Important features of the protein:****Signal peptide:**

Amino acids 1-47

**N-myristoylation site:**

Amino acids 58-64

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**FIGURE 533**

CGGGGTGTACGAAAGAGAAACCCGGAGGGCGCCGGGGACTGGGCCGGGGTCTGCAGGGCTCAG  
CTGAGCCCATGAGCTCCCAGAGCTAACCCTGAACACCCAGGCGGGCAAAGGGCTGATGTCGG  
TAGTCCCCATCCTGGAGGGGCAGGCTCTGCGCATCTGCTCCTGGC**ATG**GCGCTGCGGCACCTC  
GCCCTCCTGGCTGGCCTTCTCGTGGGAGTCGCCAGCAAGTCCATGGAGAACACGGCCCAGCTG  
CCCGAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCAGGCGCAAGTCTGTGTGGT  
CCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGA  
ACCCTCCCAGCCTACAACGGCTCCGAGTGTAGAAGCTTTGCTGGCCCCGGGTGCGCCATTCCCC  
ATGAACAGAAGCTCAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCGTGGCCGCCTCC  
CTCTTCTGGGCACGTTCTTCATTAGCTCCGGCCTCATCCTCTCCGTAGCTGGGTTCCTTCTAC  
CTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACAGAAGAAACAAAGCTCCGGCCCCTGAG  
CCTGGCGAAGCCGCTGCAATGATCCCCCGCCACAGTCCTCAGACGTGGGGTCTGCAGGAAAG  
GAGGACCCACACGACAGGGCAGACCCCCAATACCTGCTCCTCCT**TGA**AGTCCAGCTCCACCC  
GAGGACAGACGCAGCCGGCCTCCGCCAGGGCCTCCTGAGCAGCCATCGCTTCAGTGGTGTGG  
GTCAGGCGGACCCAAGAGTCAGCCCGTACGGAAGCCGCGCTACGTCAGGCGGGAGCGGCCCT  
GGACAGGGCCACGGATCCCGCTGCCTTCCCGGGGGAGGCCCGTATCAGCAATGTCTGACCTGG  
AGGCCGAGACCACGCCACGCACTTGGCGGCAGGGACCCGGAGGCCGACCCCTTGGCGGGAACC  
AGCACAAAGTGTTGGCATCGCCCGGCGCCCGGGACAGTCCTGGGCACAGCCTCGGCTCTGGGT  
CCCTCCGCCTCCCAGCGACGGACGCCAAAGGGTCCCGGGCCGCTGAGGCTCCTCCCCACCAC  
AGCCATCTCGTTTATCGGACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGC  
CTTGGGGGGTCCGGGCCCCCCCCAGGAAACACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGG  
CACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCAGGGGCTCTGCTGCCGTGCCCTC  
CAGAGCCCACAGCGGGCAGGACTCCTCCAGCACCACCACACCCAGTGGCCCCGAGACCCCTCTG  
AGAACAGTGAGGCTGGTCTCGTGCCGTTCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGC  
CTAGGAACCAGCTGCCTGAGACCAGGGTGCCTCTGGGCTGTCTCCCGCGTGGCGGAGACCCC  
AAGCACGCAGCCACCCATTTCCGGAGCTGCAGGATAGAGCTTCCTCTTGATCTCTGTTTTTAAG  
CAGAAATTCATTGTGCAGAAAAGTCTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACC  
CCCATGCCTGGCTGATCCCTGCCCACGTGGGGCAGGCCACATCTAACCCCCACAAGTCACTG  
CCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCCTGGGGTCCCTCCCGGAGTTCCTGG  
GAGAAAGGCGCCGTCGTGGCCGCCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCAGA  
CGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCCATCTGAGGGGTGGCCTGGCC  
TTCGGGGTCCCCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTG  
GGCCAGCGGGAACGTGGGGGCACTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 534**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108765
><subunit 1 of 1, 189 aa, 1 stop
><MW: 19464, pI: 9.60, NX(S/T): 4
MALRHLALLAGLLVGVASKSMNTAQLPECCVDVVGVNASCPGASLCGPGCYRRWNADGS
ASCVRCGNGTLPAYNGSECRSFAGPGAPFPMNRSSGTPGRPHPGAPRVAASLFLGTFFIS
SGLILSVAGFFYLKRSSKLPRACYRRNKAPALQPGEAAAMIPPPQSSDVGSAGKEDPPRQ
GRPPIPAPP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-18

**Transmembrane domain:**

Amino acids 111-129

**N-glycosylation sites:**

Amino acids 38-42;68-72;75-79;92-96

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 134-138

**N-myristoylation sites:**

Amino acids 11-17;36-42;43-49;59-65;69-75;122-128

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**FIGURE 535**

TGGATCTGCGGGAATGTGGGCTGGAGAGGTCCTGCCGTGGTACCAGCCTCCAGCCTGCCCCCA  
GGACTGCCCCCTGACCCAGGCGCGCCCGCTGCTCGGTGGCAGGAGGGCCGGCGGAGCGCC**ATGG**  
CCTGCATCCTGAAGAGAAAAGTCTGTGATTGCTGTGAGCTTCATAGCAGCGTTCCTTTTCCTGC  
TGGTTGTGCGTCTTGTAATGAAGTGAATTTCCCATTTGCTACTAACTGCTTTGGACAACCTG  
GTACAAAGTGGATACCATTCTCCTACACATACAGGCGGCCCCCTTCGAACTCACTATGGATACA  
TAAATGTGAAGACACAAGAGCCTTTGCAACTGGACTGTGACCTTTGTGCCATAGTGTCAAACCT  
CAGGTCAGATGGTTGGCCAGAAGGTGGGAAATGAGATAGATCGATCCTCCTGCATTTGGAGAA  
TGAACAATGCCCCCACCAAAGGTTATGAAGAAGATGTGCGCCGCATGACCATGATTCGAGTTG  
TGTCCCATACCAGCGTTCCTCTTTTGCTAAAAAACCTGATTATTTTTTCAAGGAAGCGAATA  
CTACTATTTATGTTATTTGGGGACCTTTCCGCAATATGAGGAAAGATGGCAATGGCATCGTTT  
ACAACATGTTGAAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGA  
AGCGCATGAGTTACTGTGATGGAGTTTTTAAGAAGGAAACTGGGAAGGACAGTACAGAG**TGAC**  
CATGCAGTGTTGATTGATCGAACAGCAACCACCACATACATGTCCTGCCCCACCACAAAAGGA  
AGGAAGGAATAAAAGAAAGAAAGAAAGAAACAAACAAACAAACAAACAAACTAAGCAAGACA  
AAACAAATACCCATGTCAGTGGTTCAAAGATTAAGATTGTGGCTTTGTGTAAAGTTCTTTCCC  
TTTGTAGACTTGCTGCATAATTATTCAGGTATGATGGTTACAGTTTTTTAAAGGAAGGGAAA  
TTGTGGTATGTGGTATGTAAATATTTTAAATGTTGTCTCTCTGTTTTGATCAGTTTTTGTTT  
TATTCAATTTGTCTTTATTAAATCTTATCAAAGCA

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**FIGURE 536**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108783  
><subunit 1 of 1, 210 aa, 1 stop  
><MW: 24022, pI: 9.51, NX(S/T): 1  
MACILKRKSVIAVSFIAAFLFLLVVRLVNEVNFPLLLNCFGQPGTKWIPFSYTYRRPLRT  
HYGYINVKTQEPLQLDCDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTKGYEEDVG  
RMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVGIIY  
PNAQIYVTTEKRMSYCDGVFKKETGKDSTE

**Important features of the protein:****Signal peptide:**

Amino acids 1-27

**N-glycosylation sites:**

Amino acids 148-152

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 6-10;191-195;201-205

**N-myristoylation sites:**

Amino acids 41-47;87-93;91-97;167-173;178-184



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**FIGURE 537**

GT TTTATTGACAATACATGCATCATATCTTTGACTTTGAAGGATATCTCATGTCAAAGGAAT  
CAAGTTATGATTTATAGAGGATTCAGCTGGAATACCTTGTGGGTGCTGGCTGAGGGTGGCAAA  
ACGCCTACCGAGACATGAAGGTTTTAGCCACTAGTTTTGTCCTTGGGAGCCTGGGGTTGGCCT  
TCTACCTGCCTTTGGTGGTGACTACACCTAAACACTGGCCATCCCTGAGAAGCTGCAAGAAG  
CTGTGGGGAAAGTTATCATCAATGCCACAACCTGTACTGTCACCTGTGGCCTTGGCTATAAGG  
AGGAGACCGTCTGTGAGGTGGGCCCTGATGGAGTGAGAAGGAAATGTCAGACTCAGCGCTTAGAA  
TGTCTGACCAACTGGATCTGTGGGATGCTCCATTTACCATTCTCATTGGCAAGGAATTTGAG  
CTTAGCTGTCTGAGTTCAGACATCTTGGAGTTTGGACAGGAAGCTTTCCGGTTCACCTGGAGA  
CTTGCTCGAGGTGTCATCTCCACTGACGATGAGGTCTTCAAACCCTTTCAAGCCAACTCCCAC  
TTTGTGAAGTTTAAATATGCTCAGGAGTATGACTCTGGGACATATCGCTGTGATGTGCAGCTG  
GTAAAAAACTTGAGACTTGTCAAGAGGCTCTATTTTGGGTTGAGGGTCCTTCCTCCTAACTTG  
GTGAATCTGAATTTCCATCAGTCACTTACTGAGGATCAGAAGTTAATAGATGAGGGATTGGAA  
GTTAATCTGGACAGCTACTCCAAGCCTCACCACCCAAAGTGGAAGGAAGGTGGCGTCAGCC  
TTGGGAATAGGAATTGCCATTGGAGTGTTGGTGGCGTGTTGGTGAGGATTGTCCTCTGTGCG  
CTAAGGGGGGGCCTGCAGCAGTGACAGCTTCAAGAACTTAACAGCCTTGCTCCTGAAGAACTG  
GCTGCCCAGGAAGCCAAGCTAGCTTTTTAGGGGAGTGTTCCAGCTGCTGGTAGTGGATCAGCT  
TAGAGGGAACTCTCCACAGCCAAAAGAATGAGTGGGAGAAATGGAGGGGACAATCTCCTGGG  
AGCTATGCGCAGTAACCTA ACTTCCTTATGTCCCATGGATCTCTCCTGATCTTCCCTGCCCCA  
TTGGGTACCCAGGAACTGCAAGCATTGCCTGTGTTCCCTGGGAAGAGTTCTAAGAAGCTTGCA  
TTCATTTTCTACCCTTTATGACTTGGATGCCTCCCCACCTCCATTTCCCCTCTTCTGAGCTGT  
GTATTCATGTAGAGGGATGTATTAGCCCTTTTAGTGAACATTTTTTTTCAATAAAAGTAATT  
CACAGTAA

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**FIGURE 538**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108789
><subunit 1 of 1, 255 aa, 1 stop
><MW: 28440, pI: 8.92, NX(S/T): 1
MKVLATSFVLGSLGLAFYLPLVVTTPKTLAIPEKLQEAVGKVIINATTCTVTCGLGYKEE
TVCEVGPDGVRKRCQTQRLECLTNWICGMLHFTILIGKEFELSCLSSDILEFGQEAFT
WRLARGVISTDDEVFKPFQANSHFVKFKYAEYDSGTYRCDVQLVKNLRLVKRLYFGLRV
LPPNLVNLNFHQSLTEDQKLIDEGLEVNLDSYSKPHHPKWKKKVASALGIGIAIGVVG
LVRIVLCALRGGLQQ
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-30

**Transmembrane domain:**

Amino acids 225-244

**N-glycosylation site:**

Amino acids 45-49

**N-myristoylation sites:**

Amino acids 126-132;156-162;204-210;229-235;231-237;235-241

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**FIGURE 539**

GCGCTCATCACTGGCTGGGGACAGAGCCGGGCACCAAGGAGCGACAGGATCCCGAAGAGAGAG  
AGAGAAGGCAGCGAGGGAAGGAGGACCCCGGCAGGCAGCAGCATGAAATTTCAGCCCAGCGCAC  
TACCTGCTGCCTCTCCTGCCTGCGCTGGTCCTCAGCACCCAGACAGGACTATGAAGAGCTAGAA  
AAGCAGCTGAAAGAAGTCTTTAAGGAGCGAAGCACCATTCTTCGTCAGCTGACAAAGACATCA  
AGAGAACTTGATGGAATTAAAGTCAATCTTCAGTCCTTAAAAAACGATGAGCAGTCTGCCAAA  
ACTGATGTTTCAGAACTTCTGGAATTAGGACAGAAACAAAGAGAAGAAATGAAGTCTCTTCAG  
GAGGCCCTGCAAAATCAGCTTAAGGAGACATCAGAGAAAGCAGAAAAACACCAGGCTACTATT  
AATTTTTTAAAGACTGAAGTTGAAAGAAAGAGCAAAATGATCCGAGACCTCCAGAATGAGGAT  
TCAAGGAAGAGACCAAGAGATCTCCAGTGGAGATAGTCTCCATGAGGACCATGTCAATATAC  
TTATTGATGTATCTCTTAGTACCTAGAATAGTGGAGATTTATATTAGATACAAAATAAATATGT  
GTGGAATTAATTAATAA

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**FIGURE 540**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108806  
><subunit 1 of 1, 159 aa, 1 stop  
><MW: 18865, pI: 9.76, NX(S/T): 0  
MKFSPAHYLLPLLPALVLSTRQDYEELEKQLKEVFKERSTILRQLTKTSRELDGIKVNLO  
SLKNDEQSAKTDVQKLLLELGQKQREEMKSLQEALQNQLKETSEKAEKHQATINFLKTEVE  
RKSKMIRDLQNEDSRKRPRDLQWKIVSMRTMSIYLLMYL

**Important features of the protein:****Signal peptide:**

Amino acids 1-22

**N-myristoylation site:**

Amino acids 54-60

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FIGURE 541

[illegible]

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**FIGURE 542**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108936
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19472, pI: 5.71, NX(S/T): 0
MSPSGRLCLLTIVGLILPTRGQTLKDTTSSSSADSTIMDIQVPTRAPDAVYTELQPTSPT
PTWPADETPQPQTQTQQLEGTDGPLVTDPEETHKSTKAAHPTDDTTLSERPSPSTDVQTD
PQTLKPSGFHEDDPFFYDEHTLRKRGLLVA AVLFI TGIIILTS GKCRQLSRLCRNRCR
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-21

**Transmembrane domain:**

Amino acids 147-162

**Tyrosine kinase phosphorylation site:**

Amino acids 45-52

**N-myristoylation site:**

Amino acids 146-152

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**FIGURE 543**

CGGCTCGAGGTGAGAAGGAACTGCAAGAGTGGGGCAGAGAACCAGAGTGTGAGAGCAAAACC  
TCCTCTATCTGCACATCCTGGGGACGAACCGGGCAGCCGGAGAGCTGCGGCCGGCCCAGTCCC  
GCTCCGCCCTTTGAAGGGTAAAACCCAAGGCGGGGCCTTGTTCTGGCAGAAGGGACGCT**ATGA**  
CCGCAGAATTCTCTCCCTGCTTTGCCTCGGGCTGTGTCTGGGCTACGAAGATGAGAAAAAGA  
ATGAGAAACCGCCCAAGCCCTCCCTCCACGCCTGGCCCAGCTCGGTGGTTGAAGCCGAGAGCA  
ATGTGACCCTGAAGTGTGAGGCTCATTCCAGAAATGTGACATTTGTGCTGCGCAAGGTGAACG  
ACTCTGGGTACAAGCAGGAACAGAGCTCGGCAGAAAACGAAGCTGAATTCCTTCACGGACC  
TGAAGCCTAAGGATGCTGGGAGGTACTTTTGTGCCTACAAGACAACAGCCTCCCATGAGTGGT  
CAGAAAGCAGTGAACACTTGCAGCTGGTGGTCACAGATAAACACGATGAACTTGAAGCTCCCT  
CAATGAAAACAGACACCAGAACCATCTTTGTGCGCCATCTTCAGCTGCATCTCCATCCTTCTCC  
TCTTCCTCTCAGTCTTCATCATCTACAGATGCAGCCAGCACGGTTCATCATCTGAGGAATCCA  
CCAAGAGAACCAGCCATTCCAACTTCCGGAGCARGAGGCTGCCGAGGCAGATTTATCCAATA  
TGGAAGGGTATCTCTCTCGACGGCAGACCCCCAAGGAGTGACCTATGCTGAGCTAAGCACCA  
GCGCCCTGTCTGAGGCAGCTTCAGACACCACCCAGGAGCCCCCAGGATCTCATGAATATGCGG  
CACTGAAAGT**GTA**GCAAGAAGACAGCCCTGGCCACTAAAGGAGGGGGGATCGTGCTGGCCAAG  
GTTATCGGAAATCTGGAGATGCAGATACTGTGTTTCCTTGCTCTTCGTCCATATCAATAAAAT  
TAAGTTTCTCGTCTTA

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**FIGURE 544**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119510
><subunit 1 of 1, 236 aa, 1 stop
><MW: 26079, pI: 5.05, NX(S/T): 3
MTAEFLSLLCLGLCLGYEDEKKNEKPPKPSLHAWPSSVVEAESNVTLKCQAHSQNVTFVL
RKVNDSGYKQEQSSAENEAEFPFTDLKPKDAGRYFCAYKTTASHEWSESSEHLQLVVTDK
HDELEAPSMKTDTRTIFVAIFSCISILLFLSVFIIYRCSQHGSSEESTKRTSHSKLPE
QEAAEADLSNMERVSLSTADPQGVTYAELSTSALSEAASDTTQEPPGSHEYAALKV
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-16

**Transmembrane domain:**

Amino acids 135-153

**N-glycosylation sites:**

Amino acids 44-48;55-59;64-68

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 171-175

**Tyrosine kinase phosphorylation sites:**

Amino acids 61-69;87-95

**N-myristoylation sites:**

Amino acids 12-18;203-209



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**FIGURE 545**

GGCGGCCCGGAGCTGGGAGCGCGGGGAAGGCGGTTGGGGTTCTGACAGCTGCGCGCGATCCTG  
CTCTCTCTCAGCCGCCTGTGGACATGCGCAAAGGGCCCTCTCCTGAGTCCAGATGATGCTCAT  
ACCAATGGCTTCAGTGATGGCGGTGACTGAACCGAAATGGGTCTCGGTCTGGAGCCGCTTCCT  
CTGGGTGACGCTGCTGAGCATGGTGCTGGGGTCCCTGCTGGCCCTGCTGCTGCCGCTGGGGGC  
TGTGGAGGAGCAGTGCTTGGCTGTGCTCAAAGGCCTCTACCTGCTCAGGAGCAAACCGGACAG  
GGCGCAGCATGCCGCCACCAAGTGACACGAGCCCGTCCACGGAGCTCAGCATCACCTCCAGGGG  
CGCGACGCTGCTGGTGGCCAAGACCAAGGCCTCTCCAGCGGGTAAGTTGGAAGCCAGAGCTGC  
CCTGAACCAGGCCCTGGAGATGAAGCGCCAGGGCAAGCGGGAAAAAGCCAAAAGCTCTTCAT  
GCACGCCCTCAAGATGGACCCGGACTTCGTGGACGCGCTCACCGAGTTTGGCATCTTCTCGGA  
AGAAGACAAGGACATCATCCAGGCGGACTACTTGTACACCAGAGCATTGACCATCTCACCTA  
CCATGAGAAAGCACTGGTCAACCGCGATCGGACACTGCCTCTTGTGGAAGAGATCGACCAGAG  
GTATTTACGATCATCGACAGCAAAGTGAAGAAGGTCATGTCCATCCCCAAGGGGAACCTCAGC  
TCTGCGCAGGGTCATGGAGGAGACCTACTACCATCACATCTACCACACAGTGGCCATCGAGGG  
CAACACCCTCACCTCTCGGAAATCAGGCACATCCTGGAGACCCGCTACGCCGTGCCCGGGAA  
GAGCCTGGAGGAGCAGAACGAGGTCATAGGCATGCATGCAGCCATGAAGTACATCAACACGAC  
TCTGGTTTCGCGCATCGGCTCCGTCACCATCAGCGACGTGCTGGAGATCCACAGGCGGGTGCT  
GGGCTACGTGGACCCCGTGGAAGCCGGCAGGTTTCGGACAACACAGGTCCTGGTCGGACACCA  
CATCCCTCCCCATCCGCAGGATGTGGAAAAGCAGATGCAGGAGTTTGTACAGTGGCTCAACTCC  
GAGGAAGCCATGAACCTGCACCCAGTGGAGTTTGCAGCCTTAGCCCATTTATAAACTCGTTTAC  
ATCCACCCTTTTATTGATGGCAACGGGAGGACCTCCCGTCTGCTCATGAACCTCATCCTCATG  
CAGGCGGGCTACCCGCCCATCACCATCCGCAAGGAGCAGCGGTCCGACTACTACCACGTGTTG  
GAAGCTGCCAACGAGGGCGACGTGAGGCCTTTTATTTCGCTTCATCGCCAAGTGTACTGAGACC  
ACCCTGGACACCCTGCTTTTTGCCACAACCTGAGTACTCGGTGGCACTGCCAGAAGCCCAACCC  
AACCCTCTGGGTTCAAGGAGACGCTTCCTGTGAAGCCCTTAACCCTAGAAATCCTCAGTGACA  
AAGGCTGTCCTGAGGTAGGAAA

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**FIGURE 546**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119517
><subunit 1 of 1, 458 aa, 1 stop
><MW: 51778, pI: 7.81; NX(S/T): 2
MMLIPMASVMAVTEPKWVSVWSRFLWVTLLSMVLGSLALLPLGAVEEQCLAVLKGLYL
LRSKPDRAQHAATKCTSPSTELSITSRGATLLVAKTKASPAGKLEARAALNQALEMKRQG
KREKAQKLFMHALKMDPDFVDALTEFGIFSEEDKDIIQADYLYTRALTISPYHEKALVNR
DRTLPLVEEIDQRYFSIIDSKVKKVMSIPKGNLSALRRVMEETYYHHIYHTVAIEGNTLTL
SEIRHILETRYAVPGKSLEEQNEVIGMHAAMKYINTTLVSRIGSVTISDVLEIHRRVLGY
VDPVEAGRFRFTTQVLVGHHIPHPQDVEKMQQEFVQWLNSEEAMNLHPVEFAALAHYKLV
YIHPFIDGNGRTSRLLMNLILMQAGYPPITIRKEQRSDYYHVLEAANECDVRPFIRFIK
CTETTLDTLLFATTEYSVALPEAQPNSGFKETLPVKP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-46

**N-glycosylation sites:**

Amino acids 275-279;446-450

**Tyrosine kinase phosphorylation sites:**

Amino acids 216-225;217-225;244-232

**N-myristoylation sites:**

Amino acids 35-41;235-241;266-272;368-374

**Amidation site:**

Amino acids 119-123

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**FIGURE 547**

CCTCTGTCTGTGCTCCCATCCCAGGGAGTATAGGTGGAGCCTCCAGAGCCCATGGACAGGGCA  
TGCTGGGGCTGGGCCAGCCCCAGCGGTGTCTCTAAGGCACCCCTGGGATCCCCACTGAGCTGG  
CCTACTTCAGACAGCCAGGGCCCCACCCCTCTGGCCCCCTTAGTGTCCAGCTCGTGGCCCCCTTG  
GCATTTCCACAAGACGCCAAG**ATGG**GAGATTCCCATGGGGACCCAGGGCTGCTTCTCAAAGAGC  
CTCCTGCTCTCAGCCTCAATCCTGGTCTCTGGATGCTCCAAGGCTCCCAGGCAGCTCTCTAC  
ATCCAGAAGATTCCAGAGCAGCCTCAAAAGAACCAGGACCTTCTCCTGTCAGTCCAGGGTGTC  
CCAGACACCTTCCAGGACTTCAACTGGTACCTGGGGGAGGAGACGTACGGAGGCACGAGGGCTA  
TTTACCTACATCCCTGGGATACAACGGCCTCAGAGGGATGGCAGTGCCATGGGACAGCGAGAC  
ATCGTGGGCTTCCCCAATGGTTCCATGCTGCTGCGCCGCGCCAGCCTACAGACAGTGGCACC  
TACCAAGTAGCCATTACCATCAACTCTGAATGGACTATGAAGGCCAAGACTGAGGTCCAGGTA  
GCTGAAAAGAATAAGGAGCTGCCCAGTACACACCTGCCCACCAACGCTGGGATCCTGGCGGCC  
ACCATCATTGGATCTCTTGCTGCCGGGGCCCTTCTCATCAGCTGCATTGCCTATCTCCTGGTG  
ACAAGGAAGTGGAGGGGCCAGAGCCACAGACTGCCTGCTCCGAGGGGCCAGGGATCTCTGTCC  
ATCTTGCTGCTCGGCTGTATCCCCAGTGCCTTCAGTGACGCCAGCACATGGATGGCGACCACA  
GAGAAGCCAGAATTGGGGCCCTGCTCATGATGCTGGTGACAACAACATCTATGAAGTGATGCCC  
TCTCCAGTCCTCCTGGTGTCCCCCATCAGTGACACAAGGTCCATAAACCCAGCCCCGGCCCCCTG  
CCCACACCCCCACACCTGCAGGCGGAGCCAGAGAACCACCAGTACCAGCAGGACCTGCTAAAC  
CCCGACCCTGCCCCCTACTGCCAGCTGGTGCCAACTTCC**TGAT**GGGTCTGGGCCAGGCCAGC  
CAGGGAGAAGACAAGGCCCCAGCCCTCCTCTGGGAGCCTCACACCTGAGACCAGCAGGACAAG  
GCCATTGGGGGCTGTGGGGCCGATGAGGTGGACTCAGCCAAAGACTCAGCAGCACATGGGGCA  
GGTGTCTTGGCAGGGGGACAGGAGACTGTAAACAGGCCCCAGGTCCTTGTGCAGCCCCCTGAATGC  
ACGCCCCGCTTTCGGTCTGTTCCCTTCAAGCAAGCTGGCCTGGGCCATGTGCCTGTGAAAGGCAG  
GCTCTGGCCCCCTTTCATGCCAAAGTCCCCAAGATCTGGATATCTGGGGACAAGATGGTGGC  
CTCAGGCCTGCCTCCCAGGCAGTTGGCTGGGCTCCCAACTGTCTGTCTCAATGCCCTACCCC  
AACTCCACTAGTGACCCTCAGAGTCTTCTCCCCTTAGGACAAGGCAGACACCCACCATGCGG  
GCCTCAGGTGGCAGAGAGGGCCAGCCTCACAGGCCTGTGGCCCCACACACCAGTCCCAGCAAG  
GTGACCACGGCTGCTGGACCCCTTCCCTGTTTCAGGCAGGCCCCAGCCCCCTCTCAGAACCTGCTG  
CCAGCTGCTGGTCTTGGCCCCCACCTGAATCTTACTGAGTCCCTCTGGGCAGCAGCTCCCTT  
CTCCACCCACCCAGCACCCGTCCCAATGTGGCCTCAGCTTGTCTCCCCCTTCCCCAAACT  
ATGCATTCAATCAGCAATAAATGAGCCTTTGCTGCA

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**FIGURE 548**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119535  
><subunit 1 of 1, 300 aa, 1 stop  
><MW: 32638, pI: 6.02, NX(S/T): 1  
MEIPMGTQGCFSKSLLLSASILVLWMLQGSQAALYIQKIPEQPQKNQDLLLLSVQGVPDF  
QDFNWYLGEETYGGTRLFTYIPGIQRPQRDGSAMGQRDIVGFPNGSMLLRRRAQPTDSGT  
QVAITINSEWTMKAKTEVQVAEKNKELPSTHLPTNAGILAATIIIGSLAAGALLISCIAYL  
LVTRNWRGQSHRLPAPRGQGSLSILCSAVSPVPSVTPSTWMATTEKPELGPAGDAGDNNI  
YEVMPSPVLLVSPISDTRSINPARPLPTPPHLQAEPENHQYQQDLLNPDPAPYCQLVPTS

**Important features of the protein:****Signal peptide:**

Amino acids 1-32

**Transmembrane domain:**

Amino acids 159-178

**N-glycosylation site:**

Amino acids 104-108

**N-myristoylation sites:**

Amino acids 6-12;29-35;55-61;91-97;157-163;165-171

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**FIGURE 549**

GCCACTCACACCATCTGCTAATGGGACAGCTCACTCTTCCCTCCAAACCATGGCCTTGGCTCA  
AGAGCTTCCTTGTTTCTGGAATGTTCTTTCCCTCCAGCTCCAGGTGTTGAAATTCTGCCTGGTC  
TGGGTCTCCTGTTGAAGGACGCCCTCCACTGGGAAGGATCCTCTTGCCTTACCACCTTGTCTT  
CACCAGCCCCCTGCTCCCCCTCTTCTCTTGGGGCTGTTGTCGTTGTTGATACTTTTTTTTTTGT  
GTGTTTGACACACATCTTCTTCTCACCCTCTAACACAGTTCTCAACCACAGCACTTTTGTCCC  
TGGAGATGTTGGCAGTGTCCAGAGGCGTGTTGATGGTCCCACTGGGGTGGGGGTGCTGCTGGCA  
CCAGATGGTAGGGAGATGCCAGGGGTGCTGCTCCACACCCTATGGGACACTGCACAGTACACC  
TGGCCTGTGTCCCCCACAGCGAGAGCTGGCCCTGGGCAGGCGTGGTCCCTGCGGTGTGTGTTG  
GTTGGGATCCTCCACAGTGACAGACGGTGCGCTCTGCCCACGTTTCCACACAGCTCTTTTGCT  
TGTGGAGCTCACCCTTTGTCAGAGAGCTCATTTCCCTGCGGTCTTTGGCCTGCAGAAGTAAAA  
**TG**AGGGGTGGTGAATTACACCCTGCTGGTTACACATGGAAACTCAGGAGTGAGAATTTTGT  
GGAGAGCAAGAGAGGTGAGACTGGGGTGCTGGCTGCCAGCCAGGCGGTCCCTCAGCCCCCTGGA  
GAAGCGGGGTGGGGCCTGCACACCGAGTCTTCCAGTGAGTCCAGTGATGCTCTCTCTCTC  
CTCCAGTCACTTTCTCTCCAGTGCCACTACTGCGCTTTCGATGCAGAATAATTCAGTATTT  
GGCGACTTGAAGTCGGACGAGATGGAGCTGCTCTACTCAGCCTACGGAGATGAGACAGGCGTG  
CAGTGTGCGCTGAGCCTGCAGGAGTTTGTGAAGGATGCTGGGAGCTACAGCAAGAAAGTGGTG  
GACGACCTCCTGGACCAGATCACAGGCGGAGACCACTCTAGGACGCTCTTCCAGCTGAAGCAG  
AGAAGAAATGTTCCCATGAAGCCTCCAGATGAAGCCAAGGTTGGGGACACCCTAGGAGACAGC  
AGCAGCTCTGTTCTGGAGTTCATGTGATGAAGTCCTATCCCGACGTTTCTGTGGATATCTCC  
ATGCTCAGCTCTCTGGGGAAGGTGAAGAAGGAGCTGGACCCTGACGACAGCCATTTGAACCTG  
GATGAGACGACGAAGCTCCTGCAGGACCTGCACGAAGCACAGGCGGAGCGCGGCGGCTCTCGG  
CCGTCGTCCAACCTCAGCTCCCTGTCCAACGCCTCCGAGAGGGACCAGCACCACTGGGAAGC  
CCTTCTCGCCTGAGTGTGCGGGAGCAGCCAGAGCTCACCACGACCCCTATGAGTTTCTTCAG  
TCTCCAGAGCCTGCGGCCTCTGCCAAGACCTAACTCTAGACCACCTTCAGCTCTTTTATTTTA  
TTTTTTTAGTTTTATTTTGCACGTGTAGAGTTTTTGTCTATCAGACAAGGACTTTGATCCTGTC  
CCCTTTGGCATGCGGGAAGCAGCCGCGGGGAGGTAATGAATTGTCTGTGGTATCATGTCTAGCA  
GAGTCTCCAAGCCCCACGAACCCTGAGGAGTGGAGTCATACGCGAAGGCCATATGGCCATCGT  
GTCAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGGAGTCATACACGAAG  
GGCGTGTGGCCATCGTGTGTCAGCAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGG  
AGTCATACGCGAAGGGTGTGTGGCCAGGCTGCAGAGCTGCGTGCCGTTTGTGTCCGAGCATCA  
CGTGTGGCTCCAGCCCTTGTTTCTGCCAGTGTAGACACCTCTGTCTGCCCCACTGTCTGGGG  
TCGCTCTTGGGAGGCACAGGCATGGGTGTGTCTGGCCTCATTCTGTATCAGTCCAGTGTGTTT  
CTGTATAGTTTTGTGTCTCCAGGCAGGCCATGGTAGGGGCCTCGCAGGGGCCATTGGGGAGC  
ACAGGGCCAGGCTGGGGTGAGGAGAGCTCCCCTGTTTTCTGTTTAATTGATGAGCCTGGGAAA  
GGAGTGTGTTCTGCCTGCCCGTTACAGTGGAGCGTTCCGTGTCCATAAAACGTTTTCTAACTG  
GGAA

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**FIGURE 550**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119537  
><subunit 1 of 1, 104 aa, 1 stop  
><MW: 11136, pI: 8.20, NX(S/T): 0  
MLAVSRGVLMVPLGLGVLLAPDGREMPGVLLHTLWDTAQYTWPVSP TARAGPGQAWSLRC  
VLVGILHSDRRCALPTFPHSSFACGAHPFAESSFPCGLWPAEVK

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**N-myristoylation sites:**

Amino acids 53-59;64-70;97-103

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 74-85

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**FIGURE 551**

CGCCCTTAGCATGGGTTTCTGCCGACGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCAT  
GACCTGGCCCTGGGTACCTTGCCTGCCCTTCTACCTGTGAGCTCCAGCCCCACGGCCTGGTGAAGTGAAGTGA  
GCTGTTCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTACCAGCCCTTCTCTTGTCTCTC  
CAACCGCATCCACCACCTCCATGATTCTGACTTTGCCACCTGCCAGCCTGCGGCATCTCAACCTCAAGTGGAA  
CTGCCCCGCGGTTGGCCTCAGCCCCATGCACTTCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGT  
GCCACCCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATC  
CCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCTCT  
ATTCATGGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGG  
CCTGGGCAGCCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGGCCGCAACCTGCCTTCCAGCCT  
GGAGTATCTGCTGTTGTCTTACAACCGCATCGTCAAACCTGGCGCCTGAGGACCTGGCCAACTGACCCGCCCTGCG  
TGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACACGCTCCCAACCCCTGCATGGAGTGCCTCGTCACTT  
CCCCAGCTACATCCCAGATACCTTCAAGCCCTGAGCCGCTTGAAGGCTGGTGTGAAGGACAGTTCTCTCTC  
CTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCTCTACAA  
ATGCATCACTAAAACCAAGGCCCTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCTTCAATTACCAAAA  
GAGGGTGTCTTTGCCACCTGTCTCTGGCCCCCTTCTTCGGGAGCCTGGTCCGCCCTGAAGGAGCTGGACATGCA  
CGGCATCTTCTTCCGCTCACTCGATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGTCCAGACTCTGCG  
TCTGCAGATGAAGTTCATCAACAGGCCAGCTCGGCATCTTCAAGGCTTCCCTGGCCTGCGCTACGTGGACCT  
GTCCGACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTG  
GCTGCAGCCTGGGGACCTTGTCTCCGGCCCCAGTGGACACTCCAGCTCTGAAGACTTCAGGCCCCAAGTGCAGCAC  
CCTCAACTTCACTTGGATCTGTACGGAACAACCTGGTGACCGTGCAGCCGAGATGTTTGGCCAGCTCTCGCA  
CCTGCAGTGCTGCGCCTGAGCCACAACCTGCATCTCGCAGGCAGTCAATGGCTCCAGTTCCTGCCGCTGACCGG  
TCTGCAGGTGTAGACCTGTCCACAATAAGCTGGACCTTACCACGAGCACTATTACGGAGCTACCACGACT  
GGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGACGGGCGTGGGCCACAACCTCAGCTTCGTGGC  
TCACCTGCGCACCCCTGCGCCACCTCAGCCTGGCCCAACAACATCCACAGCCAAGTGTCCAGCAGCTCTGCAG  
TACGTGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCA  
CTTCTTCCAAGGCTGAGCGGTTTGATCTGGCTGGACTTGTCCAGAACCGCCTGCACACCCCTCCTGCCCCAAAC  
CCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAG  
CCTCCACTTCTGCCCCAACTGGAAGTCTCGACCTGGCAGGAAACAGCTGAAGGCCCTGACCAATGGCAGCCT  
GCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTGAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTC  
CAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCC  
CCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCCCTCTGCACTGCGCCTGTGGGGCGGCCCTTATGGA  
CTTCTGCTGGAGGTGACAGGCTGCCGTGCCCGGTCTGCCAGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTCCA  
GGGCCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTTTCGCCCTCTC  
GCTGCTGGCTGTGGCTCTGGGCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGGTACTGCTT  
CCACCTGTGCTGGCTGGCTTCCCTGGCGGGGGCGGCAAGTGGGCGAGATGAGGATGCCCTGCCCTACGATGC  
CTTCGTGGTCTTCGACAAAACGAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGAGCTGGAGGA  
GTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCACTGGCTGCCTGGCAAAACCTCTTTGAGAA  
CCTGTGGGCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCACACGGACCGGGTCACTGGTCTCTT  
GCGCGCCAGCTTCTGCTGGCCAGCAGCGCCTGTGGAGGACCGCAAGGACGTCGTGGTGTGGTGTCTCTGAG  
CCCTGACGGCCGCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCTCTCTGGCCCCA  
CCAGCCCAGTGGTCAGCGCAGCTTCTGGGCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAA  
CCGGAACCTTCTGCCAGGGACCCACGGCCGAATAGCCGTGAGCCGAATCCTGCACGGTGCCACCTC

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**FIGURE 552**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119714
><subunit 1 of 1, 1032 aa, 1 stop
><MW: 115799, pI: 8.61, NX(S/T): 12
MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFMSMAA
PRGNVTSLSSLSSNRIHHLHDSDFAHLPRLHNLKWNCPVGLSPMHFPCHMTIEPSTFL
AVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNIMLMLDSASLAGLHALRFLFMDGNCYY
KNPCRQALEVAPGALLGLGSLTHLSLKYNNLTVVPRNLPSSLEYLLLSYNRIVKLAPEDL
ANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPPDTFSHLSRLEGLVLKDSSLSWLN
ASWFRGLGNLRVLDLSENFYKCI TKTKALQGLTQLRKLNL SFNYQKRVSFAHLSLAPSF
GSLVALKELDMHGIFFRSLDETTLRPLARL PMLQTLRLQMNFINQAQLGIFRAFPGLRYV
DLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLS
RNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHS
FTELPRLEALDLSYNSQPFQMGVGHNF SFVAHLRTLRLHLSLAHNNIHSQVSQQLCSTSL
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWL DLSQNLRLHTLLPQTLRLNLPKSLQVLR
RDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRLRLDVSCNSISFVAPGF
FSKAKELRELNLSANALKTVDSWFGPLASALQILDV SANPLHCACGA AFMDFLLEVQAA
VPGLP SRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPM LHHLCG
WDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVF DKTQSAVADWVYNELRGQLEECRG
RWALRLCLEERDWLP GKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLE
DRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHFF
YNRNFCQGPTAE
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-30

**Transmembrane domain:**

Amino acids 818-835

**N-glycosylation sites:**Amino acids 64-68;129-133;210-214;242-246;300-304;340-344;  
469-473;474-477;513-517;567-571;694-698;731-735**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 347-351

**Tyrosine kinase phosphorylation site:**

Amino acids 863-871

**N-myristoylation sites:**Amino acids 27-33;41-47;63-69;193-199;361-367;409-415;  
563-569;607-613;695-701;794-800;929-935;945-951;  
1010-1016**Amidation site:**

Amino Acids 974-978

**Leucine zipper patterns:**

Amino acids 204-226;644-666;814-836



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**FIGURE 553**

GGCGTGGGACGTGCTGCGGCGTCCTAGCTGGCTTACAGGGCGGCGGGGGTGTGTGTCCTCT  
GTTAAGAGTGCTACTCGCCCGGGGTTGATCTGTGCATGCCACTCCTGGGTGAGACGGTGAGGT  
CGGCGTCTGCGAGGACGCGGCGGTGGAGTAGAAGGGCAGCCGGAGACAGGCCCGGCGCCCTT  
CCGAGGCTAGACGGCCCCAGCTTCGCGGGGATC**ATGGC**ATTGCTGGTGGACCGAGTGCGGGGC  
CACTGGCGAATCGCCCGCGGGCTCCTGTTCAACCTGCTGGTGTCCATCTGCATTGTGTTCCCTC  
AACAAATGGATTTATGTGTACCACGGCTTCCCCAACATGAGCCTGACCCTGGTGCACCTTCGTG  
GTCACCTGGCTGGGCTTGTATATCTGCCAGAAGCTGGACATCTTTGCCCCCAAAGTCTGCCG  
CCCTCCAGGCTCCTCCTCCTGGCCCTCAGCTTCTGTGGCTTTGTGGTCTTCACTAACCTTTCT  
CTGCAGAACAAACACCATAGGCACCTATCAGCTGGCCAAGGCCATGACCACGCCGGTGATCATA  
GCCATCCAGACCTTCTGCTACCAGAAAACCTTCTCCACCAGAATCCAGCTCACGCTGATTCCCT  
ATAACTTTAGGTGTAATCCTAAATTCTTATTACGATGTGAAGTTTAATTTCTTGGAAATGGTG  
TTTGCTGCTCTTGGTGTTTTAGTTACATCCCTTTATCAAGTGTGGGTAGGAGCCAAACAGCAT  
GAATTACAAGTGAACCTCAATGCAGCTGCTGTACTACCAGGCTCCGATGTCATCTGCCATGTTG  
CTGGTTGCTGTGCCCTTCTTTGAGCCAGTGTTTGGAGAAGGAGGAATATTTGGTCCCTGGTCA  
GTTTCTGCTTTGCTTATGGTGCTGCTATCTGGAGTAATAGCTTTCATGGTGAACCTTATCAATT  
TATTGGATCATTGGGAACACTTCACCTGTCACCTATAACATGTTCCGGACACTTCAAGTTCTGC  
ATTACTTTATTCCGAGGATATGTTTTATTTAAGGATCCACTGTCCATTAATCAGGCCCTTGGC  
ATTTTATGTACATTATTTGGCATTCTCGCCTATACCCACTTTAAGCTCAGTGAACAGGAAGGA  
AGTAGGAGTAAACTGGCACAACGTCCT**TAA**TGGGTTTTTGTGGAGAAAAGAATGTTGTCCCA  
AGAAGATAAAAAATATTGTTAAGTGTGCAAGTTATTA

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**FIGURE 554**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125170
><subunit 1 of 1, 313 aa, 1 stop
><MW: 35066, pI: 9.39, NX(S/T): 5
MALLVDRVRGHWRIAAGLLFNLLVSICIVFLNKWIYVYHGFNMSLTLVHFVVTWLGLYI
CQKLDIFAPKSLPPSRLLLLALSFCGFVFTNLSLQNNNTIGTYQLAKAMTTPVIIAIQTF
CYQKTFSTRIQLTLIPITLGVILNSYYDVKFNFLGMVFAALGVLVTSLYQVWVGAKQHEL
QVNSMQLLYYQAPMSSAMLLVAVPFFEPVFGEGGIFGPWSVSALLMVLLSGVIAFMVNLS
IYWIIGNTSPVTYNMFGHFKFCITLFGGYVLFKDPLSINQALGILCTLFGILAYTHFKLS
EQEGSRSKLAQRP
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-27

**Transmembrane domains:**

Amino acids 46-60;75-90;153-167;192-208;221-237

**N-glycosylation sites:**

Amino acids 43-47;92-96;97-101;238-242

**N-myristoylation sites:**

Amino acids 17-23;57-63;140-146;155-161;162-168;283-289

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**FIGURE 555**

GTTAGGCAGAGCCAAGGTGGTTGCAGACCTGGAATCAGAACAGCTTTTAGACCAACCTGAAAG  
CAGGAATGTAAGCACTGTTTACAGAGATTTTCGTCTTTGGCTTATTGTGCCTGCAGAGTCTAG  
TGCTTCTTTGCCAGCTGTGCTGACTCAGCACTCC**ATGC**CTGTTTTCTGGAACCAAGTCCCTGGA  
GCTGGGCCATGTTTTGATTGACAGTGTGGAGCTAGCCCAGCAAGTACTCTACATGCAACCCCC  
CACCCAGGCACTACCTCTGCTCCTCCTCCATGGCCTCCTGCTACACCGGCAGCTCTATGGAAC  
AAGGCTGCAGGCACACAGGGGGCGCTGGAGTCAAGTGACTCTAACCCAGGTTCTTCAGACCCA  
AGACCAGCTGTGGGCAAGTCTTAGCAATCCCCGTGCTGCCATGCAAGAGCTGGCTGCTTCAGT  
TTTCTACGGGGGTCTCTGGGGGACACTGAGGACAGGGAGGCCCTGATTAGCCTCACACAAGC  
CTGCCTGAGCCCCAGTAGTGGGAGCTGGGTCCAGCCACACACACCTCAGTCTTTGCTGGCCAC  
GCTCATGCCCTCCCAGCTAAGGGAGCTGGATGCAATGGCAGAGTGCAAGGCCCAAGATGCACC  
TACTGCCCTCACCACC**TGA**ACCCCCGGCTCTGCGGACTGAGTGAGGGCCCCCAAGCCTGGCTGT  
TGCGACGCCAGAGTCGCGCTCTCTTGAGTGCGCTGCAGCGGAGTTACCCGTGTGGGTTCCCTG  
AGTCTCGAAGAGGCGCCAGCTTGCGGAAAGGCGACTGCGGCAACGCCTAGTGCAAGTCAACCG  
GAGGCTGGAGTCACTGCAGGATCTGCTGACCCACGTGATTGCGCAAGACGAGTCCGACGCCCC  
GTGGTCAGTGCTGGGGCCAAATGCACGGCGGCCCTCTGGAGGGCGTCTTAGAGACCGAGGCTCT  
AGAACTGAGCCAGTTGGTGGGCACGCTACAACGCGACCTTGATTGCCTGTTGCAGCAGCTGAA  
GGGCGCACCCCCGTGCCCCCTCCCGCCGCTGTGCTGCGGTGGCCCACGCTCTCTGGAAGTGGCCG  
CCTACCCTTGCTTGGCGACCTCATGCGCCGGCCGGTCCGCAGCCGCCCTGGCACTGGCTGCG  
ACAGTTGTGCGCCCGTGGGCAACTGTTGGTTCGTTACTTGGGCGTGGGCGCGGACGCGAGCAG  
TGATGTACCAGAGCGCGTCTTCCACCTGTCAGCCTTTCGCCACCCGCGCCGCTGCTGCTGGC  
ATTGCGTGGGGAAGCTGCCCTGGACCAGAATGTGCCAGCTCGAATTTCCCTGGTAGCCGAGG  
CTCGGTCTCCAGTCAGCTCCAGTATAAACGTCTGGAGATGAACAGCAACCTCTGCACTTCAG  
GGTGGAGAATGGTCCAAATCCCACGGTTCAGAGAGAGGGCTGCTGCTGATCGGGCTACAGGT  
CCTACATGCGGAGTGGGACCCAATAGCTGGAGCCTTGCAAGGACAGTCCTTCCAGCCAACCCAG  
CCCTCTGCCTCCCGTCAGCATCAGCACACAGGCCCCGGGCACCAAGTGACCTGCCAGCCCCAGC  
CGACCTGACTGTGTACTCGTGTCTGTGTACATGGGAGGGCCCCCTTGGCACCCGCTAAGCTGCA  
GAGCAGGAACATCGTGATGCATCTGCCTTTACCCACCAAGCTCACCCCCAACACCTGTGTCCA  
AAGGAGGGTCCATGTGTGCAGCCCACCCCTGTCTTGAGCCCGTCTACCAAAATAAAGTTGTAG  
TGATTCCA

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**FIGURE 556**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129594
><subunit 1 of 1, 162 aa, 1 stop
><MW: 17598, pI: 6.58, NX(S/T): 1
MPVFWNQSLELGHVLIDSVELAQQVLYMQPPTQALPLLLHGLLLHRQLYGTRLQAHGR
WSQVTLTQVLQTQDQLWASLSNPRAAMQELAASVFYGGPLGDTEDREALISLTQACLSPS
SGSWVQPHTPQSLLATLMPLPAKGAGCNGRVQGPDAPTALT
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-45

**N-glycosylation site:**

Amino acids 6-10

**N-myristoylation sites:**

Amino acids 97-103;144-150

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**FIGURE 557**

GACCTTGAGCCCTCGAAAGCGACATGGCGGTTCTCTTAAAGCTGGGCGTTCTCTGCAGTGGCC  
AAGGAGCTCGAGCTCTCCTACTCCGAAGCCGGGTGGTCAGACCCGCTTATGTGTCAGCATTTC  
TCCAGGACCAGCCTACCCAAGGACGGTGTGGTACCCAGCACATTACCTGTACCAAGCCACC  
ACTCTGGTTCCAAGGCTGCATCTCTCCACTGGACCAGTGAGAGGGTTGTCAGTGTTCCTGCTCT  
TGGGGCTGATCCCTGCTGGGTACTTGAATCCCTGCTCTGTGGTGGACTACTCTCTGGCTGCAG  
CCCTCACCCCTGCACAGTCACTGGGGCCTTGGACAAGTGGTTACCGACTACGTTTCATGGGGACA  
CCCTGCCGAAGGCTGCCAGGGCAGGCCCTTGGCACTCTCAGCTTTGACCTTTGCTGGGCTTTGC  
TACTTCAATTACCACGATGTCGGCATCTGCAGAGCGGTTGCCATGCTGTGGAAGCTCTTGACCT  
GGGTGCAGCACTTTGATTGTGTGCCTCCTTGCCTCTGCTTTACCAATGCCGTTACCTCGCAG  
TGAGGGGGGATGAAGGATAAGCCCATTGGTGGGCAGAATGTCTTCTAATTACATGGTTATTTT  
CAGAATTTATTTGTTGAGGAAGAGGTTTGAGGAGTTAGGTTTCGACCATTTCGTGAGTCTGTGTT  
CCATACTCCACTGAGTGTGGGCACTAGCTCACAGCCTCGCGGTGAGACTGAACATTTTCATGAG  
CTCATGTTGCCTTTGACCACCATTTCTTAAGGAGAGCCAGCTGATTGCTGTCAGGATAAGAGC  
ATCTCTTCAGCCAGGAGGGAGGCCTGTTCCCTCCTGAGTTAGACTTTGCATGAAGCTCGAAAG  
TATTCCTTTTGGAACCTCCCATTCTTGTTTCAGGTGACACCAGCTCTGTTGATGGCTCTGCTTC  
TAGGGAACATTTAATCAGGAGATGCTCTCAATGACTAATTTGTCTAAGTCTTAGGAAGGAGGT  
TGAGGAAAGCTGGATTTAGACAAGTTCAATTTAGGGAGTTCTCCTTGTGTTGTGGATTAAAATA  
TGACAGATTGCAAACAGACTACTCTTCAAATGTATCTCAATTGTGCAGAAGTGAGCTGTCCAA  
AAGTATAAGACTAAGTGATAAACTGTCTTCCCACCGTGGGAGTTGTTAATGAGAAAGAAAGTG  
TACTCTGAAAAACAAGGGGG

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**FIGURE 558**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129793
><subunit 1 of 1, 159 aa, 1 stop
><MW: 17014, pI: 9.38, NX(S/T): 0
MAVLLKLGVLCSGQGARALLRSRVVRPAYVSAFLQDQPTQGRCGTQHIHLSPSHHSGSK
AASLHWTSERVVSVLLGLIPAGYLNPCSVVDYSLAAATLHSHWGLGQVVTDYVHGDTL
PKAARAGLLALSALTFAGLCYFNYHVDVGICRAVAMLWKL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-15

**Transmembrane domains:**

Amino acids 71-88;126-140

**Glycosaminoglycan attachment site:**

Amino acids 12-16

**N-myristoylation sites**

Amino acids 8-14;58-64;78-84;108-114;148-154

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**FIGURE 559**

CCCAGCCCCGCGTTTCGGCTGCTCTCGAGGAGGCCGGAGTCCCCGGAGACGATGCGCCCCGCGC  
AGCCGCCTGCGCCTGCGGGAGCCGGCTGCCCTTGAGATGGAGTTGCTGCCTCTTTGGCTCTGC  
CTGGGTTTTTCACTTCCTGACCGTGGGCTGGAGGAACAGAAGCGGAACAGCCACAGCAGCCTCC  
CAAGGAGTCTGCAAGTTGGTGGGTGGAGCCGCTGACTGCCGAGGGCAGAGCCTCGCTTCGGTG  
CCCAGCAGCCTCCCGCCCCACGCCCCGGATGCTCACCTGGATGCCAACCTCTCAAGACCCTG  
TGGAATCACTCCCTCCAGCCTTACCCTCTCCTGGAGAGCCTCAGCCTGCACAGCTGCCACCTG  
GAGCGCATCAGCCGCGGCGCCTTCCAGGAGCAAGGTCACCTGCGCAGCCTGGTCCTGGGGGAC  
AACTGCCTCTCAGAGAACTACGAAGAGACGGCAGCCGCCCTCCACGCCCTGCCGGGCTGCGG  
AGGCTGGACTTGTTCAGGAAACGCCCTGACGGAGGACATGGCAGCGCTCATGCTCCAGAACCTC  
TCCTCGCTGCGGTCCGTGTCCCTGGCGGGGAACACCATCATGCGGCTGGACGACTCCGTCTTC  
GAGGGCCTGGAGCGTCTCCGGGAGCTGGATCTGCAGAGGAACTACATCTTCGAGATCGAGGGC  
GGCGCTTTCGACGGCCTGGCTGAGCTGAGGCACCTCAACCTGGCCTTCAACAACCTCCCCTGC  
ATCGTGGACTTCGGGCTCACGCGGCTGCGGGTCTCAACGTGAGCTACAACGTCTGGAGTGG  
TTCTCGCGACCGGGGAGAGGCTGCCTTCGAGCTGGAGACGCTGGACCTGTCTCACAACCAG  
CTGCTGTTCTTCCCGCTGCTGCCCCAGTACAGCAAGTTGCGGACCTCCTGCTGCGCGACAAC  
AACATGGGCTTCTACCGGGACCTGTACAACACCTCGTCGCCGAGGGAGATGGTGGCCAGTTC  
CTCCTCGTGGACGGCAACGTGACCAACATCACCACCGTCAGCCTCTGGGAAGAATTCTCCTCC  
AGCGACCTCGCAGATCTCCGCTTCCCTGGACATGAGCCAGAACCAGTTCAGTACCTGCCAGAC  
GGCTTCCTGAGGAAAATGCCTTCCCTCTCCACCTGAACCTCCACCAGAATTGCCTGATGACG  
CTTCACATTCGGGAGCACGAGCCCCCGGAGCGCTCACCGAGCTGGACCTGAGCCACAACCAG  
CTGTGCGGAGCTGCACCTGGCTCCGGGGCTGGCCAGCTGCCTGGGCAGCCTGCGCTTGTTAAAC  
CTGAGCTCCAACGACTCCTGGGCGTCCCCCTGGCCTCTTCGCCAATGCTAGGAACATCACTAC  
ACTTGACATGAGCCACAATCAGATCTCACTTTGTCCCCTGCCAGCTGCCTCGGACCGGGTGGG  
CCCCCTAGCTGTGTGGATTTTCAGGAATATGGCATCTTTAAGGAGCCTGTCTCTGGAGGGCTG  
TGGCCTGGGGGCATTGCCAGACTGCCCAATTCAGGGACCTCCCTGACCTACTTAGACCTCTC  
AAGCAACTGGGGGTTCTGAATGGGAGCCTCGCCCCACTCCAGGATGTTGCCCCCATGTTACA  
GGTCCTGTCTCTCAGGAACATGGGCCTCCACTCCAGCTTTATGGCGTTGGACTTCTCTGGGTT  
TGGGAATCTCAGGGACTTAGATCTGTGCGGGAATTGCTTGACCACCTTCCCAAGGTTTGGGGG  
CAGCCTGGCCCTGGAGACCCTGGATCTCCGTAGAACTCGCTCACAGCCCTTCCCCAGAAGGC  
TGTGTCTGAGCAGCTCTCGAGAGGTCTGCGGACCATCTACCTCAGTCAGAATCCATATGACTG  
CTGTGGGGTGGATGGCTGGGGGGCCCTGCAGCATGGGCAGACGGTGGCCGACTGGGCCATGGT  
CACCTGCAACCTCTCCTCCAAGATCATCCGCGTGACGGAGCTGCCGGAGGTGTGCTCGGGA  
CTGCAAGTGGGAGCGGCTGGACCTGGGCCTGCTCTACCTCGTGCTCATCTCCCCAGCTGCCT  
CACCCTGCTGGTGGCCTGCACTGTCTCATCGTCTCACTTTTAAGAAGCCTCTGCTTCAGGTCAT  
CAAGAGCCGCTGCCACTGGTCCTCCGTTTACTGACCTGGCTGTGTGCCAAGACTCGAAATTCG  
GTCCGCACACAACAGGACACTTTCTCTGCCAGCTTTCAAGATGTGATGCAGAGGCCAAGTCTG  
ACGAATTGAAGTTTCAATTAAATTTAATATGTTTCCATTCTCATCGCCACCCACCCCG  
CCCCACCAACCGCCCAAGTTCTTTTCCATCATTATAATTTCATCCTTATTATCTTGGTAAAT  
ATTTATTAAAGTGACTTTTTCAGAAATAAAAGGCAACGTGTCTCATAAATATTTTTTAAAAAA  
AAAAAAAAAAAAAA

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**FIGURE 560**

><subunit 1 of 1, 692 aa, 1 stop  
><MW: 76366, pI: 6.07, NX(S/T): 11  
MELLPLWLCLGFHFLTVGWRNRSGTATAASQGVCKLVGGAADCRGQSLASVPSSLPPHAR  
MLTLDANPLKTLWNHSLQYPPLLESLSLHSCHLERISRGAFQEQGHLRSLVLGDNCLSEN  
YEETAAALHALPGLRRLDLSGNALTEDMAALMLQNLSSLRSVSLAGNTIMRLDDSVFEG  
ERLRELDLQRNYIFEIEGGAFDGLAELRHLNLA FNNLPCIVDFGLTRLRVLNVSYNVLEW  
FLATGGEAAFELETDLDSHNQLLFFPLLPOYSKLR TLLLRDNNMGFYRDLYNTSSPREMV  
AQFLLVDGNVTNITTVSLWEEFSSSDLADLRFLDMSQNFQYLPDGFLRKMPSSLSHLNLH  
QNCLMTLHIREHEPPGALTELDLSHNQLSELHLAPGLASCLGSLRFLNLSSNQLLGVPPG  
LFANARNITTLDMSHNQISLCPLPAASDRVGPSPCVDFRNMA SLRSLSLEGCGLGALPDC  
PFQGTSLTYLDLSSNWGVLNGSLAPLQDVAPMLQVLSLRNMGLHSSFMALDFSGFGNLRD  
LDLSGNCLTTFFPRFGGSLALETDLRRNSLTALPQKAVSEQLSRGLRTIYLSQNPYDCCG  
VDGWGALQHGQTVADWAMVTCNLSSKIIRVTELPGGVPRDCKWERLDLGLLYLVLI LPSC  
LTLLVACTVIVLTFKKPLLQVIKSRCHWSSVY

**Important features of the protein:****Signal peptide:**

Amino acids 1-18

**Transmembrane domain:**

Amino acids 651-672

**N-glycosylation sites:**Amino acids 21-25;74-78;155-159;232-236;292-296;309-313;  
312-316;408-414;427-431;500-504;622-626**Glycosaminoglycan attachment site:**

Amino acids 533-537

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 566-570

**N-myristoylation sites:**Amino acids 24-30;39-45;45-51;141-147;199-205;245-251;  
308-314;396-402;416-422;420-426;471-477;  
484-490;497-503;522-528;545-551;555-561;610-616**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 657-668

**Leucine zipper patterns:**

Amino acids 48-70;492-514



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**FIGURE 561**

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAAC**AT**  
**GGCT**GCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGG  
CCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTG  
CAGCATGTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGT  
GAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAAC  
TTGGGCTGGAAGTGTTGAACACAGTTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCA  
TAAATACACGGAAGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGG  
AGGAAGAGATGATTTTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGA  
CTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGA  
GGAGTCTCGGGGGCGTGAACCTTGACCCTGTGCCTGAGCCCGAGGCATTCAGAGCTGATTGAGA  
GGATGGAGAAGGTGCTTTCTCAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGA  
GAGCCACCTCACACCAGCGGTCTTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACAC  
TTTTGAAGAAATTCTGCACGATAAATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAG  
TTCTCCTGCCTCGGTGGAGCGGGAGAAGACAGATGCTTACAAAGTCCTGAAAAACAGAAATGAG  
TCAGAGAGGAAGTGGACAGTGCCTTATTACATTACAGCAAAGGATTCGTTGGCATCAAAATCT  
AAGTTTGTTTTACAAAGATTGTTTT**TAG**TACTAAGCTGCCTTGGCAGTTTGCATTTTTGAGCC  
AAACAAAAATATATTATTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 562**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131639
><subunit 1 of 1, 303 aa, 1 stop
><MW: 33900, pI: 4.81, NX(S/T): 2
MAAAPGLLFWLFLVGLALWWVPGQSDL SHGRFSDLKVC GDEEC SMLMYRGK ALEDFTGPD
CRFVNFKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADET
DFVCFEGGRDDFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDPVP
EPEAFRADSEEDGEAFSESTEG LQGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDK
LKVP GSESR TGNSSPASVEREKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNL SLFYK
DCF
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-22

**N-glycosylation site:**

Amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 30-34

**Tyrosine kinase phosphorylation site:**

Amino acids 67-76

**N-myristoylation sites:**

Amino acids 205-211;225-231;277-283

**Amidation site:**

Amino acids 28-32

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**FIGURE 563**

GCCAGCCGTGGGATTAGGCTTCGCCGGCTACGATTGCGGCCCCCATCTTCTGACTTTTCCTCG  
TGTGACCCATCTTTTCAAATTCCTTACCTGAGGAAGGAGCCCGATTACAAGGATATTTACCT  
GCTCCTACCCTGATCTAGGGACGAGGATGGGAAGACCGCCTGTGGCCATGAGCCCTCCCCGGT  
GCTCCTGGGGCTAAGGCTGGGGCTGCAGCCATGGGGCTGGGTCAGCCCCAGGCCTGGTTGCTG  
GGTCTGCCCACAGCTGTGGTCTATGGCTCCCTGGCTCTCTTCACCACCATCCTGCACAATGTC  
TTCCTGCTCTACTATGTGGACACCTTTGTCTCAGTGTACAAGATCAACAAAATGGCCTTCTGG  
GTCGGAGAGACAGTGTTTCTCCTCTGGAACAGCCTCAATGACCCTCTCTTCGGTTGGCTCAGT  
GACCGGCAGTTCCTCAGCTCCCAGCCCCGCCTGTGTGGAGAGGAGCTGCTTGTGGGCAGTGAG  
GAGGCGGACAGCATCACCTTGGGCCGGTATCTCCGGCAGCTGGCACGCCATCGGAACCTTCCTG  
TGGTTCGTGAGCATGGACCTGGTGCAGGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTCGG  
GACGCCAAGGTGGAAAGACCGCTTGAGCCCAGGAGTTCGAGGCTGCAATTGAGTTATGATTGCA  
CCACTGCACTCCAGCCTGGGCGGCAGAGAAAGGCTCCATCTCTAAAAAAGAAGAGCTAAGTG  
CTGTACCTAAAACATGCAGTATATAAACTGGCTGAAGTTAGAAATAAACTGTTTTTCATGTTAT  
GAAAA

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**FIGURE 564**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131649  
><subunit 1 of 1, 153 aa, 1 stop  
><MW: 17603, pI: 7.42, NX(S/T): 0  
MGLGQPQAWLLGLPTAVVYGSLALFTTILHNVFLLYYVDTFVSVYKINKMAFWVGETVFL  
LWNSLNDPLFGWLSDRQFLSSQPRLCGEELLVGSEEADSITLGRYLRLARHRNFLWFVS  
MDLVQVQWLTPVIPALRDAKVERPLEPRSSRLQ

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**N-myristoylation sites:**

Amino acids 4-10;12-18;93-99

**Leucine zipper pattern:**

Amino acids 102-124

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**FIGURE 565**

CGGCACGAGTAAAATGGAGATAATATCACCATGCACTCAGCCCTAGCCACTGCATTGCTGTTA  
CTGATACCATTACTGCTGCTACGTCGTTTTTTTGATGGCTCAGCCCTTAGGGAAGGGGGATCA  
AGGGAGAAGCCCGGACCTTCCCGCAGGAGGTGGGCTGGGCACAGCCCTGAACCATGGAGGTCA  
CCCACCCTGAGGTCGGGACCTGGGTTCCTTCCCTATCCACTGGGGGTCCCAGCCTTTGTCTTC  
ATCTCTCCAGGTCCCAGCCCTTCACAGTGGGCACTTCCCTGCCTGTGACGGAGGCCCCAGCCA  
TCTCC

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**FIGURE 566**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131652
><subunit 1 of 1, 89 aa, 1 stop
><MW: 9688, pI: 11.49, NX(S/T): 0
MHSALATALLLLIPLLLLRFFDGSALREGGSREKPGPSRRRWAGHSPEPWRSPTLRSGP
GFPSYPLGVPAFVFISPGSPSQWALPCL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-18

**Glycosaminoglycan attachment site:**

Amino acids 58-62

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**FIGURE 567**

AGTCTAGCAGGAAAGGAGAGGGAGCTTTCCCCGAAGACCCTCCTGGACCAGCCCCAGGCTCCT  
GTGCTGGTTGCACGCCAGGGCCTGTACTGACCACCTCCACGTGCCACTGGGGCTGTAAGGAGGA  
**ATG**GCGGCCGTGGGCAGCCTGCTTGGCCTGGCAGCCTCTTCTGGCTAGGGGGCCAGAACGCC  
TCTGACCACAGCCTGTGGCTCCTGAGGAAGCCCCGAGGCTCATCCTGCCCCGGCACGGGTCAC  
CAGCTCTGCCGGCTGAGGCAGAGCACCGTGAAGGCCACCGGACCTGCACTCCGCCGCCTGCAC  
ACATCCTCCTGGCGAGCTGACAGCAGCAGGGCCTCACTCACTCGTGTGCACCGCCAGGCTTAT  
GCACGACTCTACCCCGTGCTGCTGGTGAAGCAGGATGGCTCCACCATCCACATCCGCTACAGG  
GAGCCACGGCGCATGCTGGCGATGCCCATAGATCTGGACACCCTGTCTCCTGAGGAGCGCCGG  
GCCAGGCTGCGGAAGCGTGAGGCTCAGCTCCAGTCGAGGAAGGAGTACGAGCAGGAGCTCAGT  
GATGACTTGCACTGTGGAGCGCTACCGACAGTTCTGGACCAGGACCAAGAAG**TGA**CCGTGGCTC  
CAGCCACCCCGGGACATTGCTAAGATGGGAGGGCTGTTCTTAAATCACTCGTTCTTGAAGCTGC

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**FIGURE 568**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131658
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18903, pI: 11.08, NX(S/T): 1
MAAVGSLGLAASSWLGGQNASDHSLWLLRKPRGSSCPGTGHQLCRLRQSTVKATGPALR
RLHTSSWRADSSRASLTRVHRQAYARLYPVLLVKQDGSTIHIRYREPRMLAMPIDLDTL
SPEERRARLRKREAQLQSRKEYEQELSDDLHVERYRQFWTRTKK
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-18

**N-glycosylation site:**

Amino acids 20-24

**N-myristoylation sites:**

Amino acids 5-11;9-15;17-23;18-24



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**FIGURE 569**

GGTGCCAAGGGTTTCGGGGGGGAGCACTGAGGCTTTAGCAGCTCTCCTGTATCCTCATTTCAT  
CCTCCTGTAGCAGCTGGAAAATTCAGATTACAGGTGAAATTCCTGGCTGGCAATCTTCTGTA  
TATGGACACAGTGATGTGCCAGAAGGGCTTTGCATCCCTGAGACTGAAGGAAGCTCCATTTT  
GGAGCCCTCCACACCTTGCTCTGTGTGCCTCTCATTTCTGATTTGAATTCCTATTTTGTCTATA  
TGATGAAGCTGTAATCCTAAGTTTAAAAAGGGGAGTAGGTATTGACATCATGGTAGAAATAGG  
CTGTCTTATGGAAGCTGTAGTTAGGGATCACAGCCTATTGGACCAGCCCCAGCCTTAGCAGCAG  
TTCTGTACACTGATTCTTCCAGATTAGTCTACGTTCCCTCGAACAGACCTATGCCATGGGTTA  
CAACTACAATTTGTTGTCGATTAGAGTTAACTTACAGACTCTCAAAACCCCATTTCTTGGGTT  
TAGGCAACTTCCAGAAGTAGTCATTTATTTGAATTTTAGTCTAAGATCAACTGAATTAGGGAG  
GTTTGAAAGTGTAAGCAAAATCGTACATTCCCAAACACTTTGTAAAGAAGGAATGGGTAGTG  
TCAACTAAAGGAAATGGTGTGCATCCAGCAAAAGAAAGAGACCGAAAGCAAAGTCATAAACC  
**ATG**CCACAGAGCTCAGCTGTCTGCTCCGTGTCTCTCCATACCCTTGTTGACTGTGCTCATA  
TTAGCCAGAGACCTAAGTGCTCTTGGAGGATGTCCCTGGGGCCCCCTCCCCCTCCGCTGTAC  
TGTCTACTTCTGATCCTCTCTTCTGTGTCAGGAGAGGTCCAGGCCTTCTATGAGGACCTGAGT  
GGCCGGCAGTACGTGAATGAAGTCTTCAACTTCAGCGTGGACAAGCTCTATGACCTCCTCTTC  
ACCAACTCGCCCTTCCAGCGGGATTTTCATGGAGCAGCGGCGCTTCTCTGATATCATCTTCCAT  
CCATGGAAAAAGGAGGAGAATGGAAACCAGAGCCGAGTGATTCTTTACACCATCACCTTACC  
AACCTCTGGCTCCCAAACTGCCACTGTCAGGGAGACACAGACCATGTACAAGGCGAGCCAG  
GAGAGTGAATGTTACGTGATAGATGCCGAAGTCTCACCCACGACGTGCCCTACCACGACTAC  
TTCTACACAATCGCTACACGCTCACCCGTGTGGCTCGGAACAAGAGCCGACTCAGGGTC  
TCCACAGAGCTCGCTATCGAAAACAGCCCTGGGGGTTAGTGAAAACGTTTCATCGAGAAGAAC  
TTCTGGAGTGGGCTGGAGGACTACTTCCGCCATTTAGAGAGCGAGCTGGCCAAAACGGAGAGC  
ACTTATTTGGCTGAGATGCACAGACAATCTCCAAAGAGAAGGCCAGCAAGACTACAACGGTG  
CGGAGGAGGAAGCGTCCCCATGCCCACCTGCGAGTCCCTCACCTGGAAGAGGTGATGAGCCCG  
GTCACCACGCCCACAGATGAGGATGTGGGCCACAGGATCAAACATGTGGCAGGTTCCACACAG  
ACGCGGCATATCCCGGAGGACACCCCCAACGGTTTCCACCTGCAGAGCGTGTCCAAGCTGCTG  
CTGGTTATCAGCTGTGTTCTGGTGCTGCTGGTCATCCTTAACATGATGCTCTTCTACAACTC  
TGGATGTTGGAATACACCACGCAGACCCTCACTGCCTGGCAGGGTCTAAGGCTCCAAGAAAGG  
TTACCCAGTCTCAGACAGAATGGGCCCAGCTCTTAGAGTCCCAACAAAAGTACCACGATACT  
GAGCTCCAAAAATGGAGGGAAATCATCAATCCTCAGTGATGCTCCTTGACCAGATGAAGGAC  
TCGCTCATCAACCTTCAGAACGGCATCAGGTCCCGCGACTACACGTGCGAAAGTGAAGAAAAG  
AGGAATCGCTATCAT**TGACA**AGGCAGGAACAGGGTGGCTGCAAGAGGCCTGTGCAATACATGT  
ACATAGACCATATAAATATATATATATAAATATATATATATACAGAATATAAATATATATATT  
ATATACAGATTTTAAAAAGAGATAATGCCTATGTACCAGGGAGAAGGAGCGGGCCCTCCCGC  
GCCCTGTGCTGGCCGGAGCAGCGTTTTCTTATGGTGGAGCAGCTGAGGAGGGCAGGAACCGCC  
TCTCAGCACCGACCTCCCCTGATCTCCCTCCTCCACCCCTCTGTTCCCCACCCCTTCCCTTGC  
TGGCCATTCTTGGCTTTTAGAAGGGAAATGTTGAGCCAAAGTTATGCCTGCGAAGACCCTAAG  
GTCTCAAAAGAAGTCTTAAGACGGCATTGCTTAAGGTGCTTCATTCCCTAATCCCTTTTGA  
TTTGTTCCTCAAAATAAAAGAGAATCTTTTCTCCCTAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 570**

><subunit 1 of 1, 425 aa, 1 stop  
><MW: 49786, pI: 8.84, NX(S/T): 3  
MPTSSAVLLRVLSIPLLTVLILARDLSALGGCPWGPLPLRCHCLLPDPLFCAGEVQAFYE  
DLSGRQYVNEVFNFSDKLYDLLFTNSPFQORDFMEQRRFSDIIFHPWKKEENGNSQSRVIL  
YTITLTNPLAPKTATVRETQTMKASQSECEYVIDAEVLTHDVPYHDYFYTINRYTLTRV  
ARNKSRLRVSTELRYRKQPWGLVKTFIEKNEFWSGLEDYFRHLESELAKESTYLAEMHRQ  
SPKEKASKTTTVRRRKRPFAHLRVPHLEEVMSPTTPTDEDVGHRIKHVAGSTQTRHIPE  
DTPNGFHLQSVSKLLLVISCVLVLLVILNMMLFYKLWMLEYTTQTLTAWQGLRLQERLPQ  
SQTEWAQLLESQQKYHDTLQKWREIIKSSVMMLLDQMKDSLINLQNGIRSRDYTSESEEEK  
RNRYH

**Important features of the protein:****Signal peptide:**

Amino acids 1-28

**Transmembrane domain:**

Amino acids 312-334

**N-glycosylation sites:**

Amino acids 73-77;114-118;183-187

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 97-101

**Tyrosine kinase phosphorylation sites:**

Amino acids 144-153;188-196

**N-myristoylation sites:**

Amino acids 201-207;291-297

**Leucine zipper pattern:**

325-347

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**FIGURE 571**

GTAGAGAGTGAAGCAGCAAGACTGCAGAGCCTCATCAAGAAGTGTGGAGTGAAGGGAAGGCTTCAGATGGACAAT  
TTGTGTGCTGGGGAAAAAATGGAATGTGCTGCAAATTCCTGTGGATAAGGGTGGACGGCTGCTCTGTCAACTT  
TGACCATTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTGGAAAGGTATGCATCGTGCAGAAGCGAGACAC  
TAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTGCATCGAGAGGGATGAGGTTCCGAATGTTTTCCG  
GGAGCTGCAGATCATGCAAGGGCTGGAGCACCCTTCCTGGTCAATCTGTGGTACTCCTCCAGGATGAGGAGGA  
CATGTTTCATGGTGGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAAATGTGCATTTTCACAGA  
GGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTACCACATCATCCACAG  
AGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACATGTTACATTACAGACTTCAACATAGCGACGGT  
AGTGAAAGGAGCAGAAAGGGCTTCCTCCATGGCTGGCACCAGCCCTACATGGCTCCAGAAGTATTCAGGTGTA  
CATGGACAGAGGCCCCGGATACTCGTACCCTGTGCACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCTGCG  
GGGCTGGAGGCGGTACGAAATCCACTCGGTACGCCCATCGATGAAATCCTTAACATGTTCAAGGTGGAGCGTGT  
CCACTACTCCTCCACGTGGTGCAGGGGATGGTGGCCCTGCTGAGGAAGCTCCTGACCAAGGATCCTGAGAGCCG  
CGTGTCCAGCCTTCATGACATACAGAGCGTGGCCTACTTGGCCGACATGAAGTGGGACGCGGTGTTCAAGAAGGC  
ACTGATGCGCGGCTTTGTGCCAATAAAGGGAGGTTGAAGTGCATCCACATTTGAGCTTGAAGAGATGATTCT  
AGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAAGAACAGATCCAGGGATGGCACAAGGACAGCTG  
CCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCGGAGGAATTATCATATTTCAACAGAGAGAAGCT  
CAGGAGGCAGCAGGGACAGGGCAGCCAGCTCTTGGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCT  
CCAGGACGGGTGCAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGGCCACACTTGTG  
CTGCTCAACAGGACTGCACCTCGTCTCTGCCCTGCCACCCAGAGCCCCCTTTGTGCCCTGATGGTCCCTGTCTC  
ACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGAGCTGGGAAGCCTGGGTTCTGGTCCCATCTCCAT  
GACTGATTACGTGTGACCTCAGACAAGTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTTA  
AACACTTCTGCCCCACTTCAAATTACAAGATTATGGGGAGAACCAATTAGGTAGGAAACATGAAAACTTTGA  
TATTTATAAAATCATTTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCCATTCCCCAAAGCAATCAA  
ACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTAGAGGGCACTTCCGAAAAACACAGCCCTGACAGCAA  
AATAAAGGTCTGATATGTTGGCCCTTCTATGGAACACACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTT  
CATGTGCATTCTCTGGCAGGCCACAGTCCCTCTGAGCTTGTAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC  
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCCTCATTTAAGAAGACTATCCTTACCTTTTAGTTTCAGCAGTCTT  
CACCACCACCATATCCCCAGTGCTGGGATGGCACACAGGTGTCCATTAGATGAGAGTTGGGTGCTGAGCATTG  
GTTACTCCTGCAGAGTGAATCAGCACCCCATCCAAGTGGCCCGAAAGCCAGACCTGCAGCAGAACTCTCCAAC  
TCTCTATCAGCTTTTCAAGGTTTTCTCTCCTGGGAAGGGGTGTAATAATCAGCTTGTGAGATTCTTCTTACAGAGAGT  
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAGAAAGTTTATTTTACAGG  
AGGAAAAATGGGTTTACACAAAAAGCAAACTACATTCTGATCTGCTCAGGGAGAAGCTTGCCTTTGAAGTGAAGA  
TGTTGGGATGAGCAGGGAAAGCTTAGACTTTGGAGTCAGGTTTGTGTTGAGAATCCAGCCCTGCTGGCTACTAAC  
TAACTGGGAGACCTTAGGCAAGCATGCAATCGCTCTGAATGGCAGTTTCCCTCATTTTTTAAACAGGGGATAATAAA  
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTGGATGACTCATAGAAT  
GGCCTTTTTTGTGACATAATCGTCATCATTATTTAGATACTTTCTTCCCTCACTCAGCCAGGTCAGTTTTT  
TGTGCAACAAACCTGTTTAGGATTCTTCAAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTACATCCTGC  
TGAAGTTGCACTGTGTTTTTATTTTTTCACTCACTTCTTCACTTTTTTACATGATTACTCAATCCTTGGG  
GCTGTCCATGTCTCTTAGATTCTTAAAAGACATTTAATGTATGGTTAGGTTTTATATTTTTATTTTTTAA  
AAAAGAAATAGTCAGTGTTCCTCCTTTCAACCGAGACTATTTCTGGATTGTGTGCTCCTCGTCAGTTGACTTGT  
TTTGCACACTTTTCTTTACTTCATGTCCCATCAACACCGTCTGCTCCCCACCTCCCCAGGAAATAAGGGGC  
CTGCTCCTCTCCTACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTATTGGGCTGAGTTCACGAA  
TTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGGTTCTGTTCAAGTTGGCATTCTTGTGTTG  
GAATAAACTATTTCTTGG

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**FIGURE 572**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA136110  
<subunit 1 of 1, 364 aa, 1 stop  
<MW: 42195, pI: 7.40, NX(S/T): 1  
MKYMNKQKCIERDEVNRNRFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGDLRY  
HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV  
VKGAERASSMAGTKPYMAPEVFQVYMDRGPYSGYSPVDWWSLGITAYELLRGWRPYEIHVS  
TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWD  
VFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTDSCPLNGH  
LQHCLETVREEFIIFNREKLRRQGGQGSQLLDTSRGGGQAQSKLQDGCNNLLTHTCTR  
GCSS

**Important features of the protein:****N-glycosylation site:**

Amino acids 285-289

**N-myristoylation sites:**

Amino acids 123-129;290-296;337-343;339-345;348-354

**Serine/Threonine protein kinases active-site signature:**

Amino acids 92-105

**FIGURE 573**

[illegible]

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**FIGURE 574**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139592
><subunit 1 of 1, 882 aa, 1 stop
><MW: 98428, pI: 8.89, NX(S/T): 5
MKHVTVGRNMRGCVSRSCSRQRRPQHHLPSAGPASACAAA VAVSVPATVPPKQLPLHG
QVNICGCPLLEFLLFQLLLLLPLPSRSRKPTQLTLAQLQTVSSAQLYLAPRAPLRHWTH
RRVFYFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCALVPLLGSVPPHPPAPSPCCSG
QTMLKMLSFKLLLLAVALGFFEGDAKFGERNEGSGARRRRCNLGNPPKRLKRRDRRMSQ
LELLSGGEMLCGGFYPRLSCLLSDSPGLGRLENKIFSVTNNTTECGKLEEI KCALCSPH
SQSLFHSPEREVLERDLVLP LCKDYCKEFFYTCTRGHIPGFLQTTADEFCFY YARKDGGL
CFPDFPRKQVRGPASNYLDQMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDG
SQRLFILEKEGYVKILTPEGEIFKEPYLDIHKLVSQGIKGGDERGLLSLAFHPNYKKNKG
LYVSYTTNQERWAIGPHDHILRVVEYTVSRKNPHQVDLRTARVFLEVAELHRKHLGGQLL
FGPDGFLYIIILGDGMITLDDMEEMDGLSDFTGSVLRLDLDVDTMCNVPYSIPRSNPHFNST
NQPPEVFAGHLHDPGRCAVDHRHPTDININLTILCSDSNGKNRSSARILQIIKGKDYSEEP
SLLEFKPFNSGPLVGGFVYRGCQSERLYGSYVFGDRNGNFLTLOQSPVTKQWQEKPLCLG
TSGSCRGYFSGHILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEECRATV
QPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFC RTAKCEPACRHGGVCVRPNKCLCK
KGYLG PQCEQVDRNIRRVTRAGILDQIIDMTSYLLDLTSYIV
```

**Important features of the protein:****Transmembrane domains:**

Amino acids 63-80;186-201

**N-glycosylation sites:**

Amino acids 152-156;281-285;598-602;629-633;641-645

**Glycosaminoglycan attachment site:**

Amino acids 417-421

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 856-860

**N-myristoylation sites:**

Amino acids 12-18;413-419;457-463;698-695;720-726;723-729

**EGF-like domain cysteine pattern signatures:**

Amino acids 805-817;837-849

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**FIGURE 575**

CGGCTCGAGAGCGGGGCAAACCTGCTTGGCACCTCTTCAATAGGTGACATTCAATGATAGATCT  
CTGGCTTCCTGCTCTGTTTGTCTGGTTGCCCTGGAAAGCCTGCTGCTCAGCCCATGCCCCGG  
GACTTCCTCCACCCTCACCAGGACATTCTTTCCATCTCTTGTCTCCTGTGTGCAAGTCCCTTT  
CTCCTGGATTCCATGTCTTGAATGTTTCTTAATTTACTTCCTCATTTTGGCAGAGGATGTCTT  
CCAGTTGTTTTCTGGGAATGCTAATATGCAAGTGAACCAGTGACCTGCAGTTCTGCCACACA  
GGGTTAATAACCAATCAGATTCTCTCTTTTCAAGATGGTTAACATAACAGACACCAAGAAAGG  
GAAGAGGAGCCGACAGCAGAGGGGGAAAGCTGAAAGACGCACAAAGAATGGCCATAAAAGATA  
TGAGCAACCCAGCTTTCCAGACAGTCACTTTTCCAGTGGTCATACCTGGTCTGGAAGATTC  
CCCATCATCTCGAATAAAGCTGTTGTTGCTTTTAACTCCATGGAGAGACCGAATGGAGTGAGC  
CCAGCAGGGCATGCTGGGCAAGAGAGGTCCCCGAGTCCCAAATAAGAATTTCAACTAGTATA  
AAACGAGGCAGCGAACCCACACGTGGAAGTCTGATACCGCTTGCAGAGGGGAATTGAATAGAT  
GTCTCCCTATTGGTAAGGATGTGGTTTTATTGACTTGAAATAACAAAGCCCCGAAGCAACAAC  
TGATCATCCGCGGGATGCTGCCACAAGGAATAATTGAGCACTCATTCAGACACAGGGGAAACC  
ACTGCCTCTTTCAGTCTTCTCCAGATTCCAACAGTCAGTGTTACAGCATTTACACCTTGTTT  
ACCTCCCTGAGAAGACGTTGCAGCTCACTCACCCAGTGGGCACTGGGAGCCTCTGCTCAGGT  
GGGAGACAGATGCCCCCACATGCACATCTGGTGTATGAAGCAGATACTGGGGCTTCATAA  
ACACAGAAGGGGCAGGGAAGTAGCCCCAGGGCATAGTGTGGGGCCTCCTGACTAAAAGTAGCTT  
GCAAACCCCTGCCTATAACAGCCACTTCCCTGGCAGTCATTGTGCCACTTAGGAGCCCTCCTCA  
CCGCTCTTCCCTTAGTTCCCTCACTCTGTATAGACCCTGCCAGAGCAGCTCAGGGTGGAGCAG  
CTGCAGCTTGGGACCTGCTCCAGGCAAGGCCCTATGCTACACAGTCCCTGGGGGTGAGGATT  
CCAGAGGAGTCAATTCCTACCCGCCCTCCAGGGGATGGCCGAGATGAGCGTTCCACAGGG  
AAAGTGAAAGTTGCAAGGCTGTTGCGGAAACACCAGGGGTTCATTTAGGTCTTGCTGCTCAT  
CTCACAGAAAGCCAGTCACTGAGACAAGTATTGTGAGGAAGAAGGCTTTATCCAGGTGCTAC  
AGACAGGGTGAACAAGAGATCAGTCTCAAATCCATCATCAACTGACTAAAATTAGGGGTT  
TATATAGCAGGGAAGAAATGTAACCTACATGTGGGAAAACAGGGATTAACGAGGGGCAAGGAAG  
AGGAGTTGGCCAACAGGCAGCAGGTGGTCACTGGGGAATCATGATGGGTGAGGGGTCTGGCT  
TCTCACTTTCCAGATGTGGGGATCTGGTAAATTTCACTTTCTTGATAACCGTCTGGGAGGATTG  
CTGGCTGGTTTTCTGAGAAAGGAATTCAGATGACATAAATGTAAATTTCTCCTTGGGTTTCAA  
GACTGAGAGGGTCAATTTCTAGGTTTATTCAAGAAAAACCATAAACATCAGTTCTATGGGACA  
ATTGGGCCCATTTCAGGCTCTGAGGATAAGGGTTAATGAGGGGACAGAGTCGCTGAGAGAAG  
TTCACTGGGGCCTACAAGAACTAGAGAGGCTTCCCTGGCAAAGCTCTATGCTGTCTATCCTCT  
CTTCTCTCCTTGAGGAAGATTCCAGTATAATAGACCCGAGGTGAAAAGGCTTTTGTTCAATA  
AGTAGAAAACCTGAAGGGGGGTGGGAGGCACATGGATTTGAACCAGAGACCGCTTGGCCTGCAG  
GCAAATGCTGTACCTTCAGTTGCACCCCTCACTTGTTACAGCTGTTTCTGATAAGCACTTGTG  
CAGCCCCATCAGCACCTCGATTTCTTCTTGGTGAGTCCATGGGAACAGCCCCACTGCAAACAA  
CCCATTCCCTGCTCTCCTCTTCTCTAAACCTCAACCTCCTCTACCTGGCAGTCCACAGGCC  
TACAGCTTCTCCTCAGTGGGAAAGACATCAGCTTGGAAAACCACTTGGAAAGCCAACGTTATC  
CTAGAAAAGCTTTTTTAAATGACCCAGCAGGACAAGTCTCCGGATGGCCTTGGCCAACCCGGTG  
CTTCCCTCTTTTCTTGGTTGTAGTTCTCAGAATAACTAGAGAATGTACTGGGAGTGTTGTCTT  
GAGATAAGGAGGAACCTGTCCTAAACCTGGACTCTGTTCCCATCACACCTAGAACAGGATGTCC  
TGCAACGCTTTAGCCCAATGATCCAAGTTGCCCTTGGGGTATAAACTTGACAGCAGAGGGCG  
TTCAGGGTCCCTCAGCTGCAGTGTGAAGTGGGACACACAGGTGAGACTCCATCTGCCCTGGGC  
AGGTTCCCTGAGCCTTGGGGGACCAGTTCACCCTACATCCCAGGCTTCTGTTGTCCCTTGCTG  
CCTGTAAGGAATAAAGTTGCTTTGCTTA

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**FIGURE 576**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139608
><subunit 1 of 1, 80 aa, 1 stop
><MW: 8927, pI: 3.77, NX(S/T): 0
MIDLWLPALFVLVALESLLLSPCPGTSSTLTRTFFPSLVSCVQVPFSWIPCLECFLIYFL
ILAEDVLQLFSGNANMQVNQ
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-29

**Transmembrane domain:**

Amino acids 47-62

**N-myristoylation sites:**

Amino acids 25-31



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**FIGURE 577**

ATCGGTTAGCGCCTTGCCATGATTAATCCAGAGCTGCGGGATGGCAGAGCTGATGGCTTCATA  
CATCGGATAGTTCCCAAGTTGATACAAAACCTGGAAGATTGGCCTTATGTGCTTCCTGAGTATT  
ATTATTACTACAGTTTGCATTATTATGATAGCCACATGGTCCAAGCATGCTAAACCTGTGGCA  
TGTTTCAGGGGACTGGCTTGGAGTGAGAGATAAGTGTTTCTATTTTCTGATGATACCAGAAAT  
TGGACAGCCAGTAAAATATTTTGTAGTTTGCAGAAAGCAGAACTTGCTCAGATTGATACACAA  
GAAGACATGGAATTTTTGAAGAGGTACGCAGGAACCTGATATGCACTGGATTGGACTAAGCAGG  
AAACAAGGAGATTCTTGGAAATGGACAAATGGCACCACATTCAATGGTTGGCCATCAAACCTCC  
AAATGGTCTTGCAACTGGAGCCTCCGACAATGGCTTCTTCTGCTGGGACCCCTTAGATTAGGCC  
TCTGAGGGAGCTCTGACTGCCGTTTCCCCAAAACAATGTCCCCTGTCAGCAGGAAGCAGTTAA  
ATCAGTCTTCATCCTTATCCTTAATATAACGGCAGTTAGATGTACTTCTTTAGAGGGAGTAAA  
TTTATCAATTCAGAGCAATTCATCCTCCTCTTCCATCTTTGATTACAGTTAATAGGCTATA  
AATTTTGATAATGTAGAATAAACTACAGAAAACCTTCTTG

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**FIGURE 578**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143292
><subunit 1 of 1, 160 aa, 1 stop
><MW: 18576, pI: 9.29, NX(S/T): 3
MINPELRDGRADGFIHRIVPKLIQNWKIGLMCFLSIIITTVCIIMIATWSKHAKPVACSG
DWLGVRDKCFYFSDDTRNWTASKIFCSLQKAELAQIDTQEDMEFLKRYAGTDMHWIGLSR
KQGDSWKWTNGTTFNGWPSNSKWSCNWSLRQWLLLLGPLR
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-42

**N-glycosylation sites:**

Amino acids 78-82;130-134;146-150

**N-myristoylation site:**

Amino acids 131-137

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**FIGURE 579**

TGAAGGCCTGTGAGTGAGGAATGCCTCTCACCAGCTGTGCCTGAGCTGCAGCACTCCAGCCAC  
TGCTGTCTCCTTAGCTGCTCACATATGGATACTTTACAGTTCAGGATTCCACTGCAATGAGC  
TGGTGGAGGAATAATTTCTGGATCATCTTAGCTGTGGCCATCATTGTTGTCTCTGTGGGCCTG  
GGCCTCATCCTGTACTGTGTCTGTAAGTGGCAGCTTAGACGAGGCAAGAAATGGGAAATTGCC  
AAGCCCCCTGAAACACAAGCAAGTAGATGAAGAAAAGATGTATGAGAATGTTCTTAATGAGTCG  
CCAGTTCAATTACCGCCTCTGCCACCGAGGAATTGGCCTTCTCTAGAAGACTCTTCCCCACAG  
GAAGCCCCAAGTCAGCCGCCCGCTACATACTCACTGGTAAATAAAGTTAAAAATAAGAAGACT  
GTTTCCATCCCAAGCTACATTGAGCCTGAAGATGACTATGACGATGTTGAAATCCCTGCAAAT  
ACTGAAAAAGCATCATTTTTGAAACAGCCATTTCTTCTTTTGGCAAACTGAAGAGGGTTCAC  
ACAACCTATTTTAAAACAATCAAGAATGGTTGAACTTCAGTAGGTCTCTGGGCCCTGAAAGCC  
AGTGGTGATTTTATGAAGCTCTATAAGATAAAGCACTTCCCAAACCTTAGATGAAGACACCCC  
TGCGATCGGATGACTGCAGCCAGAGGAGACACATGGGTGCTCGGCTCTGAGGACTTAGAGGGG  
TCAGCCTTGTGCTGTTGAGGAACTTTCCATGGGAAGGACCACGGGGCTCCATGGCTCCCACC  
TGTGGGAACTACTCATTTCTTGGCATTCTTTCCCCCTTCATTCCCTTTGGTTTGCATGGTTC  
TGAGTGATATTAAATCTCAGCATTTGGTTGTGCAAAAAAAAAA

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**FIGURE 580**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144844
><subunit 1 of 1, 145 aa, 1 stop
><MW: 16618, pI: 5.26, NX(S/T): 1
MDTFTVQDSTAMSWWRNFWIILAVAIIVSVGLGLILYCVCKWQLRRGKKWEIAKPLKH
KQVDEEKMYENVLNESPVQLPPLPPRNWPSLEDSSPQEAPSQPPATYSLVNKVKNKKTVS
IPSYIEPEDDYDDVEIPANTEKASF
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-35

**Tyrosine kinase phosphorylation site:**

Amino acids 61-70

**Amidation site:**

Amino acids 48-52

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**FIGURE 581**

GGCCGCCTCCGCGGGGCTGTGGGAAGCTTGGGCTGTCCCAGGACCGTCAGTCTCCTCCTCTGA  
CCCTCCCTTTCCCCTTGTGTGTAGGGCCGCGTCCCACCCCACTCGCCGGAGTCCGGGGCG  
GCCCCGGTGTCCCCTCCGAGCCTGCTGCACTCCACGTCCCCCTACCAGGGCTCCAGCCCCAG  
GGAAATCTCCGACCAGGCCCGCCAGGAGCCAGATCCAGGCTCCTGGAAGAACCATGTCCGGC  
AGCTACTGGTCATGCCAGGCACACACTGCTGCCCAAGAGGAGCTGCTGTTTGAATTATCTGTG  
AATGTTGGGAAGAGGAATGCCAGAGCTGCCGGCTGAAAATTACCCAACCAAGAGAAATCTGCAGG  
**ATG**GACTTTCTGGTCCTCTTCTTGTCTACCTGGCTTCGGTGCTGATGGGTCTTGTTCTTATC  
TGCGTCTGCTCGAAAACCCATAGCTTGAAAGGCCTGGCCAGGGGAGGAGCACAGATATTTTCC  
TGTATAATTCCAGAATGTCTTCAGAGAGCCGTGCATGGATTGCTTCATTACCTTTTCCATACG  
AGAAACCACACCTTCATTGTCCTGCACCTGGTCTTGCAAGGGATGGTTTATACTGAGTACACC  
TGGGAAGTATTTGGCTACTGTCAGGAGCTGGAGTTGTCCTTGCAATTACCTTCTTCTGCCCTAT  
CTGCTGCTAGGTGTAAACCTGTTTTTTTTTCCACCTGACTTGTGGAACCAATCCTGGCATTATA  
ACAAAAGCAAATGAATTATTATTTCTTCATGTTTATGAATTTGATGAAGTGATGTTTCCAAAG  
AACGTGAGGTGCTCTACTTGTGATTTAAGGAAACCAGCTCGATCCAAGCACTGCAGTGTGTGT  
AACTGGTGTGTGCACCGTTTCGACCATCACTGTGTTTGGGTGAACAACTGCATCGGGGCCTGG  
AACATCAGGTACTTCCTCATCTACGTCTTGACCTTGACGGCCTCGGCTGCCACCGTCGCCATT  
GTGAGCACCACCTTTCTGGTCCACTTGGTGGTGATGTCAGATTATACCAGGAGACTTACATC  
GATGACCTTGGACACCTCCATGTTATGGACACGGTCTTTCTTATTACGTACCTGTTCTGACT  
TTTCCACGGATTGTCTTCATGCTGGGCTTTGTCGTGGTTCTGAGCTTCCTCCTGGGTGGCTAC  
CTGTTGTTTGTCTGTATCTGGCGGCCACCAACCAGACTACTAACGAGTGGTACAGAGGTGAC  
TGGGCCTGGTGCCAGCGTTGTCCCCTTGTGGCCTGGCCTCCGTCAGCAGAGCCCCAAGTCCAC  
CGGAACATTCACCTCCCATGGGCTTCGGAGCAACCTTCAAGAGATCTTTCTACCTGCCTTTCCA  
TGTCATGAGAGGAAGAAACAAGAA**TGA**CAAGTGATGACTGCCTTTG

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**FIGURE 582**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144857
><subunit 1 of 1, 344 aa, 1 stop
><MW: 39787, pI: 7.44, NX(S/T): 2
MDFLVFLFLFYLASVLMGLVLICVCSKTHSLKGLARGGAQIFSCIIPECLQRAVHGLLHYL
FHTRNHTFIVLHLVLQGMVYTEYTWEVFGYCQELELSLHYLLLPYLLLGVNLEFFFTLTCTG
TNPGIITKANELLFLHVIYEFDEVMFKNVRCSTCDLRKPARSKHCSVCNWCVHRFDHHCV
WVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTFLVHLVVMSDLYQETYIDDLGHLHVM
DTVFLIQYLFLTFFPRIVFMLGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQR
CPLVAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-29

**Transmembrane domains:**

Amino acids 100-116;201-217;256-275

**N-glycosylation sites:**

Amino acids 65-69;284-290

**N-myristoylation sites:**

Amino acids 32-38;77-83;120-126;322-328

**Cell attachment sequence:**

Amino acids 292-298

**DHHC zinc finger domain:**

Amino acids 140-204

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**FIGURE 583**

CCGCGGAAGTGGCAGGCGTTTCAGAGCGTCAGAGGCTGCGGATGAGCAGACTTGGAGGACTCCAGGCCAGAGACT  
AGGCTGGGCGAAGAGTCGAGCGTGAAGGGGGCTCCGGGCCAGGGTGACAGGAGGCGTGCTTGAGAGGAAGAAGTT  
GACGGGAAGGCCAGTGCGACGGCAAATCTCGTGAACCTTGGGGGACGAATGCTCAGGATGCGGGTCCCCGCCCTC  
CTCGTCTCTCTTCTGCTTCAGAGGGAGAGCAGGCCCGTCCGCTCGCCCCATTTCTGCAACAGCCAGAGGACCTGGTG  
GTGCTGCTGGGGGAGGAAGCCCGCTGCCGTGTGCTCTGGGCGCTACTGGGGGCTAGTTCAGTGGAATAAGAGTGGG  
CTGGCCCTAGGGGGCCAAAGGGACCTACCAGGGTGGTCCCGGTACTGGATATCAGGGAATGCAGCCAATGGCCAG  
CATGACCTCCACATTAGGCCCCGTGGAGCTAGAGGATGAAGCATCATATGAATGTGAGGCTACACAAGCAGGCCCTC  
CGCTCCAGACCAGCCCAACTGCACGTGCTGGTCCCCCAGAAGCCCCCAGGTGCTGGGCGGCCCTCTGTGTCT  
CTGGTTGCTGGAGTTCCTGCGAACCTGACATGTGCGAGCCGTGGGGATGCCCGCCCTACCCCTGAATTGCTGTGG  
TTCCGAGATGGGGTCTGTGGATGGAGCCACCTTTTCATCAGACCTGCTGAAGGAAGGGACCCCTGGGTGAGTG  
GAGAGCACCTTAACCTTGACCCCTTTTCAGCCATGATGATGGAGCCACCTTTGTCTGCCGGGCCGGAGCCAGGCC  
CTGCCCACAGGAAGAGACACAGCTATCACACTGAGCCTGCAGTACCCCCAGAGGTGACTCTGTCTGCTTCGCCA  
CACACTGTGCAGGAGGGAGAGAAGGTCATTTTCTGTGCCAGGCCACAGCCAGCCCTCTGTACAGGCTACAGG  
TGGGCAAAAGGGGCTCTCCGGTGCTCGGGGCCCGGCCAAGGTTAGAGGTCGTGGCAGACGCCTCGTTCTCTG  
ACTGAGCCCGTGTCTGCGAGGTCAGCAACGCCGTGGGTAGCGCCAAACCGCAGTACTGCGCTGGATGTGCTGTT  
GGGCGGATTCTGCAGGCAAAGCCGGAGCCCGTGTCCGTGGACGTGGGGGAAGACGCTTCTTCAGCTGCGCCTGG  
CGCGGAACCCGCTTCCACGGGTAACTGGACCGCGCGGTGGCGCGCAGGTGCTGGGCTCTGGAGCCACACTG  
CGTCTTCCGTGCGTGGGGCCCGAGGACGCGAGGCGACTATGTGTGCGAGAGCTGAGGCTGGGCTATCGGGCCTGCGG  
GGCGCGCGCGGAGGCTCGGCTGACTGTGAACGCTCCCCAGTAGTGACCGCCCTGCACTCTGCGCCTGCCTTC  
CTGAGGGGCCCTGCTCGCCTCCAGTGTCTGGTTTTTCGCTCTCCCGCCAGATGCCGTGGTCTGGTCTTGGGAT  
GAGGGCTTCTGGAGGCGGGTTCGAGGGCCGTTCTGGTGGAGACATTCCTGCCCCAGAGCCGCGGGGGA  
CTGGGTCCGGGCTGATCTCTGTGCTACACATTTCCGGGACCCAGGAGTCTGACTTTAGCAGGAGCTTTAACTGC  
AGTGCCCGGAACCGGCTGGGCGAGGGAGGTGCCAGGCCAGCCTGGGCCGTAGAGACTTGTGCCCACTGTGCGG  
ATAGTGGCCGAGTGGCCGCTGCCACCACAACCTCTCCTTATGGTCATCACTGGGGTGGCCCTCTGCTGCTGGCGC  
CACAGCAAGGCCTCAGCCTCTTTCTCCGAGCAAAAGAACCTGATGCGAATCCCTGGCAGCAGCGACGGCTCCAGT  
TCACGAGGTCCTGAAGAAGAGGAGACAGGCGAGCCGCGAGGACCGGGGCCCATTTGTGCACACTGACCACAGTGAT  
CTGGTTCTGGAGGAGGAAGGGACTCTGGAGACCAAGGACCCAACCAACGGTTACTACAAGGTCCGAGGAGTCAGT  
GTGAGCCTGAGCCTTGGCGAAGCCCTGGAGGAGGTCTCTTCTGCCACCACCCTCCCCCTTGGGCCCCCAGGG  
ACCCCTACCTTCTATGACTTCAACCCACACCTGGGCATGGTCCCCCCTGCAGACTTTACAGAGCCAGGGCAGGC  
TATCTCACCACACCCACCCCTCGAGCTTTCACCAGCTACATCAAACCCACATCCTTTGGGCCCCCAGATCTGGCC  
CCCCGACTCCCCCTTCCCATATGCTGCCTTCCCCACACCTAGCCACCCGCTCTCCAGACTCACGTGTGACAT  
CTTTCCAATGGAAGAGTCTTGGGATCTCCAATTGCCATAATGGATTGTTCTGATTTCTGAGGAGCCAGGACAAG  
TTGGCGACCTTACTCCTCCAAAATGAACACAAGGGGAGGGAAGATCATTACATTTGTGAGGAGCATTTGTATA  
CAGTCAGCTCAGCCAAAGGAGATGCCCCAAGTGGGAGCAACATGGCCACCCAATATGCCCACTATTCGCCGCTG  
TAAAAGAGATTCAAGATGGCAGGTAGGCCCTTTGAGGAGAGATGGGGACAGGGCAGTGGGTGTTGGGAGTTTGGG  
GCCGGGATGGAAGTTGTTTCTAGCCACTGAAAGAAGATATTTCAAGATGACCATCTGCATTGAGAGGAAAGGTAG  
CATAGGATAGATGAAGATGAAGAGCATAACAGGCCCCACCCTGGCTCTCCCTGAGGGGAACCTTTGCTCGGCCAAT  
GGAAATGCAGCCAAGATGGCCATATACTCCCTAGGAACCCAAAATGGCCACCATCTTGATTTTACTTTCTTAA  
GACTCAGAAAGACTTGGACCCAAGGAGTGGGGATACAGTGAGAATTACCACTGTTGGGGCAAAATATTGGGATAA  
AAATATTTATGTTTAAATAATAAAAAAAGTCAAAGAGAAAAAAA

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**FIGURE 584**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145841
><subunit 1 of 1, 708 aa, 1 stop
><MW: 75093, pI: 6.65, NX(S/T): 3
MLRMRVPALLVLLFCFRGRAGPSPHFLQQPEDLVLLGEEARLPCALGAYWGLVQWTKSG
IALGGQRDLPGWSRYWISGNAANGQHDLHIRPVELEDEASYEQATQAGLRSRPAQLHVL
VPPEAPQVLGGPSVSLVAGVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKEG
TPGSVESTLTLPFFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVTLSPHTVQE
GEKVIFLCQATAQPPVTGYRWAKGGSPLVGARGPRLEVADASFLEPVSCEVSNVAGSA
NRSTALDVLFGPILQAKPEPVSVDVGEDASFSCAWRGNPLPRVTWTRRGGAQVLGSGATL
RLPSVGPEDAGDYVCRAEAGLSGLRGAAEARLTVNAPPVVTALHSAPAFLRGPARLQCL
VFASPAPDAVWVSWDEGFLEAGSQGRFLVETFPAPESRGGLGPGGLISVLHISGTQESDFS
RSFNCSARNRLGEGGAQASLGRDILLPTVRIVAGVAAATTTLLMVITGVALCCWRHASKAS
ASFSEQKNLMRIPGSSDGSSSRGPEEEETGSREDRGPVHTDHSDLVLEEEGTLETKDPT
NGYYKVRGVSVSLSLGEAPGGGLFLPPPSPLGPPGTPTFYDFNPHLGMVPPCRLYRARAG
YLTPHPRAFTSYIKPTSEFGPPDLAPGTPFFPYAAFPTPSHPRLQTHV
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**Transmembrane domain:**

Amino acids 511-531

**N-glycosylation sites:**

Amino acids 143-147;301-305;484-488

**N-myristoylation sites:**Amino acids 48-54;60-66;79-85;139-145;180-186;183-189;355-361;383-389;  
387-393;460-466;473-479;494-500;495-501;514-520;528-534;  
554-560;592-598;608-614**Amidation site:**

Amino acids 500-504

**Cell attachment sequence:**

Amino acids 149-152

**Multicopper oxidases signature 1:**

Amino acids 445-466

**Immunoglobulin domain:**

Amino acids 326-377



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**FIGURE 585**

GCCCGCCTGAGGAAGCCGTGTGCCTGGGATGCCAAGAGCCAGAGAATGGATCTTCTCCGAGTG  
GGGACATTGCTGACAATCCCGGCTTCCCGAGGCGGCTAAGAACAGGCAGTTTGTGTGCGGCTGG  
CTGCAGATACCCAGAGGCACAAAGAGACCGAAGCCACCCGGAGGGACCCACGGACGGACAGAT  
GGTAGGCGCGAACCCGAGAGGACCGGCGGAGGCTGAGCACCAGAGAGCCGCCAAGGAAGAGAAA  
CTAACCACAGCCAAGTTACCCCGCCGGCTTTCCTTCGCTGCGCTAAGGAATGAAACCCCTTCCA  
GCTCGATCTGCTCTTCGTCTGCTTCTTCCTCTTCAGTCAAGAGCTGGGCCTCCAGAAGAGAGG  
ATGCTGTCTGGTGCTGGGCTACATGGCCAAGGACAAGTTTCGGAGAATGAATGAAGGCCAAGT  
CTATTCCTTCAGCCAGCAGCCCCAGGACCAGGTGGTGGTGTGCGGACAGCCAGTGACGCTACT  
TTGCGCCATCCCCGAATACGATGGCTTCGTTCTGTGGATCAAGGACGGCTTGGCTCTGGGTGT  
GGGCAGGGACCTCTCAAGTTACCCACAGTACCTGGTGGTAGGGAACCACTGTGAGGGGAGCA  
CCACCTGAAGATCCTGAGGGCAGAGCTGCAAGACGATGCGGTGTACGAGTGCCAGGCCATCCA  
GGCCGCCATCCGCTCCCGCCCCGCACGCCTCACAGTCTGGTGCCGCTGATGACCCCGTCAT  
CCTGGGGGGCCCTGTGATCAGCCTGCGTGCGGGGGACCCCTCTCAACCTCACCTGCCACGCAGA  
CAATGCCAAGCCTGCAGCCTCCATCATCTGGTTGCGAAAGGGAGAGGTCAATGGGGCCAC  
CTATGCCAAGACCCCTGCTTCGGGACGGCAAGCGGGAGAGCATCGTCAGCACCCCTCTTCATCTC  
CCCTGGTGACGTGGAGAATGGCCAGAGCATCGTGTGTGTCGTGCCACCAACAAAGCCATCCCCGG  
AGGAAAGGAGACGTCGGTCACCATTGACATCCAGCACCCCTCCACTGGTCAACCTCTCGGTGGA  
GCCACAGCCAGTGCTGGAGGACAACGTGCTCACTTTCCACTGCTCTGCAAAGGCCAACCCAGC  
TGTCACCCAGTACAGGTGGGCCAAGCGGGCCAGATCATCAAGGAGGCATCTGGAGAGGTGTA  
CAGGACCACAGTGGACTACAGTACTTCTCAGAGCCCCGTCTCCTGTGAGGTGACCAACGCCCTG  
GGCAGCACCAACCTCAGCCGCACGGTTGACGTCTACTTTGGGCCCCGGATGACCACAGAACCC  
CAATCCTTGCTCGTGGATCTGGGCTCTGATGCCATCTTCAGCTGCGCCTGGACCGGCAACCCA  
TCCCTGACCATCGTCTGGATGAAGCGGGGCTCCGGAGTGGTCTTGAGCAATGAGAAGACCCCTG  
ACCCTCAAATCCGTGCGCCAGGAGGACGCGGGCAAGTACGTGTGCCGGGCTGGTGGTCCCCCGT  
GTGGGAGCCGGGGAGAGAGAGGTGACCCTGACCGTCAATGGACCCCCCATCATCTCCAGCACC  
CAGACCCAGCACGCCCTCCACGGCGAGAAGGGCCAGATCAAGTGCTTCATCCGAGACACGCCG  
CCGCCGGACCGCATCGCCTGGTCTTGAAGGAGAACGTTCTGGAGTCGGGCACATCGGGGCGC  
TATACGGTGGAGACCATCAGCACCGAGGAGGGCGTCATCTCCACCCTGACCATCAGCAACATC  
GTGCGGGCCGACTTCCAGACCATCTACAACGACGCGCTGGAACAGCTTCGGCTCCGACACT  
GAGATCATCCGGCTCAAGGAGCAAGGTTTCGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGAG  
TCTGTGCCGATGGCCGTATCATTTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCCTCGTCTTT  
ATGGCAACCATCGTGGCGTTCTGCTGTGCCCCTTCCCAGAGAAGTACGGGAGGGAGATCCGGG  
ATCTCAGGGAGGGGGACAGAGAAAAAGGCCAGGCTTAGGCTGCCCCGGAGAGCAAGTAAGCAG  
GAGTGCAATGAACAGGGGTCC**TAA**CAGTGCTGTGAGCTCCTGGGGCAGGGAGTGGGTCTGATG  
CATCGGTGTATGTGAGCCTGGGCAACATGGCGCCTGGCAGAGTGGGCGCTAGGCTGAGGTTGA  
CCTGGACTAGACTGAACTTCATCTGCAGGGCAGCCAGCATTTTGGATTGAACACATAGCTCTT  
TCAGTCAGGAAGTGTACAGAAAGATAGGGGGAAAAGCGGTTTGTGGTTTGTATCCTTGCTCTAC  
AAGAGCTGTTAGTCTAGAGAGACCCATCTCTACAACAAAATAAAAATAAAGAGCTGCTAGTC  
TCACCAGAAAAGCAGGTCACCTCACACAGCTGTGGGGGAGTGGGTGGGGAAGCAATAAAGGAAT  
TGCTTTGAGAAAACCTTAA

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**FIGURE 586**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA148004
><subunit 1 of 1, 600 aa, 1 stop
><MW: 65308, pI: 8.35, NX(S/T): 5
MKPFQLDLLFVCFLLFSQELGLQKRGCCCLVLGYMAKDKFRRMNEGQVYSFSQQPQDQVVV
SGQPVTLLCAIPEYDGFVLWIKDGLALGVGRDLSSYPQYLVVGNHLSGEHHLKILRAELQ
DDAVECQAIQAAIRSRPARLTVLVPPDDPVILGGPVISLRAGDPLNLTCHADNAKPAAS
IIWLRKGEVINGATYSKTLRLDGKRESIVSTLFIISPGDVENGQSIVCRATNKAIPEGKET
SVTIDIQHPPVLNLSVEPQPVLLEDNVVTFHCSAKANPAVTQYRWAKRGQIIKEASGEVYR
TTVDYTYFSEPVSCVETNALGSTNLSRTVDVYFGPRMTTEPQSLLVDLGSDAIFSCAWTG
NPSLTIVWMKRGSGVVLNNEKTLTLKSVRQEDAGKYVCRAVVPRVGAGEREVTTLTVNGPP
IISSTQTQHALHGEKGQIKCFIRSTPPPDRIAWSKENVLESSTSGRYTVETISTEEGVI
STLTISNIVRADFQTIYNCTAWNSFGSDTEIIRLKEQGSEMKGAGLEAESVPMAVIIGV
AVGAGVAFLVLMATIVAFCCARSQRSTGGRSGISGRGTEKKARLRLPRRASKQECNEQGS
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-17

**Transmembrane domain:**

Amino acids 534-555

**N-glycosylation sites:**

Amino acids 167-171;253-257;324-328;498-502

**Glycosaminoglycan attachment sites:**

Amino acids 523-527;574-578

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 204-208;370-374;588-592

**Tyrosine kinase phosphorylation sites:**

Amino acids 40-49;300-308;389-397

**N-myristoylation sites:**Amino acids 45-51;62-68;84-90;103-109;192-198;236-242;  
374-380;436-442;478-484;539-545;543-549;  
568-574**Amidation site:**

Amino acids 202-206

**Leucine zipper pattern:**

Amino acids 8-30

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**FIGURE 587**

CAAAAAAGGAGCATGTCTTCATCCATGAGAGGCCTCGAAAAATCAATGGTATTTGCATTTCTC  
CCAAGAAGGTTGCTTGCCAAAACCTTTTCGGCCATTTTCTGCTTTCAGAGTGAGACAAAGTTCA  
AAATGACAGTCTGTGAGCTCATTGAAGGCACTAGATACCCTGCCTGCAGGTACCACTATTCCC  
CCACAGAGGGGTTTTGTTCTTGTCACCTGTGATGACTTGAGGCCAGATAGTTTCCTTGGCTATG  
TTAAATAACTCAAGATCAGCTACCGAGTCTGAGATCTCTTCTCTCATGGCATTGGAGCTGGCT  
GTGCCTGAGGCAGACCTGGACCGTGGACATGGGGCAATGCCTTGAGCGGAAGGGGAAGCCACT  
GAATTTTGGGTGTCACCAGGTAAACAGAGCCCTCAGCATCTGAATAGAACTGAACAGGAACA  
GAAGAGATTACACTACATCTGAGATGGAGACCTTTCTCTGCTGCTGCTCAGCCTGGGCCTGG  
TTCTTGCAAGCATCAGAAAGCACAATGAAGATAATTAAGAAGAATTTACAGACGAAGAGA  
TGCAATATGACATGGCAAAAAGTGGCCAAGAAAAACAGACCATTGAGATATTAATGAACCCGA  
TCCTGTTAGTTAAAAATACCAGCCTCAGCATGTCCAAGGATGATATGTCTTCCACATTACTGA  
CATTCAGAAGTTTACATTATAATGACCCCAAGGGAAACAGTTCGGGTAAATGACAAAGAGTGTT  
GCAATGACATGACAGTCTGGAGAAAAGTTTCAGAAGCAAACGGATCGTGCAAGTGGAGCAATA  
ACTTCATCCGCAGCTCCACAGAAGTGATGCGCAGGGTCCACAGGGCCCCCAGCTGCAAGTTTGTA  
CAGAATCCTGGCATAAGCTGCTGTGAGAGCCTAGAACTGGAAAATACAGTGTGCCAGTTCCT  
ACAGGCAAACAATTCCCCAGGTGCCAATACCATAGTGTTACCTCATTAGAGAAGATATTGACA  
GTGCTGACAGGTCAATCTCTGATGAGCTGGTTAGTTTGTGGCTCTAAGTTGTAAATCCACAG  
AGCTTTAGGACTAGGGTCTTACTAAAGAAGGACCTCTTCTTGTTCAATCTTGTTTAAACCTTT  
CCTTAATATCTACTCTTTAGCACTATAGTGAACCTCCTGATTATTTATTCTAACTGGAGGAGTG  
AAAAATCCAAAATTGTGGATAATTCAATTAAGTTATGACTGATACCG

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**FIGURE 588**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149893
><subunit 1 of 1, 199 aa, 1 stop
><MW: 22427, pI: 6.46, NX(S/T): 3
METFPLLLLSLGLVLAEASESTMKIIKEEFTDEEMQYDMAKSGQEKQTIEILMNPILLVK
NTSLSMKDDMSSTLLTFRSLHYNDPKGNSSGNDKECCNDMTVWRKVSEANGSCKWSNNF
IRSSTEVMRRVHRAPSCKFVQNPGISCCESLELENTVCQFTTGKQFPRCQYHSVTSLEKI
LTVLTGHSLSMWLVCGSKL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-16

**N-glycosylation sites:**

Amino acids 61-65;89-93;111-115

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 105-109

**N-myristoylation sites:**

Amino acids 12-18;88-94;144-150

**Microbodies C-terminal targeting signal:**

Amino acids 197-201

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**FIGURE 589**

CAGTCCTGCCGGGACGGTGAGCGCATTTCAGCACCCCTGGACAGCACCGCGGTTGCGCTGCCTCC  
AGGGCGGCCCCGGGCTGCTCCTGCTCCGCAGAGCTACGCCCTCCCCCGGGTGCCCCGGACCC  
TGCACTTGCCGCGCTTTCCTCGCGCTGCTCTGGACCTTGCTAGCCGGCTCTGCACCTCCAG  
AAGCCGTGGGCGCGCCGCTCAGCTGCTCCATCGCCTCACTTTCCAGGCTCGCGCCCGAAGCA  
GAGCCATGAGAACCCAGGGTGCCCTGGCGAGCCGCTAGCGCCATGGGCCCCGGCGAGGCGCTG  
CTGGCGGGTCTCCTGGTGATGGTACTGGCCGTGGCGCTGCTATCCAACGCACTGGTGCTGCTT  
TGTTGCGCCTACAGCGCTGAGCTCCGCACTCGAGCCTCAGGCGTCCTCCTGGTGAATCTGTCT  
CTGGGCCACCTGCTGCTGGCGGGCGCTGGACATGCCCTTCACGCTGCTCGGTGTGATGCGCGGG  
CGGACACCGTCGGCGCCCCGGCGCATGCCAAGTCATTGGCTTCCTGGACACCTTCCTGGCGTCC  
AACGCGGCGCTGAGCGTGGCGGGCGCTGAGCGCAGACCAGTGGCTGGCAGTGGGCTTCCCACTG  
CGCTACGCCGGACGCCTGCGACCGCGCTATGCCGGCCTGCTGCTGGGCTGTGCCTGGGGACAG  
TCGCTGGCCTTCTCAGGCGCTGCACTTGGCTGCTCGTGGCTTGGCTACAGCAGCGCCTTCGCG  
TCCTGTTGCTGCGCCTGCCGCCGAGCCTGAGCGTCCGCGCTTCGCAGCCTTCACCGCCACG  
CTCCATGCCGTGGGCTTCGTGCTGCCGCTGGCGGTGCTCTGCCTCACCTCGCTCCAGGTGCAC  
CGGGTGGCACGCAGACACTGCCAGCGCATGGACACCGTCACCATGAAGGCGCTCGCGCTGCTC  
GCCGACCTGCACCCAGTGTGCGGCAGCGCTGCCTCATCCAGCAGAAGCGGGCGCCGCCACCGC  
GCCACCAGGAAGATTGGCATTGCTATTGCGACCTTCCTCATCTGCTTTGCCCCGTATGTCATG  
ACCAGGCTGGCGGAGCTCGTGCCCTTCGTACCGTGAACGCCCAGTGGGGCATCCTCAGCAAG  
TGCCTGACCTACAGCAAGGCGGTGGCCGACCCGTTACGTA CTCTGCTCCGCCGGCCGTTTC  
CGCCAAGTCCTGGCCGGCATGGTGCACCGGCTGCTGAAGAGAACCCCGCGCCAGCATCCACC  
CATGACAGCTCTCTGGATGTGGCCGGCATGGTGCACCAGCTGCTGAAGAGAACCCCGCGCCCA  
GCGTCCACCCACAACGGCTCTGTGGACACAGAGAATGATTCTGCTGCCTGCAGCAGACACACTTGA  
GGGCTGGCAGGCTCATCGCCCCACCTTCTAAGAAGCCCTGTGGAAAGGGCACTGGCCCTG  
CCACAGAGATGCCACTGGGGACCCCGAGACACCAGTGGCTTGACTTTGAGCTAAGGCTGAG

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**FIGURE 590**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149930
><subunit 1 of 1, 363 aa, 1 stop
><MW: 39332, pI: 10.42, NX(S/T): 3
MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLSLGHLLLAALDM
PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRRLRP
RYAGLLLGCAWGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAAFTATLHAVG
FVLPLAVLCLTSLQVHRVARRHRCQRM DVTMTKALALLADLHPSVRQRCCLIQQKRRRHRAT
RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLLRRP
FRQVLAGMVHRLLLKRTPRPASTHDSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ
QTH
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-24

**Transmembrane domains:**

Amino acids 46-60;85-103;130-150;175-192;246-264

**N-glycosylation sites:**

Amino acids 47-51;348-352;355-359

**Tyrosine kinase phosphorylation site:**

Amino acids 286-295

**N-myristoylation sites:**Amino acids 66-72;124-130;128-134;132-138;139-145;244-250;  
349-355**G-protein coupled receptor proteins:**

Amino acids 72-112

**7 transmembrane receptor (rhodopsin family):**

Amino acids 22-294

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**FIGURE 591**

AAC**ATG**GCTGCGGCGCCTGGGCTGCTCGTCTGGCTGCTCGTGCTCCGGCTGCCCTGGCGGGTG  
CCGGGCCAGCTGGACCCAGCACTGGCCGGCGGTTCTCGGAGCACAACTCTGCGCGGACGAC  
GAATGCAGCATGATGTACCGCGGTGAGGCTCTTGAAGATTTACAGGCCCGGATTGTCGTTTT  
GTGAATTTTAAAAAAGGTGATCCTGTATATGTTTACTATAAACTGGCAAGAGGATGGCCTGAA  
GTTTGGGCTGGAAGTGTTGGACGCACTTTTGGATATTTTCCAAAAGATTTAATCCAGGTAGTT  
CATGAATATACCAAAGAAGAGCTACAAGTTCCAACAGATGAGACGGATTTTGTGTTGTTTGTAT  
GGAGGAAGAGATGATTTTCATAATTATAATGTAGAAGAACTTTTAGGGTTTTTGGAACTGTAC  
AATTCTGCAGCTACAGATTCTGAGAAAAGCTGTAGAAAAAACTTTACAGGATATGGAAAAAAC  
CCTGAATTATCTAAGGAAAGGGAACCTGAACCTGAACCAGTAGAAGCCAACTCAGAGGAAAGT  
GATAGTGTATTCTCAGAAAACACTGAGGATCTTCAGGAACAGTTTACAACCTCAGAAGCACCAC  
TCCCATGCAAACAGCCAAGCAAATCATGCTCAGGGAGAGCAGGCTTCATTTGAATCTTTTGAA  
GAAATGCTGCAAGATAAACTAAAAGTGCCAGAAAAGTGAACAAACAAAACCAGCAATAGTTCT  
CAGGTCTCAAATGAACAGGATAAGATTGATGCCTATAAACTTTTGAAAAAAGAAATGACTCTA  
GACTTGAAAACCAAATTTGGCTCAACAGCTGATGCACTTGTATCTGATGATGAGACAACCAGA  
CTCGTTACTTCATTAGAAGATGATTTTGATGAGGAATTGGATACTGAGTATTATGCAGTTGGA  
AAGGAAGATGAGGAGAACCAAGAAGACTTTGATGAGTTGCCATTACTTACCTTTACAGATGGG  
GAAGATATGAAAACCTCCAGCAAAGTCTGGCGTTGAGAAATATCCAACAGATAAAGAGCAGAAT  
TCAAATGAAGAGGACAAGGTTCACTAACTGTGCCCCCTGGCATCAAAAATGATGATAAAAAT  
ATACTAACACCTGGGGGGACACTATCTTCTCTATTGTACAGGAGGTGAAGAAACAAGAGAT  
ACGATGGATTTAGAGAGCTCTAGTTCAGAGGAAGAAAAAGAAGATGATGATGATGCATTAGTC  
CCAGATAGCAAACAGGGGAAACCACAGTCAGCAACAGATTATAGTGACCCTGACAATGTAGAT  
GATGGTCTTTTTTATTGTAGACATTCCTAAAACAAATAATGACAAAGAAGTAAACGCAGAACAT  
CACATTAAAGGAAAAGGGAGGGAGTTCAAGGAATCCAAGAGGGGCCTGGTACAAGATGAGACA  
GAATTAGAGGATGAAAATCAAGAAGGCTTTAAACAGAGCCCATAAACTAT**TGAC**CTCTGAGG  
TTTCATTGGAAAAGAAAGTGTACTGTGCATTATCCATTACAGTAAAGGATTTCAATTGGCTTCAA  
AATCCAAAAGTTTATTTTAAAAGGTTTGTGTTAGAACTAAGCTGCCTTGGCAGTGTGCATTT  
TTGAGCCAAACAATTCAAAAATGTCATTTCTTCCCTAAATAAAAATCACCTTTTAAGCTAGAG  
CGTCCCTTACAACCTTTGAAATGTGCAATAAAGAATACCTGTGTTTTAGCTAATGTAGCATATGT  
AATTGCAAAATGATTTAGAATGTCATGAAAATATGAACATTTCTGTGGAAATGCTTTAAGA  
ACATGTATTTCCATTATCTATTTTGTAGTGTACACCAGCTGAATACGGAGCAATGGTGTTTAT  
AAGCGTTTTTTTAACTATCTGGTCACAAAGACTGTTACGCTAAAAATGTTTACTAAAAGATC  
ACTAACTATCTCCCTCTTGCTGAAGTTCTTTGTAGTAATAGCTCATAAAAATTTGTTTATT  
AATATTTAAAAA

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**FIGURE 592**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150157
><subunit 1 of 1, 499 aa, 1 stop
><MW: 56471, pI: 4.31, NX(S/T): 2
MAAAPGLLVWLLVLRPLPWRVPGQLDPSTGRRFSEHKLCADDECSMMYRGEALEDFTGPDC
RFVNFKKGDPVYVYYKLARGWPEVWAGSVGRTFGYFPKDLIQVVHEYTKHEELQVPTDETD
FVCFDGGRRDDFHNYNVEELLGFLELYNSAATDSEKAVEKTLQDMEKNPELSKEREPEPEP
VEANSEESDSVFSENTEDLQEQFTTQKHHSHANSQANHAQGEQASFESFEEMLQDKLKVP
ESENKTSNSSQVSNEQDKIDAYKLLKKEMTLDLKTKFGSTADALVSDDDETTRLVTSLED
DFDEELDTEYYAVGKEDEENQEDFDELPLLTFTDGEDMKTPAKSGVEKYPTDKEQNSNEE
DKVQLTVPPGIKNDDKNILTTWGDITFSIVTGGEETRDMDLESSSSEEEKEDDDDALVP
DSKQKGKQSATDYSDDPNVDDGLFIVDIPKTNNDKEVNAEHHIKGKGRGVQESKRGLVQD
ETELEDENQEGFKTEPIKL
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-22

**N-glycosylation sites:**

Amino acids 245-249;249-253

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 30-34

**Tyrosine kinase phosphorylation site:**

Amino acids 66-72

**N-myristoylation sites:**

Amino acids 392-398;469-475

**Amidation site:**

Amino acids 28-32

**Aminoacyl-transfer RNA synthetases class-II signature 1:**

Amino acids 47-70



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**FIGURE 593**

GGGCCAGTAGAGTGTGTCTGGGTCAGCTGAGTGACTACATCAAAGCTCCCAGCCTTGAAAAAC  
ACATGCTGTTCCCAGGCCTCAAGATATTGAAACATTAATTAGATAATTTAAAGTAGCGTTTTTC  
TTCTACA**ATGT**CTGAAGAAGTGACCTACGCGACACTCACATTTTCAGGATTCTGCTGGAGCAAG  
GAATAACCGAGATGGAAATAACCTAAGAAAAAGAGGGCATCCAGCTCCATCTCCCATTTGGCG  
TCATGCTGCTCTGGGTCTGGTAACTCTTTGCCTGATGTTGCTGATTGGGCTGGTGACGTTGGG  
GATGATGTTTTTGCAGATATCTAATGACATTAACCTCAGATTCAGAGAAATTGAGTCAACTTCA  
GAAAACCATCCAACAGCAGCAGGATAACTTATCCCAGCAACTGGGCAACTCCAACAACTTGTC  
CATGGAGGAGGAATTTCTCAAGTCACAGATCTCCAGTCTACTGAAGAGGCAGGAACAAATGGC  
CATCAAACCTGTGCCAAGAGCTAATCATTCACTTTCAGACCACAGATGTAATCCATGTCCTAA  
GATGTGGCAATGGTACCAAAATAGTTGCTACTATTTTACAACAAATGAGGAGAAAACCTGGGC  
TAACAGTAGAAAGGACTGCATAGACAAGAACTCCACCCTAGTGAAGATAGACAGTTTGGAAGA  
AAAGGATTTTCTTATGTCACAGCCATTACTCATGTTTTTCGTTCTTTTGGCTGGGATTATCATG  
GGACTCCTCTGGCAGAAGTTGGTCTGGGAAGATGGCTCTGTTCCCTCTCCATCCTTGACGT  
CTCTAACTAT**TGA**GGGTAAACACAAGCTTTCATGGAATCCTGGGAAAATTAATAATGATTGT  
GAGAATTATAAATACAGACATAAAAAGAGGAGTACAACATACTGAGAAAAGAGCTCCAGTAAC  
AAATATTGAAAGGAGATTTAGTACTAAAGAACTTGACCAGATCAATGGATCCAAAGGATGTGC  
TTATTTTCAAAAAGGAAATATTTATATTTCTCGCTGTAGTGCTGAAATTTTTTGGATTTGCGA  
GAAGACAGCTGCCCCAGTGAAGACTGAGGATTTGGATTAGTATGCTTCTTCCAAATTCTCCAA  
GAAGTAAGAGACTTGTGAGTAAGCTCATATGAGGAAAGAGGAAACTACGGTACCAGAGCAAGG  
CCGAATTCTGCA

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**FIGURE 594**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150163
><subunit 1 of 1, 232 aa, 1 stop
><MW: 26754, pI: 5.80; NX(S/T): 3
MSEEVTYATLTFQDSAGARNNRDGNLRLKRGHPAPSPIWRHAALGLVTLCLMLLIGLVTL
GMMFLQISNDINS DSEKLSQLQKTIQQQQDNLSQQLGNSNNLSMEEEFLLKSQISSLLKRQ
EQMAIKLCQELIIHTSDHRCNCPKMWQWYQNSCYFFTTNEEKTWANSRKDCIDKNSTLV
KIDSLEEKDFLMSQPLLMFSFFWLGLSWDSSGRSWFWEDGSVPSPSLYVSNY
```

**Important features of the protein:****Transmembrane domain:**

Amino acids 42-62

**N-glycosylation sites:**

Amino acids 91-95;101-105;176-180

**N-myristoylation sites:**

Amino acids 17-23;97-103

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**FIGURE 595**

CGGACGCGTGGGGAAGAGGAGGAGGAGGAAGAAGACGTGGACAAGGACCCCCATCCTACCCAG  
AACACCTGCCTGCGCTGCCGCCACTTCTCTTTAAGGGAGAGGAAAAGAGAGCCTAGGAGAACC  
**ATG**GGGGGCTGCGAAGTCCGGGAATTTCTTTTGCAATTTGGTTTCTTCTTGCCATGCTGACA  
GCGTGGCCAGGCGACTGCAGTCACGTCTCCAACAACCAAGTTGTGTTGCTTGATACAACAAC  
GTACTGGGAGAGCTAGGATGGAAAACATATCCATTAAATGGGTGGGATGCCATCACTGAAATG  
GATGAACATAATAGGCCCATTCACACATAACCAGGTATGTAATGTAATGGAACCAAACCAAAC  
AACTGGCTTCGTACAAACTGGATCTCCCGTGATGCAGCTCAGAAAATTTATGTGGAAATGAAA  
TTCACACTAAGGGATTGTAACAGCATCCCATGGGTCTTGGGGACTTGCAAAGAAACATTTAAT  
CTGTTTTATATGGAATCAGATGAGTCCCACGGAATTAAATTCAAGCCAAACCAGTATACAAAG  
ATCGACACAATTGCTGCTGATGAGAGTTTACCCAGATGGATTGGGTGATCGCATCCTCAA  
CTCAACACTGAAATTCGTGAGGTGGGGCCTATAGAAAGGAAAGGATTTATCTGGCTTTTCAA  
GACATTGGGGCGTGCAATTGCCCTGGTTTCAGTCCGTGTTTCTACAAGAAATGCCCCCTTCACT  
GTTTCGTAACCTGGCCATGTTTCCTGATACCATTCGAAGGGTTGATTCTCCTCTTTGGTTGAA  
GTACGGGGTTCTTGTGTGAAGAGTGCTGAAGAGCGTGACACTCCTAAACTGTATTGTGGAGCT  
GATGGAGATTGGCTGGTTCCTCTTGGAAGGTGCATCTGCAGTACAGGATATGAAGAAATTGAG  
GGTCTTGCCATGGAGCCTCAAAGGCCGCTGCTTCT**TAG**TTGGCCATCTTGGCCCCACCCGA  
AACAGTAACCTTTGAAGAATAAAAGAAAAAGCAAAAGAGTAGCATTACTAAAATATTAAACGG  
TTACATTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 596**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA153579
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32368, pI: 5.32, NX(S/T): 0
MGGCEVREFLLQFGFFLPMLTAWPGDCSHVSNNQVVLLDTTTVLGELGWKTYPLNGWDAI
TEMDEHNRPIHTYQVCNVMENQNNWLRNWNISRDAAQKIYVEMKFTLRDCNSIPWVLGT
CKETFNLFYMESESHGIKFKPNQYTKIDTIAADESFTQMDLGDRILKLNTEIREVGPIE
RKGFYLAFAQDIGACIALVSVRVFYKKCPFTVRNLMFPDTIPRVDSSSLVEVRGSCVKSA
EERDTPKLYCGADGDWLVPLGRCICSTGYEEIEGSCHGASKGRCF
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-22

**N-myristoylation sites:**

Amino acids 192-198;274-280;278-284

**Receptor tyrosine kinase class V signature 1:**

Amino acids 192-209

**Ephrin receptor ligand binding domain:**

Amino acids 34-207

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**FIGURE 597**

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCA  
GGACAGAGAGTGCACAAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGG  
ATTCCAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGG  
CAGCACAGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTT  
GCTGTCCTTGGCACTGGGCCGAAGCCAGTGGTCCTTTCTCTGGAGAGGCTTGTGGGGCCTCA  
GGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTCTGGGACAGTGACATACTCTGCCT  
GCCTGGGGACATCGTGCCTGCTCCGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCT  
GGTGTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGC  
CGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGG  
GGTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCC  
TACTGCCCGCTGCGTCTCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTC  
TGTGGGCTCTGTGGTATATGACTGCTTCCAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTC  
CTATACTCAGCCAGGTACGAGAAGGAACTCAACCACACACAGCAGCTGCCTGCCCTGCCCTG  
GCTCAACGTGTCAGCAGATGGTGACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCA  
CTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCCTAAAACCCCGGTGGCACAAAA  
CCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCCTGCCTCTGTATTCA  
GGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCTTCAGGGAGGACCCCCG  
CGCACACCAGAACCTCTGGCAAGCCGCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCT  
GGACGCACCGTGCTCGCTGCCCCGAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCC  
CTGCCAGCCACTGGTCCCACCGCTTTCCTGGGAGAACGTCACTGTGGACAAGGTTCTCGAGTT  
CCATTGCTGAAAGGCCACCCTAACCTCTGTGTTTCAAGGTGAACAGCTCGGAGAAGCTGCAGCT  
GCAGAGTGTCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTGTTGGAGAC  
ACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCCAGTGGCTGTACTTCACTACC  
CAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTACAAGACCTGCAGTCAGG  
CCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCCATGGACAAATA  
CATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCGCTGCGCTTTCCT  
CATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAACAGGACGTCCG  
CTCGGGGGCGGCCGCCAGGGGCCGCGCGGCTCTGCTCCTCTACTCAGCCGATGACTCGGGTTT  
CGAGCGCCTGGTGGGCGCCCTGGCGTCGGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGA  
CCTGTGGAGCCGTGCTGAACTGAGCGCGCAGGGGCCCGTGGCTTGGTTTACGCGCAGCGGCG  
CCAGACCCTGCAGGAGGGCGGCGTGGTGGTCTTGCTCTTCTCTCCCGGTGCGGTGGCGCTGTG  
CAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGGGCGCACGGCCCGCACGACGCCTTCCG  
CGCCTCGCTCAGCTGCGTGCTGCCCCGACTTCTTGCAAGGGCCGGGCGCCCGGAGCTACGTGGG  
GGCCTGCTTCGACAGGCTGCTCCACCCGGACGCCGTACCCGCCCTTTTCCGCACCGTGCCCGT  
CTTCACACTGCCCTCCCAACTGCCAGACTTCTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCG  
TTCCGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAG  
CTACTTCCATCCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGG  
GGCGGGGGACGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

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**FIGURE 598**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA164625
><subunit 1 of 1, 705 aa, 1 stop
/><MW: 76970, pI: 6.00, NX(S/T): 9
MPVPWFLLSLALGRSPVVLRLVGPQDATHCSPGLSCLWDSILCLPGDIVPAPGP
VLAPTHLQTELVLRQCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRN
ASLQAQVVLVSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYT
QPRYEKELNHTQQLPALPWLNV SADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWH
KNLTGPGIITLNLHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLT
LQSWLLDAPCSLPAAEALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCV
QVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRA
ARLGEYLLQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSILL
LKKDHAKGWLRLKQDVRSAAAARGRAALLYSADDSGFERLVGALASALCQLPLRVAV
DLWSRRELSAQGPVAFWFAQRQTLEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGP
HDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHPDAVPALFRTVPVFTLPSQLPDFLG
ALQQPRAPRSGRQLQERAEQVSRAALQPALDSYFHPPGTPAPGRGVGPAGPGAGDGT
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-20

**Transmembrane domain:**

Amino acids 453-473

**N-glycosylation sites:**Amino acids 118-122;186-190;198-202;211-215;238-242;  
248-252;334-338;357-360;391-395;**Glycosaminoglycan attachment site:**

Amino acids 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 552-556

**N-myristoylation sites:**Amino acids 107-113;152-158;319-325;438-444;516-522;612-618;  
692-698;696-702;700-706

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**FIGURE 599**

GGTCCTTA**ATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC  
TGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA  
TCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT  
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCCTGGGGAAGAACTAA  
ATGTCACAACGGCCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACTTACAG  
AGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCCAA  
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG  
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA  
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA  
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA  
GTGCAGGAGCACCACTCGCCATGTCTCAGGCACAACCCAACTCAGGGCCACAGCCACCACCC  
TCATCCTTTGCTGCCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCATCT**GA**GGAGAGT  
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC  
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT  
CATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCCTTTTGCCAACAATTTTA  
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA  
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTCTTCTCTTTTGTGGAAAA  
TCAAGTACTTCTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAATAATCACG  
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAGAATTTTAAATTATTTAAT  
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA  
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 600**

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF  
 YDCGNKTVTPVSPPLGKKLVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS  
 CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD  
 CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLLCCLLIILPCFILPGI

**Important features:**

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 224-246

**N-glycosylation site.**

amino acids 68-72, 82-86

**N-myristoylation site.**

amino acids 200-206, 210-216

**Amidation site.**

amino acids 77-81



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**FIGURE 601**

GCAGTCAGAGACTTCCCCTGCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTT  
GCTTCCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCA  
CCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATG  
GGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCCGGC  
GCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTGT  
GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACCAGCTCT  
CCAATACTGGTCAAGACACCATTTCTCAAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGT  
TGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAAC  
TCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGA  
AATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAGTTGGGAGGACTGTAAAT  
ATTTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAAACAAACAAGAAGACCTGGAATTTG  
CCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGCGCCCTGACA  
GTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCCATATTATAA  
TAGATGTCACCAGCCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAA  
AGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGA  
GCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCCCTCTGCAACTACAAAT  
AGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACATTGGGAAATGGAACATAA  
TCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTGTTTCTCTGTTTCAGGATCAC  
CAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGC  
CACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGC  
TCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGGA  
ATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAG  
TAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATTCTTT  
TTGTTTGTTCAGTTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGT  
CCATGCCGTTTCCCAACAGGGATGTCACCTGATATGAGAATCTCAAATCTCAATGCCTTATAA  
GCATTCCCTCCTGTGTCCATTAAAGACTCTGATAATTGTCTCCCCTCCATAGGAATTTCTCCCA  
GGAAAGAAATATATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCTTCAG  
AGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCTTA  
TTTTCTTCCATTGACCCATATTTATACCTTTTCAGGTACTGAAGATTTAATAATAATAAATGTA  
AATACTGTGAAAAA

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**FIGURE 602**

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVLVLI  
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY  
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY  
SEFFYSYWTGLLRPD SGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEL  
KRCVCERRAGMVKPESLHVPPETLGEGD

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**FIGURE 603**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC  
CAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT  
GTCTGGATGGGCGGCCAGCGATGACCCCATTTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT  
GAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGCATGC  
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA  
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA  
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG  
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG  
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT  
GGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC  
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG  
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA  
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCCTAAACTGG  
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGACATGACCTGGAGGGG  
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTGGGATTTGTGAATAAA  
CTTGATACACCA

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**FIGURE 604**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675  
><subunit 1 of 1, 247 aa, 1 stop  
><MW: 25335, pI: 7.00, NX(S/T): 0  
MHLARLVGSCSLLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR  
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA  
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN  
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

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**FIGURE 605**

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAG**ATGG**  
TCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCACG  
GCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACATCT  
TCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATTACACC  
TTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGCAACGGTTTCTTCATCCAGGACC  
AGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCCAGGAGC  
ACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTACGTGGAGA  
TGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTGCTCGGCCGAGACG  
GCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTTCCATCCCAG  
TCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTCTGG**TAGA**AAGA  
GTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCCAGGAATTTTGC  
TACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGAAAAGGGTTTGGG  
CGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGGGCCCCCAAGGGTG  
TCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAA  
AGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACTCACCTGGCTCCAGCC  
TCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGGAGTGGTTTAAAGAGCT  
GGTGTGTTGGGGACTCAATAAACCTCACTGACTTTTTTAGCAATAAAGCTTCTCATCAGGGTTG  
CAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 606**

&gt;&lt;/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

&gt;&lt;subunit 1 of 1, 188 aa, 1 stop

&gt;&lt;MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQI  
HLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSFYV  
EMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW**Signal peptide:**

amino acids 1-20

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**FIGURE 607**

GCATTTGCCACTGGTTGCAGATCAGGCGGACGAGGAGCCGGGAAGGCAGAGCC**ATGT**GGCTGC  
CCCCTGCTCTGCTCCTTCTCAGCCTCTCAGGCTGTTTCTCCATCCAAGGCCAGAGTCTGTGA  
GAGCCCCAGAGCAGGGGTCCCTGACGGTTCAATGCCACTATAAGCAAGGATGGGAGACCTACA  
TTAAGTGGTGGTGCCGAGGGGTGCGCTGGGATACATGCAAGATCCTCATTGAAACCAGAGGGT  
CGGAGCAAGGAGAGAAGAGTGACCGTGTGTCCATCAAGGACAATCAGAAAGACCGCACGTTCA  
CTGTGACCATGGAGGGGCTCAGGCGAGATGACGCAGATGTTTACTGGTGTGGGATTGAAAGAA  
GAGGACCTGACCTTGGGACTCAAGTGAAAGTGATCGTTGACCCAGAGGGAGCGGCTTCCACAA  
CAGCAAGCTCACCTACCAACAGCAATATGGCAGTGTTTCATCGGCTCCCACAAGAGGAACCACT  
ACATGCTCCTGGTATTTGTGAAGGTGCCCATCTTGCTCATCTTGGTCACTGCCATCCTCTGGT  
TGAAGGGGTCTCAGAGGGTCCCTGAGGAGCCAGGGGAACAGCCTATCTACATGAACTTCTCCG  
AACCTCTGACTAAAGACATGGCCACT**TAG**AGAGATGGATCTGCAGAGCCTTCCCTGCCCTGGCC  
ACGTTTCCAGAAGAGACTCGGGCTGTGGAAGGAACATCTACGAGTCCTCGGGATGCAGTGACT  
GAGATAGGGGCCCTGGGCCTCCGCCCTGGCCTTGGAGCTGGTGGGCACCTCCCTGTTCTGCAC  
AGCTCAGGGACTTAGCCAGGTCTCTCCTGAGCCACCATCACCTCCTGGGGTGCCAGCACCTG  
TTCTCTTGGTCAGGAGCTGTAGAGATGGAGCTCAAGCACTGGACGACTCTGTCCCCACTGCTG  
GAATAACTCGGGCACAGAGCATGGGACCAAAGTACAGAAAGAGGTTGGGGGAGACCCCCCAG  
CCCTAGACTTCCATCATTCCGGAGACCAACTCAACACCGTCTTTGCCTGAGAACCTGATATATCC  
GTGTTTTTAAATTTTTTTTTTCTAGCAAAGTTGGGTTTTAATGACTTATGTTTCATAGGAAAC  
CTCTCTGATCCCACACACAAGGAGGGTGATTCTGGGATGAGTTCCTGGTTCTAGGGCATGAGG  
GGCTGGATGGACCTGTCCCCAGGGAGGACATGGCTCTGAGTCCACAGGGCTGAGGAGGCAAT  
GGGAACCTCCCTGGCCCGGCCCGGTGCTTGCTCCCCCTCCACCTCTTCCTCCTCCTAGCT  
CCCCAAGCTCCCTGCCTATTCCCCACCTCCGAGGGGCTGCAGCTTGGGAGCCTCCTCAGCAT  
GACAGCTTGGGTCTCCTCCCCAAAAGAGCCTGTCAGGCCTCAAGAACCACCTCCAGGTGGGGA  
GGGCAGTAACGAAAACCATCGCAGGAAATGGCACCCTCCCTTTTCGGTGATGTTGAAATCATG  
TTACTAATGAAAACGTCTCTAGGGAAGTGGTCTGTCTCCTCACAGGCTTCACCCACGGCGAT  
GAGGCCCTTGAATGTGGTCACTTTGTGCTGTATGGTTGAGGGACCCTCACACCAAAGGGACCT  
TCCCATGTGAGATGTGCTCCCGCCCCCACCTGCCACAAGCAAACACACCACACATGTTCCGC  
ATGTTGCCCTTTGAACACCCATGAGGACGCCTCCAACCTGCTCTTGGTTCTAATAGGGAGTAC  
TGACTGTCAGCAGTGGATAAAGGAGAGGGGACCCTCTGGTCCCTAGCATGGCACCAGAGCCT  
CCCCTCTTCTTGCTCTCAGCCAAAGAGAAACTTCTCTGACTTTGAACTGAATTTAGGTCTC  
TGGCCAATGATGGGCCTGAAAATTCATAATGGCCAGAGAGGAGAGTTGAGCCCGGCTAAGA  
TCCCCTGAGTCATTCTGTGAGGGACCAAGACCCACAGTCCACCAGCCCCAGGGCCCTACCTCC  
TGGAATGCTTTCCTGGATCCAGCTTCCCAGAGATCCGACCAGACCCAGGGACCGGCACCGC  
TCCGCGGGAGGGAAAGCCAAAGCATGGTGCTTCACCAGCTGGACTCAGGGGCGAGGGGACATG  
GGCGCTTGTCAACGTGATGTCACTTTTTCCACCGTTTCTTCTGTTGATATTCAATGAATC  
CGTCAATCTCTCTGGGAAA

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**FIGURE 608**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA105849
><subunit 1 of 1, 201 aa, 1 stop
><MW: 22689, pI: 7.41, NX(S/T): 1
MWLPPALLLLSLSGCFSIQGPESVRAPEQGSALTVOCHYKQGWETIYIKWWCRGVRWDTCKI
LIETRGSEQGEKSDRVSIKDNQKDRTFTVTMEGLRRDDADVWCGIERRGPDLTQVKVI
VDPEGAASTTASSPTNSNMAVFIGSHKRNHYMLLVFVKVPILLILVTAILWLKGSQRVPE
EPGEQPIYMNFFSEPLTKDMAT
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-17

**Transmembrane domain:**

Amino acids 151-170

**N-glycosylation site:**

Amino acids 190-194

**Tyrosine kinase phosphorylation site:**

Amino acids 95-103

**N-myristoylation sites:**

Amino acids 66-72;125-131

**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 5-16



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**FIGURE 609**

GATGGCGCAGCCACAGCTTCTGTGAGATTCTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG  
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA  
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT  
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG  
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG  
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCCTCTAGT  
CTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG  
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT  
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT  
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC  
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC  
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA  
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG  
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG  
GAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT  
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT  
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCGATGATTGTCTTTATGCATCCCC  
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT  
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTTACTTGGACATG  
AAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT  
ACAGTAAAAAATAACCTTGTAATTCTAGAAGAGTGGCTAGGGGGGTATTTCATTTGTAT  
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC  
TACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG  
ACCATCCCCAGTAGACTCCCCAGTCCCATTAATTGTGTATCTTCCAGCCAGGAATCCTACACGG  
CCAGCATGTATTTCTACAAATAAAGTTTTCTTGCATACCAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 610**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSEL
RPEIFSSREAWQFFLLWSPDFRPMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVI
ATNLQEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVF
KNYQTPDHYT LRKISSLAN SFLT IKKDLRL SHAHMTCHCGEEAMKKYSQILSHFEKLEPQ
AAVVKALGELDILLQWMEETE
```

**Important features of the protein:****Signal peptide:**

Amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

Amino acids 192-196;225-229

**N-myristoylation sites:**

Amino acids 42-48;46-52;136-142